

(2) INFORMATION FOR SEQ ID NO:625:

(A) LENGTH: 405 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..405

(D) OTHER INFORMATION: / Ceres Seq. ID 1498752

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:625:

Met	Ile	Gln	Gln	Ala	Met	Met	Gln	Gln	His	Pro	Ser	Leu	Tyr	His	Pro
1				5					10					15	
Gly	Val	Met	Ala	Pro	Pro	Gln	Met	Glu	Pro	Leu	Pro	Ser	Gly	Asn	Leu
			20					25					30		
Pro	Pro	Gly	Phe	Asp	Pro	Thr	Thr	Cys	Arg	Ser	Val	Tyr	Ala	Gly	Asn
		35				40						45			
Ile	His	Thr	Gln	Val	Thr	Glu	Ile	Leu	Leu	Gln	Glu	Ile	Phe	Ala	Ser
	50					55					60				
Thr	Gly	Pro	Ile	Glu	Ser	Cys	Lys	Leu	Ile	Arg	Lys	Asp	Lys	Ser	Ser
65					70					75					80
Tyr	Gly	Phe	Val	His	Tyr	Phe	Asp	Arg	Arg	Cys	Ala	Ser	Met	Ala	Ile
				85					90					95	
Met	Thr	Leu	Asn	Gly	Arg	His	Ile	Phe	Gly	Gln	Pro	Met	Lys	Val	Asn
			100					105					110		
Trp	Ala	Tyr	Ala	Thr	Gly	Gln	Arg	Glu	Asp	Thr	Ser	Ser	His	Phe	Asn
		115				120						125			
Ile	Phe	Val	Gly	Asp	Leu	Ser	Pro	Glu	Val	Thr	Asp	Ala	Ala	Leu	Phe
	130					135					140				

Asp	Ser	Phe	Ser	Ala	Phe	Asn	Ser	Cys	Ser	Asp	Ala	Arg	Val	Met	Trp
145					150					155					160
Asp	Gln	Lys	Thr	Gly	Arg	Ser	Arg	Gly	Phe	Gly	Phe	Val	Ser	Phe	Arg
				165					170						175
Asn	Gln	Gln	Asp	Ala	Gln	Thr	Ala	Ile	Asn	Glu	Met	Asn	Gly	Lys	Trp
			180					185						190	
Val	Ser	Ser	Arg	Gln	Ile	Arg	Cys	Asn	Trp	Ala	Thr	Lys	Gly	Ala	Thr
			195				200					205			
Phe	Gly	Glu	Asp	Lys	His	Ser	Ser	Asp	Glu	Lys	Ser	Val	Val	Glu	Leu
	210					215					220				
Thr	Asn	Gly	Ser	Ser	Glu	Asp	Gly	Arg	Glu	Leu	Ser	Asn	Glu	Asp	Ala
225					230					235					240
Pro	Glu	Asn	Asn	Pro	Gln	Phe	Thr	Thr	Val	Tyr	Val	Gly	Asn	Leu	Ser
			245						250					255	
Pro	Glu	Ile	Thr	Gln	Leu	Asp	Leu	His	Arg	Leu	Phe	Tyr	Thr	Leu	Gly
			260					265					270		
Ala	Gly	Val	Ile	Glu	Glu	Val	Arg	Val	Gln	Arg	Asp	Lys	Gly	Phe	Gly
	275						280					285			
Phe	Val	Arg	Tyr	Asn	Thr	His	Asp	Glu	Ala	Ala	Leu	Ala	Ile	Gln	Met
	290					295					300				
Gly	Asn	Ala	Gln	Pro	Phe	Leu	Phe	Ser	Arg	Gln	Ile	Arg	Cys	Ser	Trp
305					310					315					320
Gly	Asn	Lys	Pro	Thr	Pro	Ser	Gly	Thr	Ala	Ser	Asn	Pro	Leu	Pro	Pro
			325						330					335	
Pro	Ala	Pro	Ala	Ser	Val	Pro	Ser	Leu	Ser	Ala	Met	Asp	Leu	Leu	Ala
			340					345					350		
Tyr	Glu	Arg	Gln	Leu	Ala	Leu	Ala	Lys	Met	His	Pro	Gln	Ala	Gln	His
		355					360					365			
Ser	Leu	Arg	Gln	Ala	Gly	Leu	Gly	Val	Asn	Val	Ala	Gly	Gly	Thr	Ala
	370					375					380				
Ala	Met	Tyr	Asp	Gly	Gly	Tyr	Gln	Asn	Val	Ala	Ala	Ala	His	Gln	Gln
385					390					395					400
Leu	Met	Tyr	Tyr	Gln											
				405											

(2) INFORMATION FOR SEQ ID NO:626:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 400 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..400

(D) OTHER INFORMATION: / Ceres Seq. ID 1498753

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:626:

Met	Met	Gln	Gln	His	Pro	Ser	Leu	Tyr	His	Pro	Gly	Val	Met	Ala	Pro
1				5					10					15	
Pro	Gln	Met	Glu	Pro	Leu	Pro	Ser	Gly	Asn	Leu	Pro	Pro	Gly	Phe	Asp
		20						25					30		
Pro	Thr	Thr	Cys	Arg	Ser	Val	Tyr	Ala	Gly	Asn	Ile	His	Thr	Gln	Val
		35					40					45			
Thr	Glu	Ile	Leu	Leu	Gln	Glu	Ile	Phe	Ala	Ser	Thr	Gly	Pro	Ile	Glu
	50					55					60				
Ser	Cys	Lys	Leu	Ile	Arg	Lys	Asp	Lys	Ser	Ser	Tyr	Gly	Phe	Val	His
65					70					75					80
Tyr	Phe	Asp	Arg	Arg	Cys	Ala	Ser	Met	Ala	Ile	Met	Thr	Leu	Asn	Gly
				85					90					95	
Arg	His	Ile	Phe	Gly	Gln	Pro	Met	Lys	Val	Asn	Trp	Ala	Tyr	Ala	Thr
			100					105					110		
Gly	Gln	Arg	Glu	Asp	Thr	Ser	Ser	His	Phe	Asn	Ile	Phe	Val	Gly	Asp

115	120	125
Leu Ser Pro Glu Val Thr Asp Ala Ala Leu Phe Asp Ser Phe Ser Ala		
130	135	140
Phe Asn Ser Cys Ser Asp Ala Arg Val Met Trp Asp Gln Lys Thr Gly		
145	150	155
Arg Ser Arg Gly Phe Gly Phe Val Ser Phe Arg Asn Gln Gln Asp Ala		
165	170	175
Gln Thr Ala Ile Asn Glu Met Asn Gly Lys Trp Val Ser Ser Arg Gln		
180	185	190
Ile Arg Cys Asn Trp Ala Thr Lys Gly Ala Thr Phe Gly Glu Asp Lys		
195	200	205
His Ser Ser Asp Glu Lys Ser Val Val Glu Leu Thr Asn Gly Ser Ser		
210	215	220
Glu Asp Gly Arg Glu Leu Ser Asn Glu Asp Ala Pro Glu Asn Asn Pro		
225	230	235
Gln Phe Thr Thr Val Tyr Val Gly Asn Leu Ser Pro Glu Ile Thr Gln		
245	250	255
Leu Asp Leu His Arg Leu Phe Tyr Thr Leu Gly Ala Gly Val Ile Glu		
260	265	270
Glu Val Arg Val Gln Arg Asp Lys Gly Phe Gly Phe Val Arg Tyr Asn		
275	280	285
Thr His Asp Glu Ala Ala Leu Ala Ile Gln Met Gly Asn Ala Gln Pro		
290	295	300
Phe Leu Phe Ser Arg Gln Ile Arg Cys Ser Trp Gly Asn Lys Pro Thr		
305	310	315
Pro Ser Gly Thr Ala Ser Asn Pro Leu Pro Pro Ala Pro Ala Ser		
325	330	335
Val Pro Ser Leu Ser Ala Met Asp Leu Leu Ala Tyr Glu Arg Gln Leu		
340	345	350
Ala Leu Ala Lys Met His Pro Gln Ala Gln His Ser Leu Arg Gln Ala		
355	360	365
Gly Leu Gly Val Asn Val Ala Gly Gly Thr Ala Ala Met Tyr Asp Gly		
370	375	380
Gly Tyr Gln Asn Val Ala Ala Ala His Gln Gln Leu Met Tyr Tyr Gln		
385	390	395
		400

(2) INFORMATION FOR SEQ ID NO:627:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1552 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1552
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498754

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:627:

gctgcttaga	ttttgttttc	ttcattgtcg	tcgtcggagt	gaattaggga	ttcgagaatg	60
acgatgaact	cgcttccgag	gagatttggg	aagaatcatg	gctatttgga	tcgagattat	120
cgaaacggaa	gacgatctgg	ttcagattcc	gatgaagaat	tgaagggatt	gagtcacgaa	180
gagtatagga	ggcagaaacg	gcttaagatg	aggaaatcag	ccaagttctg	cttttgggag	240
aacacaccga	gtccacctag	agatcagaac	gaggattccg	atgagaacgc	cgacgagatt	300
caggacaaga	acggcggcga	aagagatgat	aattcgaaaag	ggaaagaaaag	gaaaggtaaa	360
tctgactcgg	aatctgaatc	tgatggtttg	agatctagga	agaggaagag	taagagctcg	420
aggtcaaagc	gcaggagaaa	gagatcttat	gacagcgata	gtgaatccga	agggagtga	480
agtgattcgg	aagaggaaga	taggagacga	aggaggaaga	gttcttctaa	gaggaagaag	540
agtagaagca	gccgtagtgt	taggaaaaag	cgaagtcata	ggagaaagac	gaaatacagt	600
gactctgatg	agagcagcga	tgaagatagt	aaagctgaga	ttagtgcttc	ttcgtctggg	660
gaggaagaag	ataccaagtc	aaagagcaag	aggcgggaaga	aatcttcgga	ttctagttca	720

aaacgaagca	agggagagaa	gacgaagtca	gggagtgaca	gcgatggtag	tgaggaagat	780
tcgaagatgc	aagtagacga	aacggtaaga	acactgagct	agaacttgat	gaagaagagt	840
tgaagaagtt	caaagagatg	attgaattaa	agaagaaatc	ttcagctggt	gatgaagagg	900
aagaagaagg	tgatgttggt	ccaatgccat	tacctaaagc	tgaaggtcac	atcagttatg	960
gtggtgcttt	aagaccgggt	gaaggagacg	ccrttgcvca	gtatgttcag	caaggtaaag	1020
gtatcccacg	tagaggagaa	gtgggtctta	acgctgaaga	gattcagaag	tttgaggatc	1080
ttggttatgt	gatgagtggg	agtaggcac	aaaggatgaa	tgctattcgt	attagaaaag	1140
aaaaccaggt	ttacagtgtc	gaagacaaac	gggcattggc	catgtttaac	tacgaggaga	1200
aggcgaagcg	cgaggctaag	gttatgtctg	atctgcagcg	gcttgtgcag	cgccatatgg	1260
gagaagaggt	ggggccaaat	catgaccctt	tcgggtgctg	aaagactgaa	gaagatgatg	1320
attgattttg	cttggtcttc	tgcttctgtt	atgtgggtac	tcactcttatg	ctttatcttg	1380
ttgaatgttc	cttatttgca	tcatatgatac	tgctgtttgc	tacttgcccg	ttaatgagct	1440
tcgtagttta	tgtcttaatc	tactatgtat	ccgttaaatg	gcttcatagt	ttatgcgtta	1500
atctgctatg	tatcacatga	ttgtgtttgt	gtgtcaaaga	taatagattc	tg	

(2) INFORMATION FOR SEQ ID NO:628:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 254 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..254

(D) OTHER INFORMATION: / Ceres Seq. ID 1498755

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:628:

Met	Thr	Met	Asn	Ser	Leu	Pro	Arg	Arg	Phe	Gly	Lys	Asn	His	Gly	Tyr
1			5					10						15	
Leu	Asp	Arg	Asp	Tyr	Arg	Asn	Gly	Arg	Arg	Ser	Gly	Ser	Asp	Ser	Asp
			20					25					30		
Glu	Glu	Leu	Lys	Gly	Leu	Ser	His	Glu	Glu	Tyr	Arg	Arg	Gln	Lys	Arg
			35				40					45			
Leu	Lys	Met	Arg	Lys	Ser	Ala	Lys	Phe	Cys	Phe	Trp	Glu	Asn	Thr	Pro
	50					55					60				
Ser	Pro	Pro	Arg	Asp	Gln	Asn	Glu	Asp	Ser	Asp	Glu	Asn	Ala	Asp	Glu
65					70					75					80
Ile	Gln	Asp	Lys	Asn	Gly	Gly	Glu	Arg	Asp	Asp	Asn	Ser	Lys	Gly	Lys
			85					90					95		
Glu	Arg	Lys	Gly	Lys	Ser	Asp	Ser	Glu	Ser	Glu	Ser	Asp	Gly	Leu	Arg
			100					105					110		
Ser	Arg	Lys	Arg	Lys	Ser	Lys	Ser	Arg	Ser	Lys	Arg	Arg	Arg	Lys	
			115					120					125		
Arg	Ser	Tyr	Asp	Ser	Asp	Ser	Glu	Ser	Glu	Gly	Ser	Glu	Ser	Asp	Ser
			130				135						140		
Glu	Glu	Glu	Asp	Arg	Arg	Arg	Arg	Arg	Lys	Ser	Ser	Ser	Lys	Arg	Lys
145					150					155					160
Lys	Ser	Arg	Ser	Ser	Arg	Ser	Phe	Arg	Lys	Lys	Arg	Ser	His	Arg	Arg
			165						170					175	
Lys	Thr	Lys	Tyr	Ser	Asp	Ser	Asp	Glu	Ser	Ser	Asp	Glu	Asp	Ser	Lys
			180					185					190		
Ala	Glu	Ile	Ser	Ala	Ser	Ser	Ser	Gly	Glu	Glu	Glu	Asp	Thr	Lys	Ser
			195					200					205		
Lys	Ser	Lys	Arg	Arg	Lys	Lys	Ser	Ser	Asp	Ser	Ser	Ser	Lys	Arg	Ser
			210				215					220			
Lys	Gly	Glu	Lys	Thr	Lys	Ser	Gly	Ser	Asp	Ser	Asp	Gly	Thr	Glu	Glu
225					230					235					240
Asp	Ser	Lys	Met	Gln	Val	Asp	Glu	Thr	Val	Arg	Thr	Leu	Ser		
			245						250						

(2) INFORMATION FOR SEQ ID NO:629:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 252 amino acids

(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..252
(D) OTHER INFORMATION: / Ceres Seq. ID 1498756
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:629:
Met Asn Ser Leu Pro Arg Arg Phe Gly Lys Asn His Gly Tyr Leu Asp
1 5 10 15
Arg Asp Tyr Arg Asn Gly Arg Arg Ser Gly Ser Asp Ser Asp Glu Glu
20 25 30
Leu Lys Gly Leu Ser His Glu Glu Tyr Arg Arg Gln Lys Arg Leu Lys
35 40 45
Met Arg Lys Ser Ala Lys Phe Cys Phe Trp Glu Asn Thr Pro Ser Pro
50 55 60
Pro Arg Asp Gln Asn Glu Asp Ser Asp Glu Asn Ala Asp Glu Ile Gln
65 70 75 80
Asp Lys Asn Gly Gly Glu Arg Asp Asp Asn Ser Lys Gly Lys Glu Arg
85 90 95
Lys Gly Lys Ser Asp Ser Glu Ser Glu Ser Asp Gly Leu Arg Ser Arg
100 105 110
Lys Arg Lys Ser Lys Ser Ser Arg Ser Lys Arg Arg Arg Lys Arg Ser
115 120 125
Tyr Asp Ser Asp Ser Glu Ser Glu Gly Ser Glu Ser Asp Ser Glu Glu
130 135 140
Glu Asp Arg Arg Arg Arg Arg Lys Ser Ser Ser Lys Arg Lys Lys Ser
145 150 155 160
Arg Ser Ser Arg Ser Phe Arg Lys Lys Arg Ser His Arg Arg Lys Thr
165 170 175
Lys Tyr Ser Asp Ser Asp Glu Ser Ser Asp Glu Asp Ser Lys Ala Glu
180 185 190
Ile Ser Ala Ser Ser Ser Gly Glu Glu Asp Thr Lys Ser Lys Ser
195 200 205
Lys Arg Arg Lys Lys Ser Ser Asp Ser Ser Ser Lys Arg Ser Lys Gly
210 215 220
Glu Lys Thr Lys Ser Gly Ser Asp Ser Asp Gly Thr Glu Glu Asp Ser
225 230 235 240
Lys Met Gln Val Asp Glu Thr Val Arg Thr Leu Ser
245 250

(2) INFORMATION FOR SEQ ID NO:630:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 204 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..204
(D) OTHER INFORMATION: / Ceres Seq. ID 1498757
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:630:
Met Arg Lys Ser Ala Lys Phe Cys Phe Trp Glu Asn Thr Pro Ser Pro
1 5 10 15
Pro Arg Asp Gln Asn Glu Asp Ser Asp Glu Asn Ala Asp Glu Ile Gln
20 25 30
Asp Lys Asn Gly Gly Glu Arg Asp Asp Asn Ser Lys Gly Lys Glu Arg
35 40 45
Lys Gly Lys Ser Asp Ser Glu Ser Glu Ser Asp Gly Leu Arg Ser Arg
50 55 60

Lys Arg Lys Ser Lys Ser Ser Arg Ser Lys Arg Arg Arg Lys Arg Ser
65 70 75 80
Tyr Asp Ser Asp Ser Glu Ser Glu Gly Ser Glu Ser Asp Ser Glu Glu
85 90 95
Glu Asp Arg Arg Arg Arg Arg Lys Ser Ser Ser Lys Arg Lys Lys Ser
100 105 110
Arg Ser Ser Arg Ser Phe Arg Lys Lys Arg Ser His Arg Arg Lys Thr
115 120 125
Lys Tyr Ser Asp Ser Asp Glu Ser Ser Asp Glu Asp Ser Lys Ala Glu
130 135 140
Ile Ser Ala Ser Ser Ser Gly Glu Glu Glu Asp Thr Lys Ser Lys Ser
145 150 155 160
Lys Arg Arg Lys Lys Ser Ser Asp Ser Ser Ser Lys Arg Ser Lys Gly
165 170 175
Glu Lys Thr Lys Ser Gly Ser Asp Ser Asp Gly Thr Glu Glu Asp Ser
180 185 190
Lys Met Gln Val Asp Glu Thr Val Arg Thr Leu Ser
195 200

(2) INFORMATION FOR SEQ ID NO:631:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1275 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1275
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498758

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:631:

aatctttttt	tttttgctta	ttattttttt	gactttgata	tcccatcagt	tcatcttctt	60
cttcttcttc	tgatcaacca	tggtgtgtgc	tataagtgtc	gcagtctctt	taccttcctc	120
caagtcattc	tctctctcca	ccaaaatctc	ctctgtatcc	cctcaaagga	ttttcctcaa	180
gaagagcaca	gtgtgtttaca	gaagagtgtg	gtcagtgaag	gctcaggtga	caacagatac	240
taccgaggca	ccaccagtta	aagtagtcaa	ggagtctaag	aaacaggaag	aagggattgt	300
tgtcaacaaa	ttcaaacctt	agaaccctta	cactgggtgc	tgctttttga	acaccaagat	360
caccgggtgat	gacgtctccg	gtgagacttg	gcacattgtc	ttcaccaccg	aaggtgaggt	420
tccgtataga	gaaggacaat	cgataggagt	gattccagag	ggaatagaca	agaacgggaa	480
gccgcacaag	ctcaggcttt	actctatcgc	gagtagtgcc	attggtgact	ttggagactc	540
caagaccgtt	tctctctgtg	tcaagagact	agttttacaca	aatgatggcg	gagagattgt	600
taaggggggtc	tgctccaact	tcttggtgtga	cttgaagccg	ggtgatgaag	ctaagatcac	660
tggacctgtt	ggcaaggaaa	tgcttatgcc	aaaagacccc	aatgccacca	tcatcatgct	720
tggaacagga	actggaatag	ctccattcag	atcatttttg	tggaaaatgt	tctttgagga	780
gcacgaggac	tacaagttca	atggtttggc	gtggcttttc	ttgggtgtac	ccagaagcag	840
ctcactgcta	tacaaggagg	agtttgagaa	gatgaaggag	aagaaccagg	acaacttcag	900
gctggacttt	gcggtgagca	gagagcagac	gaacgagaag	ggagagaaaa	tgtacattca	960
gacaagaatg	gcagagtatg	cagaaagagc	tgtgggagtt	gctgaagaaa	gacaacacct	1020
ttgtttacat	gtgtggtctt	aagggtatgg	agaagggtat	cgatgacatt	atggtctcgc	1080
ttgctgctaa	agatgggata	gattggttgg	agtacaagaa	gcaattgaag	aggagtgaac	1140
agtggaatgt	tgaagtctac	taagggaagct	tctgagggag	taattatata	atgtagataa	1200
aaagcttcag	atgcattgtg	aaatcttcat	atctgcttct	tttttctttc	tcaaggattt	1260
tcaatcaaaa	catcc					

(2) INFORMATION FOR SEQ ID NO:632:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 320 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide

2025 RELEASE UNDER E.O. 14176

(B) LOCATION: 1..320

(D) OTHER INFORMATION: / Ceres Seq. ID 1498759

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:632:

Met	Ala	Ala	Ala	Ile	Ser	Ala	Ala	Val	Ser	Leu	Pro	Ser	Ser	Lys	Ser
1				5				10						15	
Ser	Ser	Leu	Leu	Thr	Lys	Ile	Ser	Ser	Val	Ser	Pro	Gln	Arg	Ile	Phe
			20					25					30		
Leu	Lys	Lys	Ser	Thr	Val	Cys	Tyr	Arg	Arg	Val	Val	Ser	Val	Lys	Ala
			35				40					45			
Gln	Val	Thr	Thr	Asp	Thr	Thr	Glu	Ala	Pro	Pro	Val	Lys	Val	Val	Lys
	50					55				60					
Glu	Ser	Lys	Lys	Gln	Glu	Gly	Ile	Val	Val	Asn	Lys	Phe	Lys	Pro	
65				70				75						80	
Lys	Asn	Pro	Tyr	Thr	Gly	Arg	Cys	Leu	Leu	Asn	Thr	Lys	Ile	Thr	Gly
			85					90						95	
Asp	Asp	Ala	Pro	Gly	Glu	Thr	Trp	His	Ile	Val	Phe	Thr	Thr	Glu	Gly
		100					105					110			
Glu	Val	Pro	Tyr	Arg	Glu	Gly	Gln	Ser	Ile	Gly	Val	Ile	Pro	Glu	Gly
	115					120					125				
Ile	Asp	Lys	Asn	Gly	Lys	Pro	His	Lys	Leu	Arg	Leu	Tyr	Ser	Ile	Ala
	130					135					140				
Ser	Ser	Ala	Ile	Gly	Asp	Phe	Gly	Asp	Ser	Lys	Thr	Val	Ser	Leu	Cys
145				150				155						160	
Val	Lys	Arg	Leu	Val	Tyr	Thr	Asn	Asp	Gly	Gly	Glu	Ile	Val	Lys	Gly
			165					170						175	
Val	Cys	Ser	Asn	Phe	Leu	Cys	Asp	Leu	Lys	Pro	Gly	Asp	Glu	Ala	Lys
		180					185					190			
Ile	Thr	Gly	Pro	Val	Gly	Lys	Glu	Met	Leu	Met	Pro	Lys	Asp	Pro	Asn
	195					200					205				
Ala	Thr	Ile	Ile	Met	Leu	Gly	Thr	Gly	Thr	Gly	Ile	Ala	Pro	Phe	Arg
	210					215					220				
Ser	Phe	Leu	Trp	Lys	Met	Phe	Phe	Glu	Glu	His	Glu	Asp	Tyr	Lys	Phe
225				230				235						240	
Asn	Gly	Leu	Ala	Trp	Leu	Phe	Leu	Gly	Val	Pro	Arg	Ser	Ser	Ser	Leu
			245					250						255	
Leu	Tyr	Lys	Glu	Glu	Phe	Glu	Lys	Met	Lys	Glu	Lys	Asn	Pro	Asp	Asn
		260					265						270		
Phe	Arg	Leu	Asp	Phe	Ala	Val	Ser	Arg	Glu	Gln	Thr	Asn	Glu	Lys	Gly
	275					280						285			
Glu	Lys	Met	Tyr	Ile	Gln	Thr	Arg	Met	Ala	Glu	Tyr	Ala	Glu	Arg	Ala
	290					295					300				
Val	Gly	Val	Ala	Glu	Glu	Arg	Gln	His	Leu	Cys	Leu	His	Val	Trp	Ser
305				310				315						320	

(2) INFORMATION FOR SEQ ID NO:633:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1854 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1854

(D) OTHER INFORMATION: / Ceres Seq. ID 1498760

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:633:

atatacttttc	tctgtttaca	ttctcgtttc	cgaggagaaa	agtctcgatc	ttctggatct	60
gggggtttggt	ttgggtttggg	gttgactcgg	ttttgactcg	ggacaagtcg	tctcgtgaga	120
tggatgtctc	tcgtttatta	gtatctcttt	gagagtctgt	ctttctgggt	tcaatagatt	180
cttatagttt	cgcttagaaa	cacgcacaaa	aagatgtcgt	tgaagcatca	tcacagagga	240

```
ttagagctct ctgcttcgaa gagttttgtc tcaaagaaat ggactttatt tctctgtatc 300
ggttttcttct gcgcaggaat tctcttctcc gacagaatgt ggccagagcc tgaatccaat 360
gttgatcaaa gggacacagt agcatcagat gaacggctgc ggtagagtc tgaggactgt 420
gattcatcaa aaaagggttt taaagcgtga atcgaaagac atccttgag atgtttacaa 480
gagtcagat gcaattcaaa cgcttgataa aacgatttca aagctggaaa cagaactggc 540
cgatgcaaga gctgcgcaag aatctatcat gaatggttca ccagtttctg atgactttaa 600
gctccctgaa aatgtcacta aaagaaagta tctgatggtt gttggtgtta atactgcgtt 660
tagcagcaga aagcgcaggg attcagtcctg tgctacttgg atgcctcccg gtgaggagag 720
aaagaagctc gaggaagaga aagggatcgt gatgcggttt gtgataggcc atagtcttac 780
tcccggtgga attcttgata gagcgattca ggctgaagaa agtaaacaatg gagacttctt 840
gaggctggat catgttgaaag gttatctcga gctgtcagca aagactaaaaa cttactttac 900
cacggctttt gcaatgtggg atgcagactt ctacgtcaaa gtcgatgatg atgtgcatgt 960
aaatatagcc acgcttgag cagaattagc aagataccgg atgaagcccc gagtgtacat 1020
tggttgcatg aaatctggac ctgttcttgc tcagaaagga gtgagatata atgaaccga 1080
atactggaaa tttggagaag agggtaacaa atacttccgc catgccacag gtcagctcta 1140
tgcaatatcc agggagtgtg cgtcttacat atcgataaac caaaacgtac ttcacaaata 1200
tgtgaatgaa gatgtctctt taggatcatg gtttcttgga ttagatgtgg agcatgtaga 1260
tgaccgtagg ctatgttggt gtacaacaga ttgtgagtgg aaggcgcagg cgggcaacat 1320
ctgtgttgcc tcgttcgatt ggagctgcag tgggatttgt agatcagcgg ataggatgaa 1380
ggatgttcat cgtaggtgtg gagaaggtga aaaggccctt ctggctgcat ctttctgaaa 1440
cacaataact aaagaaacac attgaggaag aagagtacag agacaaatcc gctcgacagt 1500
ctacacttgg tagtatagac acacagtcaa actctctcta tatatgtatg tatgtatgta 1560
tgtatgtatc ttgtgaaact agatgagaag ggtgcttttt gccctccttt cttgtttctt 1620
tatgcttttc tcaattctct gaaggtctgg agttctttgc acacagaaaa tgcagatttt 1680
agctgcaaag gcggactcca tgagtgcacc ttcagagtca tttcattgag gcgttttctc 1740
tgcccttttg gcttttcttc ttcatttctt tttggatttt gcctattttg ttcatttttt 1800
cctttgccat gattgtggtg aaacatgggt tgtttatgtg tgtacttgaa acgc
```

(2) INFORMATION FOR SEQ ID NO:634:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 289 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..289
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498761

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:634:

```
Met Asn Gly Ser Pro Val Ser Asp Asp Phe Lys Leu Pro Glu Thr Val
1          5          10          15
Thr Lys Arg Lys Tyr Leu Met Val Val Gly Val Asn Thr Ala Phe Ser
20          25          30
Ser Arg Lys Arg Arg Asp Ser Val Arg Ala Thr Trp Met Pro Pro Gly
35          40          45
Glu Glu Arg Lys Lys Leu Glu Glu Glu Lys Gly Ile Val Met Arg Phe
50          55          60
Val Ile Gly His Ser Ser Thr Pro Gly Gly Ile Leu Asp Arg Ala Ile
65          70          75          80
Gln Ala Glu Glu Ser Lys His Gly Asp Phe Leu Arg Leu Asp His Val
85          90          95
Glu Gly Tyr Leu Glu Leu Ser Ala Lys Thr Lys Thr Tyr Phe Thr Thr
100         105         110
Ala Phe Ala Met Trp Asp Ala Asp Phe Tyr Val Lys Val Asp Asp Asp
115         120         125
Val His Val Asn Ile Ala Thr Leu Gly Ala Glu Leu Ala Arg Tyr Arg
130         135         140
Met Lys Pro Arg Val Tyr Ile Gly Cys Met Lys Ser Gly Pro Val Leu
145         150         155         160
Ala Gln Lys Gly Val Arg Tyr His Glu Pro Glu Tyr Trp Lys Phe Gly
165         170         175
```

Glu	Glu	Gly	Asn	Lys	Tyr	Phe	Arg	His	Ala	Thr	Gly	Gln	Leu	Tyr	Ala
			180					185					190		
Ile	Ser	Arg	Glu	Leu	Ala	Ser	Tyr	Ile	Ser	Ile	Asn	Gln	Asn	Val	Leu
		195					200				205				
His	Lys	Tyr	Val	Asn	Glu	Asp	Val	Ser	Leu	Gly	Ser	Trp	Phe	Leu	Gly
	210					215					220				
Leu	Asp	Val	Glu	His	Val	Asp	Asp	Arg	Arg	Leu	Cys	Cys	Gly	Thr	Thr
225					230					235					240
Asp	Cys	Glu	Trp	Lys	Ala	Gln	Ala	Gly	Asn	Ile	Cys	Val	Ala	Ser	Phe
				245					250					255	
Asp	Trp	Ser	Cys	Ser	Gly	Ile	Cys	Arg	Ser	Ala	Asp	Arg	Met	Lys	Asp
		260					265						270		
Val	His	Arg	Arg	Cys	Gly	Glu	Gly	Glu	Lys	Ala	Leu	Leu	Ala	Ala	Ser
		275					280					285			

Phe

(2) INFORMATION FOR SEQ ID NO:635:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 267 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..267

(D) OTHER INFORMATION: / Ceres Seq. ID 1498762

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:635:

Met	Val	Val	Gly	Val	Asn	Thr	Ala	Phe	Ser	Ser	Arg	Lys	Arg	Arg	Asp
1				5					10					15	
Ser	Val	Arg	Ala	Thr	Trp	Met	Pro	Pro	Gly	Glu	Glu	Arg	Lys	Lys	Leu
		20					25						30		
Glu	Glu	Glu	Lys	Gly	Ile	Val	Met	Arg	Phe	Val	Ile	Gly	His	Ser	Ser
		35				40						45			
Thr	Pro	Gly	Gly	Ile	Leu	Asp	Arg	Ala	Ile	Gln	Ala	Glu	Glu	Ser	Lys
	50					55					60				
His	Gly	Asp	Phe	Leu	Arg	Leu	Asp	His	Val	Glu	Gly	Tyr	Leu	Glu	Leu
65				70						75				80	
Ser	Ala	Lys	Thr	Lys	Thr	Tyr	Phe	Thr	Thr	Ala	Phe	Ala	Met	Trp	Asp
			85						90					95	
Ala	Asp	Phe	Tyr	Val	Lys	Val	Asp	Asp	Val	His	Val	Asn	Ile	Ala	
		100					105					110			
Thr	Leu	Gly	Ala	Glu	Leu	Ala	Arg	Tyr	Arg	Met	Lys	Pro	Arg	Val	Tyr
		115				120						125			
Ile	Gly	Cys	Met	Lys	Ser	Gly	Pro	Val	Leu	Ala	Gln	Lys	Gly	Val	Arg
	130					135					140				
Tyr	His	Glu	Pro	Glu	Tyr	Trp	Lys	Phe	Gly	Glu	Gly	Asn	Lys	Tyr	
145				150						155				160	
Phe	Arg	His	Ala	Thr	Gly	Gln	Leu	Tyr	Ala	Ile	Ser	Arg	Glu	Leu	Ala
			165						170					175	
Ser	Tyr	Ile	Ser	Ile	Asn	Gln	Asn	Val	Leu	His	Lys	Tyr	Val	Asn	Glu
		180					185						190		
Asp	Val	Ser	Leu	Gly	Ser	Trp	Phe	Leu	Gly	Leu	Asp	Val	Glu	His	Val
		195				200						205			
Asp	Asp	Arg	Arg	Leu	Cys	Cys	Gly	Thr	Thr	Asp	Cys	Glu	Trp	Lys	Ala
	210					215					220				
Gln	Ala	Gly	Asn	Ile	Cys	Val	Ala	Ser	Phe	Asp	Trp	Ser	Cys	Ser	Gly
225					230					235					240
Ile	Cys	Arg	Ser	Ala	Asp	Arg	Met	Lys	Asp	Val	His	Arg	Arg	Cys	Gly
			245						250					255	

Glu Gly Glu Lys Ala Leu Leu Ala Ala Ser Phe

260 265
(2) INFORMATION FOR SEQ ID NO:636:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 245 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..245
(D) OTHER INFORMATION: / Ceres Seq. ID 1498763
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:636:
Met Pro Pro Gly Glu Glu Arg Lys Lys Leu Glu Glu Glu Lys Gly Ile
1 5 10 15
Val Met Arg Phe Val Ile Gly His Ser Ser Thr Pro Gly Gly Ile Leu
20 25 30
Asp Arg Ala Ile Gln Ala Glu Glu Ser Lys His Gly Asp Phe Leu Arg
35 40 45
Leu Asp His Val Glu Gly Tyr Leu Glu Leu Ser Ala Lys Thr Lys Thr
50 55 60
Tyr Phe Thr Thr Ala Phe Ala Met Trp Asp Ala Asp Phe Tyr Val Lys
65 70 75 80
Val Asp Asp Asp Val His Val Asn Ile Ala Thr Leu Gly Ala Glu Leu
85 90 95
Ala Arg Tyr Arg Met Lys Pro Arg Val Tyr Ile Gly Cys Met Lys Ser
100 105 110
Gly Pro Val Leu Ala Gln Lys Gly Val Arg Tyr His Glu Pro Glu Tyr
115 120 125
Trp Lys Phe Gly Glu Glu Gly Asn Lys Tyr Phe Arg His Ala Thr Gly
130 135 140
Gln Leu Tyr Ala Ile Ser Arg Glu Leu Ala Ser Tyr Ile Ser Ile Asn
145 150 155 160
Gln Asn Val Leu His Lys Tyr Val Asn Glu Asp Val Ser Leu Gly Ser
165 170 175
Trp Phe Leu Gly Leu Asp Val Glu His Val Asp Asp Arg Arg Leu Cys
180 185 190
Cys Gly Thr Thr Asp Cys Glu Trp Lys Ala Gln Ala Gly Asn Ile Cys
195 200 205
Val Ala Ser Phe Asp Trp Ser Cys Ser Gly Ile Cys Arg Ser Ala Asp
210 215 220
Arg Met Lys Asp Val His Arg Arg Cys Gly Glu Gly Glu Lys Ala Leu
225 230 235 240
Leu Ala Ala Ser Phe
245

(2) INFORMATION FOR SEQ ID NO:637:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 865 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
(A) NAME/KEY: -
(B) LOCATION: 1..865
(D) OTHER INFORMATION: / Ceres Seq. ID 1498764
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:637:
accataaaaaaa aaactcaaga gagactttgt ggccatggca gcctctctcc aatccaccgc 60
tacattcctc cagtcggcga agatcgccac cgctccttct cgcggaagtt ctcacctccg 120
atcgactcaa gccgtcggca aatcttttgg gctcgaaact tcctcggctc gcctcacttg 180
ctccttccag tctgacttta aggacttcac cggtaaagtc tccgacgctg tcaaaatcgc 240

cggattcgct	cttgccacct	ctgctctcgt	cgtctcggga	gcaagtgcgg	agggagctcc	300
aaagagattg	acctatgacg	agatcgaagg	acccttcgag	gttgcttcag	acggaagcgt	360
caatttcaag	gaagaagatg	gaatcgacta	tgctgcagtc	acagtccaac	ttccaggagg	420
tgaacgtgtg	ccattccttt	tcacagtcaa	acagcttgac	tcctcaggca	aaccagacag	480
cttcaccgga	aaattcttgg	ttccatcgta	ccgtggctct	tccttcttgg	acccaaaggg	540
ccgtgggtgga	tccacaggat	atgacaacgc	cgtggcattg	ccagctggag	gcagaggaga	600
cgaggaggag	cttgtaaagg	agaacgtgaa	gaacactgcc	gcttcagtgg	gagagatcac	660
tctgaaagtg	acaaagagca	agccggagac	aggagaggtg	atcgagagtgt	tcgagagtct	720
tcagccgtcg	gatactgact	tgggtgctaa	ggtaccaaag	gatgtgaaga	tccaaggggt	780
gtggtatggt	caacttgagt	gatcatgtta	ttatatatttc	cgttgattgt	gtttgatgat	840
aatgataaca	tcttttgatg	ctttc				

(2) INFORMATION FOR SEQ ID NO:638:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 266 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..266

(D) OTHER INFORMATION: / Ceres Seq. ID 1498765

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:638:

Pro	Lys	Lys	Lys	Leu	Lys	Arg	Asp	Phe	Val	Ala	Met	Ala	Ala	Ser	Leu	
1				5					10					15		
Gln	Ser	Thr	Ala	Thr	Phe	Leu	Gln	Ser	Ala	Lys	Ile	Ala	Thr	Ala	Pro	
			20					25						30		
Ser	Arg	Gly	Ser	Ser	His	Leu	Arg	Ser	Thr	Gln	Ala	Val	Gly	Lys	Ser	
			35				40					45				
Phe	Gly	Leu	Glu	Thr	Ser	Ser	Ala	Arg	Leu	Thr	Cys	Ser	Phe	Gln	Ser	
			50				55				60					
Asp	Phe	Lys	Asp	Phe	Thr	Gly	Lys	Cys	Ser	Asp	Ala	Val	Lys	Ile	Ala	
65					70				75					80		
Gly	Phe	Ala	Leu	Ala	Thr	Ser	Ala	Leu	Val	Ser	Gly	Ala	Ser	Ala		
			85					90						95		
Glu	Gly	Ala	Pro	Lys	Arg	Leu	Thr	Tyr	Asp	Glu	Ile	Glu	Gly	Pro	Phe	
			100				105						110			
Glu	Val	Ala	Ser	Asp	Gly	Ser	Val	Asn	Phe	Lys	Glu	Glu	Asp	Gly	Ile	
			115				120					125				
Asp	Tyr	Ala	Ala	Val	Thr	Val	Gln	Leu	Pro	Gly	Gly	Glu	Arg	Val	Pro	
			130				135				140					
Phe	Leu	Phe	Thr	Val	Lys	Gln	Leu	Asp	Ser	Ser	Gly	Lys	Pro	Asp	Ser	
145					150					155				160		
Phe	Thr	Gly	Lys	Phe	Leu	Val	Pro	Ser	Tyr	Arg	Gly	Ser	Ser	Phe	Leu	
			165					170						175		
Asp	Pro	Lys	Gly	Arg	Gly	Gly	Ser	Thr	Gly	Tyr	Asp	Asn	Ala	Val	Ala	
			180				185						190			
Leu	Pro	Ala	Gly	Gly	Arg	Gly	Asp	Glu	Glu	Glu	Leu	Val	Lys	Glu	Asn	
			195				200					205				
Val	Lys	Asn	Thr	Ala	Ala	Ser	Val	Gly	Glu	Ile	Thr	Leu	Lys	Val	Thr	
			210				215				220					
Lys	Ser	Lys	Pro	Glu	Thr	Gly	Glu	Val	Ile	Gly	Val	Phe	Glu	Ser	Leu	
225					230					235				240		
Gln	Pro	Ser	Asp	Thr	Asp	Leu	Gly	Ala	Lys	Val	Pro	Lys	Asp	Val	Lys	
			245					250						255		
Ile	Gln	Gly	Val	Trp	Tyr	Gly	Gln	Leu	Glu							
			260				265									

(2) INFORMATION FOR SEQ ID NO:639:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 255 amino acids
- (B) TYPE: amino acid

2025 RELEASE UNDER E.O. 14176

(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..255
 (D) OTHER INFORMATION: / Ceres Seq. ID 1498766
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:639:
Met Ala Ala Ser Leu Gln Ser Thr Ala Thr Phe Leu Gln Ser Ala Lys
1 5 10 15
Ile Ala Thr Ala Pro Ser Arg Gly Ser Ser His Leu Arg Ser Thr Gln
 20 25 30
Ala Val Gly Lys Ser Phe Gly Leu Glu Thr Ser Ser Ala Arg Leu Thr
 35 40 45
Cys Ser Phe Gln Ser Asp Phe Lys Asp Phe Thr Gly Lys Cys Ser Asp
50 55 60
Ala Val Lys Ile Ala Gly Phe Ala Leu Ala Thr Ser Ala Leu Val Val
65 70 75 80
Ser Gly Ala Ser Ala Glu Gly Ala Pro Lys Arg Leu Thr Tyr Asp Glu
 85 90 95
Ile Glu Gly Pro Phe Glu Val Ala Ser Asp Gly Ser Val Asn Phe Lys
 100 105 110
Glu Glu Asp Gly Ile Asp Tyr Ala Ala Val Thr Val Gln Leu Pro Gly
 115 120 125
Gly Glu Arg Val Pro Phe Leu Phe Thr Val Lys Gln Leu Asp Ser Ser
130 135 140
Gly Lys Pro Asp Ser Phe Thr Gly Lys Phe Leu Val Pro Ser Tyr Arg
145 150 155 160
Gly Ser Ser Phe Leu Asp Pro Lys Gly Arg Gly Gly Ser Thr Gly Tyr
 165 170 175
Asp Asn Ala Val Ala Leu Pro Ala Gly Gly Arg Gly Asp Glu Glu Glu
 180 185 190
Leu Val Lys Glu Asn Val Lys Asn Thr Ala Ala Ser Val Gly Glu Ile
195 200 205
Thr Leu Lys Val Thr Lys Ser Lys Pro Glu Thr Gly Glu Val Ile Gly
210 215 220
Val Phe Glu Ser Leu Gln Pro Ser Asp Thr Asp Leu Gly Ala Lys Val
225 230 235 240
Pro Lys Asp Val Lys Ile Gln Gly Val Trp Tyr Gly Gln Leu Glu
 245 250 255

(2) INFORMATION FOR SEQ ID NO:640:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2144 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
(B) LOCATION: 1..2144
(D) OTHER INFORMATION: / Ceres Seq. ID 1498771

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:640:

aaggaatcga	aaaccagaa	gaggactcag	tgaacaaatt	tcttcaggtt	aaatttcctc	60
actattctac	tgtgtttttg	ttctcagaat	cctcgaaaat	cgtaatatgt	tttttcgtat	120
gctcctaaaa	tctgggcaat	tcattagatt	tcgttgcgta	gataaactta	agcttgatgt	180
attcttttgt	acaatgtaat	tctgttttagt	tctataactt	ggaatcactc	taagtgtaat	240
gtatatgtat	gcgaagtcaa	atgttgctga	atttttgctc	tcctgcattt	ttccccaatt	300
ttttctgagc	cagtattgtg	aaaaattgga	gtctgagaaa	actgaaaagt	ttaatgtatt	360
ctcatttaat	cagtgttcat	agattcacta	gttgtttgac	cagggcttag	gcttaatcat	420
tcttgtgaca	cttggttttc	ttttaaatct	gttttgatgt	tcagttttct	ttggaagcta	480
tatacccata	aacttaaaat	gaataaagat	ggaagcttta	gctgatataa	tttgggtgtt	540

tctttctttc ttccttgggtg tgaagctgtt tcaaaatgtc tcggaggtat gatagtcgca 600
ccacgatctt ctcaccggaa ggtcgtctct accaggttga atatgctatg gaagctattg 660
gcaatgctgg ttctgccatt ggaatcttgg caaaagacgg agtggtgttg gttggtgaga 720
agaaagtcac ttctaaactt cttcaaacct cttcatccat ggagaaaatg tacaagatcg 780
atgaccatgt ggcttgtgca gttgctggtg taatgtctga tgccaacatt ctgattaaca 840
ctgctcgagt tcaagctcag cgttacacct ttatgtacca agagccaatg cccgttttagc 900
agctggttca gtctctttgt gacaccaagc aaggatacac ccagtttggg ggtctccgcc 960
cgtttgaggt ttcctttctt tttgcaggct gggacaggaa ccacggggtt cagctgtata 1020
tgagtgacct aagtggaaac tatggtggat ggcaagctgc agctggttga gcaaataatc 1080
aagcggctca gtctattctt aagcaagact ataaggatga tgcaacgagg gaagaagtgg 1140
ttcagctcgc tatcaagggt ttgagcaaga cgatggacag cacgagcttt acagctgaaa 1200
aactcgagct tgctgagttg tatctgactc cttcaaaatg tgtaagtac catgttcact 1260
cgcctgactc gctcactaag ctcttgggtt agcatggtgt gactcaacca gccgcagaaa 1320
cttcctaagc tagaaactgg tgacagtttt acctgaccgc cctggttact gtagatgtcc 1380
atttgctttc tttccctttg gagatatcgt atcagaatca atttaccact ctgattatgt 1440
catgtgattc atttggttgg actatctttt atcttgagat tgatcttctt ctagtctaaa 1500
gtaaaagttg acttttagagg ttttattcaa taaatgaatg agcaatcacc aacgggcccc 1560
ttagaaaagg cataacattc attgattgag gtaacgggtt ttaatggctc aaattaacga 1620
agaatcagaa tctctttaag tttcaccacg tcgatttaac ggtcaagagt gtctgtttat 1680
taacagaaca gtaaaaatgt taccgctcaa agcgtatatc ttgagcgcca aatgggaattt 1740
cattggtaca atgcccagaa gttctgggcc agaactggcc tcattgtaag agatttttta 1800
ggagatttat gcagacttgg aaaaacaagt tttctctctt tggattatct acaaaatatt 1860
atttacttaa gtagttgtca gttagacaat gccctgaatc caaggaattg tatcgaccgg 1920
gattgaagag accattcttg catcgtctct tctttttgca gcacgcgat tgtatgaaac 1980
attgatggcc agatctttct tctataagtc aatcaaccgg ccaccggaat taccctaaaa 2040
acatagaaaa tatgttgaaa tatattgaga cattagtcac cgactatgac taagtgtcac 2100
aaacttttgt gtgataggat tcaatcaatc caatggatct tagt

(2) INFORMATION FOR SEQ ID NO:641:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 107 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..107
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498772

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:641:

Met Ser Arg Arg Tyr Asp Ser Arg Thr Thr Ile Phe Ser Pro Glu Gly
1 5 10 15
Arg Leu Tyr Gln Val Glu Tyr Ala Met Glu Ala Ile Gly Asn Ala Gly
20 25 30
Ser Ala Ile Gly Ile Leu Ala Lys Asp Gly Val Val Leu Val Gly Glu
35 40 45
Lys Lys Val Thr Ser Lys Leu Leu Gln Thr Ser Ser Ser Met Glu Lys
50 55 60
Met Tyr Lys Ile Asp Asp His Val Ala Cys Ala Val Ala Gly Ile Met
65 70 75 80
Ser Asp Ala Asn Ile Leu Ile Asn Thr Ala Arg Val Gln Ala Gln Arg
85 90 95
Tyr Thr Phe Met Tyr Gln Glu Pro Met Pro Val
100 105

(2) INFORMATION FOR SEQ ID NO:642:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 83 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..83
(D) OTHER INFORMATION: / Ceres Seq. ID 1498773

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:642:

```
Met Glu Ala Ile Gly Asn Ala Gly Ser Ala Ile Gly Ile Leu Ala Lys
1           5           10           15
Asp Gly Val Val Leu Val Gly Glu Lys Lys Val Thr Ser Lys Leu Leu
           20           25           30
Gln Thr Ser Ser Ser Met Glu Lys Met Tyr Lys Ile Asp Asp His Val
           35           40           45
Ala Cys Ala Val Ala Gly Ile Met Ser Asp Ala Asn Ile Leu Ile Asn
           50           55           60
Thr Ala Arg Val Gln Ala Gln Arg Tyr Thr Phe Met Tyr Gln Glu Pro
65           70           75           80
Met Pro Val
```

(2) INFORMATION FOR SEQ ID NO:643:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 102 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..102
(D) OTHER INFORMATION: / Ceres Seq. ID 1498774

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:643:

```
Met Ser Asp Pro Ser Gly Asn Tyr Gly Gly Trp Gln Ala Ala Ala Val
1           5           10           15
Gly Ala Asn Asn Gln Ala Ala Gln Ser Ile Leu Lys Gln Asp Tyr Lys
           20           25           30
Asp Asp Ala Thr Arg Glu Glu Val Gln Leu Ala Ile Lys Val Leu
           35           40           45
Ser Lys Thr Met Asp Ser Thr Ser Phe Thr Ala Glu Lys Leu Glu Leu
           50           55           60
Ala Glu Leu Tyr Leu Thr Pro Ser Lys Cys Val Lys Tyr His Val His
65           70           75           80
Ser Pro Asp Ser Leu Thr Lys Leu Leu Val Lys His Gly Val Thr Gln
           85           90           95
Pro Ala Ala Glu Thr Ser
           100
```

(2) INFORMATION FOR SEQ ID NO:644:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1245 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
(B) LOCATION: 1..1245
(D) OTHER INFORMATION: / Ceres Seq. ID 1498775

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:644:

```
attgcttttg ctctgtatag tcaactgattt aggggtttttc gaatctgaac ttcttctttt 60
ttgagtttcc aaagcaatgg cggcgctcgca agataagttg gataagatga aacttaggca 120
agattaccgg aatttatggc actccgatct catgggcacc gtcaccgccg acactcccta 180
ttgctgcatc tcgtgtctgt gtggaccttg tgtgtcatac atgcttcgga gaagagcact 240
ttacaatgac atgtcaaggt atacttgctg tgctggatat atgccctgta gtggaaggtg 300
tggagaaagc aaatgtcctc aactttgcct tgccactgag gtcttccttt gcttcggaaa 360
ctctgtggcc tctaccgcgt ttcttctgca ggatgaattc aacatccaga caacacaatg 420
```

```
cgacaattgc ataattggat ttatgttctg cctcagccaa gttgcttgca tattctctat 480
agttgcttgc attgttggtg gtgatgaact ttccgaggct tctcagatac tctcttgctg 540
tgctgatatg gtctactgca cggctctgcgc atgtatgcag acacaacaca aacttgagat 600
ggacaaaaga gatggagtgt ttggatcgca gccaatgggt gtgccaccag ctcagcagat 660
gtctcgtttt gatcaacctg tccctcctcc agtcggatac cctcagtcgt atccaccgcc 720
tgctcaaggc taccctcctg catcttacct gcctcccggt tctcctcagc attaagaaat 780
ttaaccagta tcttcatttt atgtgtcaga atagggacac ccgcaatgac aaccggaggc 840
tgtatagagt ctgatttcga gacaatggcg gattttctga taaaggcggc tcagataaca 900
agtgcgttgc agagagagca tggaaagtca cacaaggagt ttgtgaaaag tttatgcacc 960
aacaagaca tagctgagct tagaaaccga gtcgaagcat ttgctttgca gtatgagatg 1020
cctgcttctc ttattcgaat tgaatgaaag aaaactccac acaacagctt tatttacagt 1080
tgaattttat cttatctctg ggtcaatttt tttttttttt tttggagttc tatcttgtaa 1140
attagagtaa atatatatgt atattgggat tgatttgcac tttttttttc cattgtaatt 1200
ctgtaaacad tttgataaat gggaatgatt actacaaatt tactt
```

(2) INFORMATION FOR SEQ ID NO:645:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 232 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..232
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498776

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:645:

```
Met Ala Ala Ser Gln Asp Lys Leu Asp Lys Met Lys Leu Arg Gln Asp
1          5          10          15
Tyr Arg Asn Leu Trp His Ser Asp Leu Met Gly Thr Val Thr Ala Asp
20          25          30
Thr Pro Tyr Cys Cys Ile Ser Cys Leu Cys Gly Pro Cys Val Ser Tyr
35          40          45
Met Leu Arg Arg Arg Ala Leu Tyr Asn Asp Met Ser Arg Tyr Thr Cys
50          55          60
Cys Ala Gly Tyr Met Pro Cys Ser Gly Arg Cys Gly Glu Ser Lys Cys
65          70          75          80
Pro Gln Leu Cys Leu Ala Thr Glu Val Phe Leu Cys Phe Gly Asn Ser
85          90          95
Val Ala Ser Thr Arg Phe Leu Leu Gln Asp Glu Phe Asn Ile Gln Thr
100         105         110
Thr Gln Cys Asp Asn Cys Ile Ile Gly Phe Met Phe Cys Leu Ser Gln
115         120         125
Val Ala Cys Ile Phe Ser Ile Val Ala Cys Ile Val Gly Ser Asp Glu
130         135         140
Leu Ser Glu Ala Ser Gln Ile Leu Ser Cys Cys Ala Asp Met Val Tyr
145         150         155         160
Cys Thr Val Cys Ala Cys Met Gln Thr Gln His Lys Leu Glu Met Asp
165         170         175
Lys Arg Asp Gly Val Phe Gly Ser Gln Pro Met Gly Val Pro Pro Ala
180         185         190
Gln Gln Met Ser Arg Phe Asp Gln Pro Val Pro Pro Pro Val Gly Tyr
195         200         205
Pro Gln Ser Tyr Pro Pro Pro Ala Gln Gly Tyr Pro Pro Ala Ser Tyr
210         215         220
Pro Pro Pro Gly Tyr Pro Gln His
225         230
```

(2) INFORMATION FOR SEQ ID NO:646:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 222 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:

(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..222
 (D) OTHER INFORMATION: / Ceres Seq. ID 1498777
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:646:
Met Lys Leu Arg Gln Asp Tyr Arg Asn Leu Trp His Ser Asp Leu Met
1 5 10 15
Gly Thr Val Thr Ala Asp Thr Pro Tyr Cys Cys Ile Ser Cys Leu Cys
 20 25 30
Gly Pro Cys Val Ser Tyr Met Leu Arg Arg Arg Ala Leu Tyr Asn Asp
 35 40 45
Met Ser Arg Tyr Thr Cys Cys Ala Gly Tyr Met Pro Cys Ser Gly Arg
 50 55 60
Cys Gly Glu Ser Lys Cys Pro Gln Leu Cys Leu Ala Thr Glu Val Phe
65 70 75 80
Leu Cys Phe Gly Asn Ser Val Ala Ser Thr Arg Phe Leu Leu Gln Asp
 85 90 95
Glu Phe Asn Ile Gln Thr Thr Gln Cys Asp Asn Cys Ile Ile Gly Phe
 100 105 110
Met Phe Cys Leu Ser Gln Val Ala Cys Ile Phe Ser Ile Val Ala Cys
 115 120 125
Ile Val Gly Ser Asp Glu Leu Ser Glu Ala Ser Gln Ile Leu Ser Cys
 130 135 140
Cys Ala Asp Met Val Tyr Cys Thr Val Cys Ala Cys Met Gln Thr Gln
145 150 155 160
His Lys Leu Glu Met Asp Lys Arg Asp Gly Val Phe Gly Ser Gln Pro
 165 170 175
Met Gly Val Pro Pro Ala Gln Gln Met Ser Arg Phe Asp Gln Pro Val
 180 185 190
Pro Pro Pro Val Gly Tyr Pro Gln Ser Tyr Pro Pro Pro Ala Gln Gly
 195 200 205
Tyr Pro Pro Ala Ser Tyr Pro Pro Pro Gly Tyr Pro Gln His
210 215 220

(2) INFORMATION FOR SEQ ID NO:647:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 207 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide
(B) LOCATION: 1..207

(D) OTHER INFORMATION: / Ceres Seq. ID 1498778

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:647:

Met Gly Thr Val Thr Ala Asp Thr Pro Tyr Cys Cys Ile Ser Cys Leu
1 5 10 15
Cys Gly Pro Cys Val Ser Tyr Met Leu Arg Arg Arg Ala Leu Tyr Asn
 20 25 30
Asp Met Ser Arg Tyr Thr Cys Cys Ala Gly Tyr Met Pro Cys Ser Gly
 35 40 45
Arg Cys Gly Glu Ser Lys Cys Pro Gln Leu Cys Leu Ala Thr Glu Val
 50 55 60
Phe Leu Cys Phe Gly Asn Ser Val Ala Ser Thr Arg Phe Leu Leu Gln
65 70 75 80
Asp Glu Phe Asn Ile Gln Thr Thr Gln Cys Asp Asn Cys Ile Ile Gly
 85 90 95
Phe Met Phe Cys Leu Ser Gln Val Ala Cys Ile Phe Ser Ile Val Ala
 100 105 110

Cys Ile Val Gly Ser Asp Glu Leu Ser Glu Ala Ser Gln Ile Leu Ser
115 120 125
Cys Cys Ala Asp Met Val Tyr Cys Thr Val Cys Ala Cys Met Gln Thr
130 135 140
Gln His Lys Leu Glu Met Asp Lys Arg Asp Gly Val Phe Gly Ser Gln
145 150 155 160
Pro Met Gly Val Pro Pro Ala Gln Gln Met Ser Arg Phe Asp Gln Pro
165 170 175
Val Pro Pro Pro Val Gly Tyr Pro Gln Ser Tyr Pro Pro Pro Ala Gln
180 185 190
Gly Tyr Pro Pro Ala Ser Tyr Pro Pro Pro Gly Tyr Pro Gln His
195 200 205

(2) INFORMATION FOR SEQ ID NO:648:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1182 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1182
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498779

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:648:

aataggtcag agagaacatt tcttattggt ttagtttgac gtctggtctc tgttttgcwt	60
cttttctaatac aacccatagc ttctattctt tttcttcttt cagcagtggt ttcaagaaaa	120
tgctagtaat actttttgtg tctgtcaatt tcaggagaaa aggcattttc tttgtcgcca	180
tcgatttgaa ccggccccta tctgaacaag ggccatttga tgttgttttg cataagttgt	240
tgggaaaaga gtgggaagag gttattgagg attaccaaca aaaacaccca gaagtgaactg	300
tgcttgatcc tccaggatca atacagcgta tatataatcg acaatcgaatg cttcagggtg	360
tggcagattt gaaactgtca gattgcagtg gcagcctttt tgttccaaag caaatgggtg	420
tcttgaaaga ttcagcagct agtgctgatg cagttgtgga agctggtctc aaatttccac	480
tagttgcaag ccgctctgga tcgatgggac tgcaaaagtca catcaattgt acttggctta	540
tgacaggcgc tcgcttgagc agcttgatcc gccttttagtc cttcaagagt ttgttaatca	600
tgggtggagtt atgttcaagg tatttgtggt ggggtgatgt ataaaagtca tgagacgggt	660
ttctctacca aatgtgagta attgtgaaaa agccaaagt tgggctgtct tccaattccc	720
aagggtttca tcagctgtg cttcagctga taacgcagac ttggaccctc gtgttgctga	780
gctacctcca aagcctttcc tcgaggcgct tgtgaaagag ctaagaagct tattgggact	840
tcggcttttc aacatagaca tgatcaggga acatgggagc aaaaacgtgt tttatgttat	900
tgacatcaac tattttcctg gttacggaaa actgccagac tacgagcaag tctttgtaga	960
tttcttccaa aatctggcgc aggtcaata taagaagaga caacattgta aatgaaagaa	1020
aatggcgcca gtttttagat ggtctactaa gaagcgacaa ataataaaat gtctaattat	1080
ggatttgtac agaatttagc tctcccttat ggaagcagta tcagataaac aagttttgat	1140
tactgatttt gaattttcag tgaaataaac gtctcttcac cc	

(2) INFORMATION FOR SEQ ID NO:649:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 152 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..152
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498780

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:649:

Met Leu Val Ile Leu Phe Val Ser Val Asn Phe Arg Arg Lys Gly Ile
1 5 10 15
Phe Phe Val Ala Ile Asp Leu Asn Arg Pro Leu Ser Glu Gln Gly Pro
20 25 30
Phe Asp Val Val Leu His Lys Leu Leu Gly Lys Glu Trp Glu Glu Val

Met	Arg	Arg	Phe	Ser	Leu	Pro	Asn	Val	Ser	Asn	Cys	Glu	Lys	Ala	Lys
1				5					10					15	
Val	Asp	Gly	Val	Phe	Gln	Phe	Pro	Arg	Val	Ser	Ser	Ala	Ala	Ala	Ser
			20					25					30		

Ala Asp Asn Ala Asp Leu Asp Pro Arg Val Ala Glu Leu Pro Pro Lys
35 40 45
Pro Phe Leu Glu Ala Leu Val Lys Glu Leu Arg Ser Leu Leu Gly Leu
50 55 60
Arg Leu Phe Asn Ile Asp Met Ile Arg Glu His Gly Ser Lys Asn Val
65 70 75 80
Phe Tyr Val Ile Asp Ile Asn Tyr Phe Pro Gly Tyr Gly Lys Leu Pro
85 90 95
Asp Tyr Glu Gln Val Phe Val Asp Phe Phe Gln Asn Leu Ala Gln Val
100 105 110
Lys Tyr Lys Lys Arg Gln His Cys Lys
115 120

(2) INFORMATION FOR SEQ ID NO:652:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 733 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..733
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498783

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:652:

acwtctttca aggaaatagt aagtaaatac agtagagaag taagagaagt gggattttaa	60
atagaggaat taatatcaga gagcttaggt ttagaaaaag attacatgaa gaaagtgctt	120
ggtgaacaag gtcaacacat ggcagtaaac tattatcctc catgtcctga acctgagctc	180
acttacggtt tacctgctca taccgaccca aacgccctaa ccattcttct tcaagacact	240
actgtttgcg gtctccagat cttgatcgac ggctcagtgg tccgccgttaa tccacatcct	300
gatgcttttg tcatcaacat aggtgaccag ttacaggcat taagtaatgg agtatacaaa	360
agtgtttggc gtcgcgctgt aacaaacaca gaaaatccga gactatcggc cgcacgcgtt	420
ctgtgcccag ctgactgtgc tgtcatgagc ccggccaagc ccttggtggga agctgaggac	480
gatgaaacga aaccagtcta caaagatttc acttatgcag agtattacaa gaagtttttg	540
agtaggaatc tggaccaaga acatttcctc gagaattttc taaacaacta agatacatat	600
atctttggcc tttgtgtttg tctagtaggc atatatatac aagtcaataa cagcattgat	660
gttcgattct acattctac caacattttg ttctagacgt atgataatag taggaatcat	720
gatcatatgt ctt	

(2) INFORMATION FOR SEQ ID NO:653:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 196 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..196
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498784

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:653:

Xaa Ser Phe Lys Ile Val Ser Lys Tyr Ser Arg Glu Val Arg Glu	
1 5 10 15	
Val Gly Phe Lys Ile Glu Glu Leu Ile Ser Glu Ser Leu Gly Leu Glu	
20 25 30	
Lys Asp Tyr Met Lys Lys Val Leu Gly Glu Gln Gly Gln His Met Ala	
35 40 45	
Val Asn Tyr Tyr Pro Pro Cys Pro Glu Pro Glu Leu Thr Tyr Gly Leu	
50 55 60	
Pro Ala His Thr Asp Pro Asn Ala Leu Thr Ile Leu Leu Gln Asp Thr	
65 70 75 80	
Thr Val Cys Gly Leu Gln Ile Leu Ile Asp Gly Gln Trp Phe Ala Val	
85 90 95	

Asn Pro His Pro Asp Ala Phe Val Ile Asn Ile Gly Asp Gln Leu Gln
100 105 110
Ala Leu Ser Asn Gly Val Tyr Lys Ser Val Trp Arg Arg Ala Val Thr
115 120 125
Asn Thr Glu Asn Pro Arg Leu Ser Val Ala Ser Phe Leu Cys Pro Ala
130 135 140
Asp Cys Ala Val Met Ser Pro Ala Lys Pro Leu Trp Glu Ala Glu Asp
145 150 155 160
Asp Glu Thr Lys Pro Val Tyr Lys Asp Phe Thr Tyr Ala Glu Tyr Tyr
165 170 175
Lys Lys Phe Trp Ser Arg Asn Leu Asp Gln Glu His Phe Leu Glu Asn
180 185 190
Phe Leu Asn Asn
195

(2) INFORMATION FOR SEQ ID NO:654:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 161 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..161

(D) OTHER INFORMATION: / Ceres Seq. ID 1498785

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:654:

Met Lys Lys Val Leu Gly Glu Gln Gly Gln His Met Ala Val Asn Tyr
1 5 10 15
Tyr Pro Pro Cys Pro Glu Pro Glu Leu Thr Tyr Gly Leu Pro Ala His
20 25 30
Thr Asp Pro Asn Ala Leu Thr Ile Leu Leu Gln Asp Thr Thr Val Cys
35 40 45
Gly Leu Gln Ile Leu Ile Asp Gly Gln Trp Phe Ala Val Asn Pro His
50 55 60
Pro Asp Ala Phe Val Ile Asn Ile Gly Asp Gln Leu Gln Ala Leu Ser
65 70 75 80
Asn Gly Val Tyr Lys Ser Val Trp Arg Arg Ala Val Thr Asn Thr Glu
85 90 95
Asn Pro Arg Leu Ser Val Ala Ser Phe Leu Cys Pro Ala Asp Cys Ala
100 105 110
Val Met Ser Pro Ala Lys Pro Leu Trp Glu Ala Glu Asp Asp Glu Thr
115 120 125
Lys Pro Val Tyr Lys Asp Phe Thr Tyr Ala Glu Tyr Tyr Lys Lys Phe
130 135 140
Trp Ser Arg Asn Leu Asp Gln Glu His Phe Leu Glu Asn Phe Leu Asn
145 150 155 160
Asn

(2) INFORMATION FOR SEQ ID NO:655:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 150 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..150

(D) OTHER INFORMATION: / Ceres Seq. ID 1498786

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:655:

Met Ala Val Asn Tyr Tyr Pro Pro Cys Pro Glu Pro Glu Leu Thr Tyr

1	5	10	15
Gly Leu Pro	Ala His Thr Asp Pro	Asn Ala Leu Thr Ile Leu Leu Gln	
	20	25	30
Asp Thr Thr	Val Cys Gly Leu Gln Ile Leu Ile Asp Gly Gln Trp Phe		
	35	40	45
Ala Val Asn	Pro His Pro Asp Ala Phe Val Ile Asn Ile Gly Asp Gln		
	50	55	60
Leu Gln Ala	Leu Ser Asn Gly Val Tyr Lys Ser Val Trp Arg Arg Ala		
65		70	75
Val Thr Asn	Thr Glu Asn Pro Arg Leu Ser Val Ala Ser Phe Leu Cys		
	85	90	95
Pro Ala Asp	Cys Ala Val Met Ser Pro Ala Lys Pro Leu Trp Glu Ala		
	100	105	110
Glu Asp Asp	Glu Thr Lys Pro Val Tyr Lys Asp Phe Thr Tyr Ala Glu		
	115	120	125
Tyr Tyr Lys	Lys Phe Trp Ser Arg Asn Leu Asp Gln Glu His Phe Leu		
	130	135	140
Glu Asn Phe	Leu Asn Asn		
145	150		

(2) INFORMATION FOR SEQ ID NO:656:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1676 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1676
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498789

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:656:

attaagacg	gatgttgtaa	ttaa	acac	ct	acca	acagac	aaaatcaaaa	gataggaagc	60
cacgtatgc	tatat	tttag	tgaagc	tttt	gata	aaaaca	agcgttgggc	tcttccaaat	120
atcaaaaca	gttttttt	ttt	gttggc	t	tata	attcac	ctgagaaaaa	caatatcaat	180
cggctcg	ttt	tctctc	tca	gtgtt	cttc	agtagtc	ctgagatcgta	taagagattc	240
gaaacccta	tctatca	att	tgatc	ctgtc	cattc	tctgt	tattgtttga	gaattgtgca	300
atccgatgg	gacgatgc	ac	ggagtgg	tg	ctccc	agaag	gacaaatgaa	aatgcgaagc	360
ttatcatac	gacaatc	gtg	ggagtgg	tgt	ttgg	ttttt	tgttgggtatc	acattaccat	420
taggttc	ctt	tagaa	agatt	agc	ttac	ctt	caggccttat	gtcatctctt	480
tgtcagatg	gaaattgt	tt	tctgg	tggca	gatcac	ctga	agatattggt	tcaagaaagt	540
ctcctaag	at	atgtt	cca	accaat	ccgc		atggtgcaga	actacttcct	600
tagtggc	aga	acagatt	tc	tacttgc	gcc		gattatggg	tgaacctagt	660
agaagaagc	aaagt	atctc		gtaact	ttta		cagttggatt	tgagcagaga	720
atgcagctg	taaga	agttt		tctga	agatt		tccaaatatt	gttattccat	780
gaacaactg	gtggg	accag		tttg	agtgg	t	ctaaaaatgc	aatacatatc	840
agcaaacaa	atgg	tgg	t	gca	aa	gagat	ttttgcatcc	tgatgttg	900
agtatata	t	at	atggg	at	ga	atc	cttg	gatcgagca	960
ttacttgt	ct	gaa	attgt	ag	ttgc	agatca	gtgacaatct	ttacaatttt	1020
tttcaggt	ac	gtt	gag	ttag	tt	aaga	agca	tggtttggag	1080
gccaacaac	ggact	tacat		ggg	aa	atgac		aaagaggaga	1140
agaaacta	ag	gaaaa	accag		gat	ggtgc	ag	tgatccacat	1200
tgttgag	att	atggc	acctg		tatt	tttct	ag	agaagcatgg	1260
tcagaatg	at	ctt	gttcatg		gat	ggg	tct	cgattttgct	1320
tgctcatg	ag	att	gg	tg	tag	attc		acagtggatt	1380
ccttgga	agt	cagg	gtg	agt	cgg	aggagg		gaaatctcca	1440
atgcagaa	c	gaat	ggac	ga	gtt	ccagaa		tcgcgtggca	1500
ggaacaac	a	agg	t	aaag		gtt	gg	gcctcttctt	1560
gcttacg	ttt	ccct	gat	caa	gtg	agtgtg	ga	ggagagagat	1620
tttaaa	acat	ctc	agat	ata	tct	acattat		tagcttttta	
								cctaata	
								tatat	
								ttcttc	

(2) INFORMATION FOR SEQ ID NO:657:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 217 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..217
(D) OTHER INFORMATION: / Ceres Seq. ID 1498790
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:657:

Met	Gly	Thr	Met	His	Arg	Ser	Gly	Ala	Pro	Arg	Arg	Thr	Asn	Glu	Asn
1				5					10					15	
Ala	Lys	Leu	Ile	Ile	Thr	Thr	Ile	Val	Gly	Val	Val	Phe	Gly	Phe	Phe
			20					25					30		
Val	Gly	Ile	Thr	Leu	Pro	Leu	Gly	Ser	Phe	Arg	Lys	Ile	Ser	Leu	Pro
			35				40					45			
Ser	Gly	Leu	Met	Ser	Ser	Leu	Asp	Val	Ala	Met	Ser	Asp	Gly	Lys	Leu
	50					55					60				
Phe	Ser	Gly	Gly	Arg	Ser	Pro	Glu	Asp	Ile	Gly	Ser	Arg	Lys	Ser	Pro
65				70					75					80	
Lys	Ile	Tyr	Val	Pro	Thr	Asn	Pro	His	Gly	Ala	Glu	Leu	Leu	Pro	Pro
			85						90				95		
Gly	Ile	Ile	Val	Ala	Glu	Thr	Asp	Phe	Tyr	Leu	Arg	Arg	Leu	Trp	Gly
			100					105					110		
Glu	Pro	Ser	Glu	Asp	Leu	Lys	Lys	Lys	Pro	Lys	Tyr	Leu	Val	Thr	Phe
		115				120						125			
Thr	Val	Gly	Phe	Glu	Gln	Arg	Asn	Asn	Ile	Asn	Ala	Ala	Val	Lys	Lys
	130					135					140				
Phe	Ser	Glu	Asp	Phe	Gln	Ile	Leu	Leu	Phe	His	Tyr	Asp	Gly	Arg	Thr
145				150						155				160	
Thr	Glu	Trp	Asp	Gln	Phe	Glu	Trp	Ser	Lys	Asn	Ala	Ile	His	Ile	Ser
			165						170				175		
Ala	Lys	Lys	Gln	Thr	Lys	Trp	Trp	Tyr	Ala	Lys	Arg	Phe	Leu	His	Pro
		180						185					190		
Asp	Val	Val	Ser	Ala	Tyr	Glu	Tyr	Ile	Phe	Ile	Trp	Asp	Glu	Asp	Leu
	195					200						205			
Gly	Val	Glu	His	Phe	Asn	Ala	Asp	Arg							
	210				215										

(2) INFORMATION FOR SEQ ID NO:658:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 214 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..214
(D) OTHER INFORMATION: / Ceres Seq. ID 1498791
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:658:

Met	His	Arg	Ser	Gly	Ala	Pro	Arg	Arg	Thr	Asn	Glu	Asn	Ala	Lys	Leu
1				5					10					15	
Ile	Ile	Thr	Thr	Ile	Val	Gly	Val	Val	Phe	Gly	Phe	Phe	Val	Gly	Ile
			20					25					30		
Thr	Leu	Pro	Leu	Gly	Ser	Phe	Arg	Lys	Ile	Ser	Leu	Pro	Ser	Gly	Leu
		35				40					45				
Met	Ser	Ser	Leu	Asp	Val	Ala	Met	Ser	Asp	Gly	Lys	Leu	Phe	Ser	Gly
	50					55				60					
Gly	Arg	Ser	Pro	Glu	Asp	Ile	Gly	Ser	Arg	Lys	Ser	Pro	Lys	Ile	Tyr
65				70					75				80		
Val	Pro	Thr	Asn	Pro	His	Gly	Ala	Glu	Leu	Leu	Pro	Pro	Gly	Ile	Ile

				85					90					95			
Val	Ala	Glu	Thr	Asp	Phe	Tyr	Leu	Arg	Leu	Trp	Gly	Glu	Pro	Ser			
				100				105				110					
Glu	Asp	Leu	Lys	Lys	Lys	Pro	Lys	Tyr	Leu	Val	Thr	Phe	Thr	Val	Gly		
		115					120					125					
Phe	Glu	Gln	Arg	Asn	Asn	Ile	Asn	Ala	Ala	Val	Lys	Lys	Phe	Ser	Glu		
		130					135					140					
Asp	Phe	Gln	Ile	Leu	Leu	Phe	His	Tyr	Asp	Gly	Arg	Thr	Thr	Glu	Trp		
				145		150				155					160		
Asp	Gln	Phe	Glu	Trp	Ser	Lys	Asn	Ala	Ile	His	Ile	Ser	Ala	Lys	Lys		
				165					170					175			
Gln	Thr	Lys	Trp	Trp	Tyr	Ala	Lys	Arg	Phe	Leu	His	Pro	Asp	Val	Val		
			180					185					190				
Ser	Ala	Tyr	Glu	Tyr	Ile	Phe	Ile	Trp	Asp	Glu	Asp	Leu	Gly	Val	Glu		
		195					200					205					
His	Phe	Asn	Ala	Asp	Arg												
				210													

(2) INFORMATION FOR SEQ ID NO:659:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 166 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..166
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498792

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:659:

Met	Ser	Ser	Leu	Asp	Val	Ala	Met	Ser	Asp	Gly	Lys	Leu	Phe	Ser	Gly		
1				5				10				15					
Gly	Arg	Ser	Pro	Glu	Asp	Ile	Gly	Ser	Arg	Lys	Ser	Pro	Lys	Ile	Tyr		
			20					25				30					
Val	Pro	Thr	Asn	Pro	His	Gly	Ala	Glu	Leu	Leu	Pro	Pro	Gly	Ile	Ile		
			35				40					45					
Val	Ala	Glu	Thr	Asp	Phe	Tyr	Leu	Arg	Arg	Leu	Trp	Gly	Glu	Pro	Ser		
		50				55				60							
Glu	Asp	Leu	Lys	Lys	Lys	Pro	Lys	Tyr	Leu	Val	Thr	Phe	Thr	Val	Gly		
				65		70				75				80			
Phe	Glu	Gln	Arg	Asn	Asn	Ile	Asn	Ala	Ala	Val	Lys	Lys	Phe	Ser	Glu		
				85				90					95				
Asp	Phe	Gln	Ile	Leu	Leu	Phe	His	Tyr	Asp	Gly	Arg	Thr	Thr	Glu	Trp		
			100					105					110				
Asp	Gln	Phe	Glu	Trp	Ser	Lys	Asn	Ala	Ile	His	Ile	Ser	Ala	Lys	Lys		
			115				120					125					
Gln	Thr	Lys	Trp	Trp	Tyr	Ala	Lys	Arg	Phe	Leu	His	Pro	Asp	Val	Val		
			130			135					140						
Ser	Ala	Tyr	Glu	Tyr	Ile	Phe	Ile	Trp	Asp	Glu	Asp	Leu	Gly	Val	Glu		
			145		150				155						160		
His	Phe	Asn	Ala	Asp	Arg												
				165													

(2) INFORMATION FOR SEQ ID NO:660:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1373 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1373

(D) OTHER INFORMATION: / Ceres Seq. ID 1498801

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:660:

atgctttgtc	tttagtttaa	ccgccgcac	ctctctctct	ggtcggagaa	atctccagat	60
ttggtcattt	ctccaatctt	ctcggaaccc	taattttaacc	aaacctctcc	tccttcagat	120
tcattcttct	cctaattctc	ctaaaagctc	aaacctttct	ctcaatcaat	tctaaacaat	180
ggcaacagaa	gcaacaacca	aattcccaga	atccgatctc	cgtccaatcc	cacaaccacc	240
ggattttcat	ccagcaatca	tcgttccagc	tcaaaacaca	actcttaa	tctggcaact	300
aatggtcgcc	ggttcaatcg	ctggctcagt	cgaacacatg	gctatgtttc	cagtagatac	360
agtcaaaacc	catatgcaag	ctcttcgttc	atgtccgatt	aaaccaatcg	gaatccgtca	420
agctttccgt	tcaattatca	aaaccgatgg	accttctgct	ttatatagag	gtatttgggc	480
tatgggactt	ggtgctggac	cagctcacgc	tgtttatttc	tcattctatg	aagtctctaa	540
gaagttttta	tccggtggaa	accctaataa	ctctgctgca	cacgctat	ccggtgtttt	600
cgctactata	tctagtgatg	ctgtgtttac	tccaatggat	atggttaagc	aaaggttgca	660
aattgggaat	ggaacttata	aaggagtttg	ggattgtatc	aagagagtaa	cgcgtgagga	720
agggtttggg	gctttttacg	cttcgtatag	aactactgtg	ttgatgaatg	ctccgtttac	780
cgctgtgcat	ttcactactt	atgaggcggt	taagagaggt	ttgagggaga	tgtttcctga	840
gcatgctgtt	ggagtagagg	atgaggaagg	ttggttgatt	tatgctactg	ctggagctgc	900
ggctgggtgg	ttagcggctg	ctgtaactac	tccgcttgat	gttggttaaga	cgcagttgca	960
atgtcagggt	gtgtgtgggt	gtgaccgttt	caagagcagt	tcaataagcg	atgtgttccg	1020
tacaatagt	aagaaagacg	gttatagagg	acttgctaga	ggatggctac	caagaatgct	1080
cttccatgct	ccagcagctg	cgatttgctg	gtccacttat	gaaacagtca	aatctttctt	1140
tcaagatctc	aatggtgaag	caaacgcagc	ttgaaaagac	acaaacatac	atgcgtttgg	1200
cataattttac	ttgcttgatt	caggtcattg	attcttcata	gagctagcta	ctggttggtt	1260
agtattaaca	ctagctctta	gagaagatct	ctgtttgtat	aatttatattg	ttttcttcac	1320
gcaataatgt	tgtcagatta	gagttacaac	aaccccaagg	ccttttttct	ggt	

(2) INFORMATION FOR SEQ ID NO:661:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 331 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..331

(D) OTHER INFORMATION: / Ceres Seq. ID 1498802

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:661:

Met	Ala	Thr	Glu	Ala	Thr	Thr	Lys	Phe	Pro	Glu	Ser	Asp	Leu	Arg	Pro	
1				5					10					15		
Ile	Pro	Gln	Pro	Pro	Asp	Phe	His	Pro	Ala	Ile	Ile	Val	Pro	Ala	Gln	
			20					25					30			
Asn	Thr	Thr	Leu	Lys	Phe	Trp	Gln	Leu	Met	Val	Ala	Gly	Ser	Ile	Ala	
		35					40					45				
Gly	Ser	Val	Glu	His	Met	Ala	Met	Phe	Pro	Val	Asp	Thr	Val	Lys	Thr	
		50				55					60					
His	Met	Gln	Ala	Leu	Arg	Ser	Cys	Pro	Ile	Lys	Pro	Ile	Gly	Ile	Arg	
65					70					75				80		
Gln	Ala	Phe	Arg	Ser	Ile	Ile	Lys	Thr	Asp	Gly	Pro	Ser	Ala	Leu	Tyr	
			85						90					95		
Arg	Gly	Ile	Trp	Ala	Met	Gly	Leu	Gly	Ala	Gly	Pro	Ala	His	Ala	Val	
			100					105					110			
Tyr	Phe	Ser	Phe	Tyr	Glu	Val	Ser	Lys	Lys	Phe	Leu	Ser	Gly	Gly	Asn	
		115					120				125					
Pro	Asn	Asn	Ser	Ala	Ala	His	Ala	Ile	Ser	Gly	Val	Phe	Ala	Thr	Ile	
						135					140					
Ser	Ser	Asp	Ala	Val	Phe	Thr	Pro	Met	Asp	Met	Val	Lys	Gln	Arg	Leu	
145					150					155				160		
Gln	Ile	Gly	Asn	Gly	Thr	Tyr	Lys	Gly	Val	Trp	Asp	Cys	Ile	Lys	Arg	
			165					170					175			
Val	Thr	Arg	Glu	Glu	Gly	Phe	Gly	Ala	Phe	Tyr	Ala	Ser	Tyr	Arg	Thr	
			180					185					190			

Thr Val Leu Met Asn Ala Pro Phe Thr Ala Val His Phe Thr Thr Tyr
195 200 205
Glu Ala Val Lys Arg Gly Leu Arg Glu Met Phe Pro Glu His Ala Val
210 215 220
Gly Val Glu Asp Glu Glu Gly Trp Leu Ile Tyr Ala Thr Ala Gly Ala
225 230 235 240
Ala Ala Gly Gly Leu Ala Ala Ala Val Thr Thr Pro Leu Asp Val Val
245 250 255
Lys Thr Gln Leu Gln Cys Gln Gly Val Cys Gly Cys Asp Arg Phe Lys
260 265 270
Ser Ser Ser Ile Ser Asp Val Phe Arg Thr Ile Val Lys Lys Asp Gly
275 280 285
Tyr Arg Gly Leu Ala Arg Gly Trp Leu Pro Arg Met Leu Phe His Ala
290 295 300
Pro Ala Ala Ala Ile Cys Trp Ser Thr Tyr Glu Thr Val Lys Ser Phe
305 310 315 320
Phe Gln Asp Leu Asn Gly Glu Ala Asn Ala Ala
325 330

(2) INFORMATION FOR SEQ ID NO:662:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 290 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..290
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498803

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:662:

Met Val Ala Gly Ser Ile Ala Gly Ser Val Glu His Met Ala Met Phe
1 5 10 15
Pro Val Asp Thr Val Lys Thr His Met Gln Ala Leu Arg Ser Cys Pro
20 25 30
Ile Lys Pro Ile Gly Ile Arg Gln Ala Phe Arg Ser Ile Ile Lys Thr
35 40 45
Asp Gly Pro Ser Ala Leu Tyr Arg Gly Ile Trp Ala Met Gly Leu Gly
50 55 60
Ala Gly Pro Ala His Ala Val Tyr Phe Ser Phe Tyr Glu Val Ser Lys
65 70 75 80
Lys Phe Leu Ser Gly Gly Asn Pro Asn Asn Ser Ala Ala His Ala Ile
85 90 95
Ser Gly Val Phe Ala Thr Ile Ser Ser Asp Ala Val Phe Thr Pro Met
100 105 110
Asp Met Val Lys Gln Arg Leu Gln Ile Gly Asn Gly Thr Tyr Lys Gly
115 120 125
Val Trp Asp Cys Ile Lys Arg Val Thr Arg Glu Glu Gly Phe Gly Ala
130 135 140
Phe Tyr Ala Ser Tyr Arg Thr Thr Val Leu Met Asn Ala Pro Phe Thr
145 150 155 160
Ala Val His Phe Thr Thr Tyr Glu Ala Val Lys Arg Gly Leu Arg Glu
165 170 175
Met Phe Pro Glu His Ala Val Gly Val Glu Asp Glu Glu Gly Trp Leu
180 185 190
Ile Tyr Ala Thr Ala Gly Ala Ala Gly Gly Leu Ala Ala Val
195 200 205
Thr Thr Pro Leu Asp Val Val Lys Thr Gln Leu Gln Cys Gln Gly Val
210 215 220
Cys Gly Cys Asp Arg Phe Lys Ser Ser Ser Ile Ser Asp Val Phe Arg
225 230 235 240
Thr Ile Val Lys Lys Asp Gly Tyr Arg Gly Leu Ala Arg Gly Trp Leu

Pro Arg Met Leu Phe His Ala Pro Ala Ala Ala Ile Cys Trp Ser Thr
245 250 255
260 265 270
Tyr Glu Thr Val Lys Ser Phe Phe Gln Asp Leu Asn Gly Glu Ala Asn
275 280 285
Ala Ala
290

(2) INFORMATION FOR SEQ ID NO:663:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 278 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..278

(D) OTHER INFORMATION: / Ceres Seq. ID 1498804

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:663:

Met Ala Met Phe Pro Val Asp Thr Val Lys Thr His Met Gln Ala Leu
1 5 10 15
Arg Ser Cys Pro Ile Lys Pro Ile Gly Ile Arg Gln Ala Phe Arg Ser
20 25 30
Ile Ile Lys Thr Asp Gly Pro Ser Ala Leu Tyr Arg Gly Ile Trp Ala
35 40 45
Met Gly Leu Gly Ala Gly Pro Ala His Ala Val Tyr Phe Ser Phe Tyr
50 55 60
Glu Val Ser Lys Lys Phe Leu Ser Gly Gly Asn Pro Asn Asn Ser Ala
65 70 75 80
Ala His Ala Ile Ser Gly Val Phe Ala Thr Ile Ser Ser Asp Ala Val
85 90 95
Phe Thr Pro Met Asp Met Val Lys Gln Arg Leu Gln Ile Gly Asn Gly
100 105 110
Thr Tyr Lys Gly Val Trp Asp Cys Ile Lys Arg Val Thr Arg Glu Glu
115 120 125
Gly Phe Gly Ala Phe Tyr Ala Ser Tyr Arg Thr Thr Val Leu Met Asn
130 135 140
Ala Pro Phe Thr Ala Val His Phe Thr Thr Tyr Glu Ala Val Lys Arg
145 150 155 160
Gly Leu Arg Glu Met Phe Pro Glu His Ala Val Gly Val Glu Asp Glu
165 170 175
Glu Gly Trp Leu Ile Tyr Ala Thr Ala Gly Ala Ala Ala Gly Gly Leu
180 185 190
Ala Ala Ala Val Thr Thr Pro Leu Asp Val Val Lys Thr Gln Leu Gln
195 200 205
Cys Gln Gly Val Cys Gly Cys Asp Arg Phe Lys Ser Ser Ser Ile Ser
210 215 220
Asp Val Phe Arg Thr Ile Val Lys Lys Asp Gly Tyr Arg Gly Leu Ala
225 230 235 240
Arg Gly Trp Leu Pro Arg Met Leu Phe His Ala Pro Ala Ala Ala Ile
245 250 255
Cys Trp Ser Thr Tyr Glu Thr Val Lys Ser Phe Phe Gln Asp Leu Asn
260 265 270
Gly Glu Ala Asn Ala Ala
275

(2) INFORMATION FOR SEQ ID NO:664:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1186 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1186

(D) OTHER INFORMATION: / Ceres Seq. ID 1498808

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:664:

```
accatccact ctactcaaca tggactcctc caaactctca tctctctctc tttgcctctt      60
cctcatttgc attatctatc tcccccaaca ttctctcgca tgcggctctt gcaacccacg      120
gaagggcgga aagcactccc ctaagctacc agttcctccg gtgaccgtcc ctaagctacc      180
agttcctccg gtgaccgtcc ctaagctacc agtccctccg gtgaccgtcc ctaagctacc      240
cgttcctcct gtgaccatcc ctaagctacc cgttccacca gtgactgtac ctaagctacc      300
cgttcctcct gtgaccgtcc ccaagctacc cgttcctcca gtgaccgtcc ccaagctacc      360
cgttcctcca gtgacagtcc ctaagctacc cgttcccccg gtaactgtac ctaagctacc      420
cgttcctcca gtgaccgtcc ctaagctacc ccttcctccg atttcagggc taccataacc      480
tccagtggta ggtcccaatc tgccattgcc accttgcca attgtaggtc ctattcttcc      540
accgggaaca accccaccag ccacaggagg gaaggactgt cctccaccgc cagggagcgt      600
aaagccacca tcagggggcg ggaaggcgag atgtccaata gacacgctga agttaggtgc      660
ttgcgtcgac ttgttgggag gtttagtaaa gatagggtt ggggatccag cagttaacaa      720
atgttgctcg ttacttaaac gcctcgttga aatcgaaagg gcggcttgct tctgcactac      780
cctcaagctc aaagctcttg acctcaatct ttatgtccct gatgctcttc agcttctcct      840
tacctgtggc aaaaatccac ctccgggcta cacttggtcc atatgataaa ctcactccac      900
ttataaagga tgctttggag aaaaaagtga gaagagaatg gcagagctcc aatctttcct      960
gtcttgggtt accaaatata tcatatcaaa tcctatccct ttgattcttt cctctatcgt     1020
tcccttatgc ttgtatcatt aattaatgtg tgcttttttag attaatgatt cttctcttgt     1080
attaaagtat gatttgaaat cctttttttt tctctatctc tttttattga attgattgaa     1140
ctgcgttcac gatactgtca aaaagagaga aaaagagtac aatttt
```

(2) INFORMATION FOR SEQ ID NO:665:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 294 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..294

(D) OTHER INFORMATION: / Ceres Seq. ID 1498809

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:665:

```
Pro Ser Thr Leu Leu Asn Met Asp Ser Ser Lys Leu Ser Ser Leu Ser
1          5          10          15
Leu Cys Leu Phe Leu Ile Cys Ile Ile Tyr Leu Pro Gln His Ser Leu
20          25          30
Ala Cys Gly Ser Cys Asn Pro Arg Lys Gly Gly Lys His Ser Pro Lys
35          40          45
Leu Pro Val Pro Pro Val Thr Val Pro Lys Leu Pro Val Pro Pro Val
50          55          60
Thr Val Pro Lys Leu Pro Val Pro Pro Val Thr Val Pro Lys Leu Pro
65          70          75          80
Val Pro Pro Val Thr Ile Pro Lys Leu Pro Val Pro Pro Val Thr Val
85          90          95
Pro Lys Leu Pro Val Pro Pro Val Thr Val Pro Lys Leu Pro Val Pro
100          105          110
Pro Val Thr Val Pro Lys Leu Pro Val Pro Pro Val Thr Val Pro Lys
115          120          125
Leu Pro Val Pro Pro Val Thr Val Pro Lys Leu Pro Val Pro Pro Val
130          135          140
Thr Val Pro Lys Leu Pro Leu Pro Pro Ile Ser Gly Leu Pro Ile Pro
145          150          155          160
Pro Val Val Gly Pro Asn Leu Pro Leu Pro Pro Leu Pro Ile Val Gly
165          170          175
Pro Ile Leu Pro Pro Gly Thr Thr Pro Pro Ala Thr Gly Gly Lys Asp
```

	180		185		190										
Cys	Pro	Pro	Pro	Gly	Ser	Val	Lys	Pro	Pro	Ser	Gly	Gly	Lys		
	195					200					205				
Ala	Thr	Cys	Pro	Ile	Asp	Thr	Leu	Lys	Leu	Gly	Ala	Cys	Val	Asp	Leu
	210					215					220				
Leu	Gly	Gly	Leu	Val	Lys	Ile	Gly	Leu	Gly	Asp	Pro	Ala	Val	Asn	Lys
	225				230					235					240
Cys	Cys	Pro	Leu	Leu	Lys	Gly	Leu	Val	Glu	Ile	Glu	Ala	Ala	Ala	Cys
			245						250						255
Leu	Cys	Thr	Thr	Leu	Lys	Leu	Lys	Ala	Leu	Asp	Leu	Asn	Leu	Tyr	Val
			260					265						270	
Pro	Asp	Ala	Leu	Gln	Leu	Leu	Leu	Thr	Cys	Gly	Lys	Asn	Pro	Pro	Pro
		275					280					285			
Gly	Tyr	Thr	Cys	Ser	Ile										
	290														

(2) INFORMATION FOR SEQ ID NO:666:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 288 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..288

(D) OTHER INFORMATION: / Ceres Seq. ID 1498810

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:666:

Met	Asp	Ser	Ser	Lys	Leu	Ser	Ser	Leu	Ser	Leu	Cys	Leu	Phe	Leu	Ile
1				5				10						15	
Cys	Ile	Ile	Tyr	Leu	Pro	Gln	His	Ser	Leu	Ala	Cys	Gly	Ser	Cys	Asn
			20					25					30		
Pro	Arg	Lys	Gly	Gly	Lys	His	Ser	Pro	Lys	Leu	Pro	Val	Pro	Pro	Val
		35					40					45			
Thr	Val	Pro	Lys	Leu	Pro	Val	Pro	Pro	Val	Thr	Val	Pro	Lys	Leu	Pro
		50				55				60					
Val	Pro	Pro	Val	Thr	Val	Pro	Lys	Leu	Pro	Val	Pro	Pro	Val	Thr	Ile
				70						75				80	
Pro	Lys	Leu	Pro	Val	Pro	Pro	Val	Thr	Val	Pro	Lys	Leu	Pro	Val	Pro
			85					90					95		
Pro	Val	Thr	Val	Pro	Lys	Leu	Pro	Val	Pro	Pro	Val	Thr	Val	Pro	Lys
		100						105					110		
Leu	Pro	Val	Pro	Pro	Val	Thr	Val	Pro	Lys	Leu	Pro	Val	Pro	Pro	Val
		115						120					125		
Thr	Val	Pro	Lys	Leu	Pro	Val	Pro	Pro	Val	Thr	Val	Pro	Lys	Leu	Pro
		130				135					140				
Leu	Pro	Pro	Ile	Ser	Gly	Leu	Pro	Ile	Pro	Pro	Val	Val	Gly	Pro	Asn
				150						155					160
Leu	Pro	Leu	Pro	Pro	Leu	Pro	Ile	Val	Gly	Pro	Ile	Leu	Pro	Pro	Gly
			165						170					175	
Thr	Thr	Pro	Pro	Ala	Thr	Gly	Gly	Lys	Asp	Cys	Pro	Pro	Pro	Pro	Gly
			180					185					190		
Ser	Val	Lys	Pro	Pro	Ser	Gly	Gly	Gly	Lys	Ala	Thr	Cys	Pro	Ile	Asp
		195					200					205			
Thr	Leu	Lys	Leu	Gly	Ala	Cys	Val	Asp	Leu	Leu	Gly	Gly	Leu	Val	Lys
		210					215					220			
Ile	Gly	Leu	Gly	Asp	Pro	Ala	Val	Asn	Lys	Cys	Cys	Pro	Leu	Leu	Lys
				230						235					240
Gly	Leu	Val	Glu	Ile	Glu	Ala	Ala	Ala	Cys	Leu	Cys	Thr	Thr	Leu	Lys
			245						250					255	
Leu	Lys	Ala	Leu	Asp	Leu	Asn	Leu	Tyr	Val	Pro	Asp	Ala	Leu	Gln	Leu
			260					265					270		

Leu Leu Thr Cys Gly Lys Asn Pro Pro Pro Gly Tyr Thr Cys Ser Ile
275 280 285

(2) INFORMATION FOR SEQ ID NO:667:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1777 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1777
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498811

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:667:

gaagacgaag	aagaagaaga	agaagaagaa	agcttgagac	tttctctctg	tgtgcaattt	60
cgaaatcgat	aaagacttca	actttcggtt	ctaacaatga	caatttccgt	atagtttgat	120
tttgtccacc	tctttcaccg	attacctgat	ttcatcgctg	gcgttagtca	tcaaatggga	180
gctcgttgct	caaagtcttc	attctgcttg	ttcccttctc	acttcaaadc	cgcttcagtt	240
ctcgagtctc	ctgatatcga	gaatggagga	aaagtgtggc	cgacttttaa	ggaattcaaa	300
ttggagcagc	tgaaatctgc	gaccggaggt	ttctcttcag	acaacattgt	atcagaacac	360
ggcgagaaa	ctccaaacgt	tgtctacaga	ggaaggcttg	atgatggctg	tttgattgct	420
gtcaaacgat	tcaatcgctt	tgcttgggct	gatcatcgac	agttcctgga	tgaagctaaa	480
gctgttggga	gcttgaggag	tgatagatta	gcaaacttga	ttggatgttg	ctttgaagga	540
gaagagagat	tactagtctg	tgagtttatg	cctcatgaaa	cgcttgcaaa	gcatcttttc	600
cactgggaga	ataatccgat	gaaatgggag	atgagattaa	gagttgcatt	gtgttttagca	660
caagcattgg	aattattgtg	taataaaggg	gagagctttg	tatcatgatc	tcaatgctta	720
cagggttttg	tttgacaagg	atgggaatcc	cagggtgtct	tgttttggac	tcatgaaaaa	780
tagcagagat	gggaagagtt	atagcacaaa	cttggcattt	actcctccag	agtatttgcg	840
aacgggtaga	gttacaccag	agagtgttgt	attcagtttt	ggaaccggtt	tgctcgatct	900
catgagtggg	aaacatatct	caccgagtcg	tgcgcttgac	ctaatacagag	gcaagaactg	960
tgcaatgtta	atggattctg	ctctcgaggg	tcattttctc	aacgaagacg	gaactgagct	1020
agtacgctta	gccacacgtt	gtctgcagta	tgaagctcga	gaaagaccaa	atgtgaaatc	1080
tctcgtgact	tcacttgtca	cactccagaa	ggaatctgat	gtagcttcct	acgttcttat	1140
gggtataccc	catgaaaccg	aggctgaaga	agagtctccg	ctttctttga	cacccttttg	1200
tgatgcatgc	ttaagagtgg	atcttacagc	catacaggaa	atactcagta	agattggata	1260
caaggatgat	gaaggaattg	ccaatgagct	ctcgtttcaa	atgtggacca	atcagatgca	1320
ggaatctctc	aattcgaaga	agcaaggcga	cttagctttc	cgttccaaag	attttacaac	1380
cgcggtcgat	tgctacactc	agttcataga	tgggggaaca	atggtgtcac	caacagtaac	1440
cgcacggcgg	tgctgtgcat	atctgatgaa	cgacaacgca	caagaggctc	tgacagatgc	1500
attgcagaca	caggttgtgt	ctccggattg	gccaaaccgc	ttgtatctgc	aagcggcttg	1560
cttgttcaag	ctgggtatgg	aagccgatgc	tcagcaagct	cttaaggatg	ggactacatt	1620
ggaagctaag	aagagtaaca	agcgctgata	aaatagcggt	ttcaaaaagct	tttgtatatg	1680
ctttattttg	tttcttttct	ctctatttcc	atctatatgc	gcatacatac	acatatgcgg	1740
gtgtatttat	tatatatgtg	catatacttt	tgatgcc			

(2) INFORMATION FOR SEQ ID NO:668:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 291 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..291
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498812

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:668:

Met	Lys	Asn	Ser	Arg	Asp	Gly	Lys	Ser	Tyr	Ser	Thr	Asn	Leu	Ala	Phe
1			5						10					15	
Thr	Pro	Pro	Glu	Tyr	Leu	Arg	Thr	Gly	Arg	Val	Thr	Pro	Glu	Ser	Val

20	25	30
Val Phe Ser Phe Gly Thr	Val Leu Asp Leu Met Ser Gly Lys His	
35	40	45
Ile Pro Pro Ser His Ala Leu Asp Leu Ile Arg Gly Lys Asn Cys Ala		
50	55	60
Met Leu Met Asp Ser Ala Leu Glu Gly His Phe Ser Asn Glu Asp Gly		
65	70	75
Thr Glu Leu Val Arg Leu Ala Thr Arg Cys Leu Gln Tyr Glu Ala Arg		
85	90	95
Glu Arg Pro Asn Val Lys Ser Leu Val Thr Ser Leu Val Thr Leu Gln		
100	105	110
Lys Glu Ser Asp Val Ala Ser Tyr Val Leu Met Gly Ile Pro His Glu		
115	120	125
Thr Glu Ala Glu Glu Glu Ser Pro Leu Ser Leu Thr Pro Phe Gly Asp		
130	135	140
Ala Cys Leu Arg Val Asp Leu Thr Ala Ile Gln Glu Ile Leu Ser Lys		
145	150	155
Ile Gly Tyr Lys Asp Asp Glu Gly Ile Ala Asn Glu Leu Ser Phe Gln		
165	170	175
Met Trp Thr Asn Gln Met Gln Glu Ser Leu Asn Ser Lys Lys Gln Gly		
180	185	190
Asp Leu Ala Phe Arg Ser Lys Asp Phe Thr Thr Ala Val Asp Cys Tyr		
195	200	205
Thr Gln Phe Ile Asp Gly Gly Thr Met Val Ser Pro Thr Val His Ala		
210	215	220
Arg Arg Cys Leu Ser Tyr Leu Met Asn Asp Asn Ala Gln Glu Ala Leu		
225	230	235
Thr Asp Ala Leu Gln Thr Gln Val Val Ser Pro Asp Trp Pro Thr Ala		
245	250	255
Leu Tyr Leu Gln Ala Ala Cys Leu Phe Lys Leu Gly Met Glu Ala Asp		
260	265	270
Ala Gln Gln Ala Leu Lys Asp Gly Thr Thr Leu Glu Ala Lys Lys Ser		
275	280	285
Asn Lys Arg		
290		

(2) INFORMATION FOR SEQ ID NO:669:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 248 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..248
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498813

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:669:

Met Ser Gly Lys His Ile Pro Pro Ser His Ala Leu Asp Leu Ile Arg		
1	5	10
Gly Lys Asn Cys Ala Met Leu Met Asp Ser Ala Leu Glu Gly His Phe		
20	25	30
Ser Asn Glu Asp Gly Thr Glu Leu Val Arg Leu Ala Thr Arg Cys Leu		
35	40	45
Gln Tyr Glu Ala Arg Glu Arg Pro Asn Val Lys Ser Leu Val Thr Ser		
50	55	60
Leu Val Thr Leu Gln Lys Glu Ser Asp Val Ala Ser Tyr Val Leu Met		
65	70	75
Gly Ile Pro His Glu Thr Glu Ala Glu Glu Glu Ser Pro Leu Ser Leu		
85	90	95
Thr Pro Phe Gly Asp Ala Cys Leu Arg Val Asp Leu Thr Ala Ile Gln		
100	105	110

Glu Ile Leu Ser Lys Ile Gly Tyr Lys Asp Asp Glu Gly Ile Ala Asn
115 120 125
Glu Leu Ser Phe Gln Met Trp Thr Asn Gln Met Gln Glu Ser Leu Asn
130 135 140
Ser Lys Lys Gln Gly Asp Leu Ala Phe Arg Ser Lys Asp Phe Thr Thr
145 150 155 160
Ala Val Asp Cys Tyr Thr Gln Phe Ile Asp Gly Gly Thr Met Val Ser
165 170 175
Pro Thr Val His Ala Arg Arg Cys Leu Ser Tyr Leu Met Asn Asp Asn
180 185 190
Ala Gln Glu Ala Leu Thr Asp Ala Leu Gln Thr Gln Val Val Ser Pro
195 200 205
Asp Trp Pro Thr Ala Leu Tyr Leu Gln Ala Ala Cys Leu Phe Lys Leu
210 215 220
Gly Met Glu Ala Asp Ala Gln Gln Ala Leu Lys Asp Gly Thr Thr Leu
225 230 235 240
Glu Ala Lys Lys Ser Asn Lys Arg
245

(2) INFORMATION FOR SEQ ID NO:670:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 227 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..227
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498814

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:670:

Met Leu Met Asp Ser Ala Leu Glu Gly His Phe Ser Asn Glu Asp Gly
1 5 10 15
Thr Glu Leu Val Arg Leu Ala Thr Arg Cys Leu Gln Tyr Glu Ala Arg
20 25 30
Glu Arg Pro Asn Val Lys Ser Leu Val Thr Ser Leu Val Thr Leu Gln
35 40 45
Lys Glu Ser Asp Val Ala Ser Tyr Val Leu Met Gly Ile Pro His Glu
50 55 60
Thr Glu Ala Glu Glu Glu Ser Pro Leu Ser Leu Thr Pro Phe Gly Asp
65 70 75 80
Ala Cys Leu Arg Val Asp Leu Thr Ala Ile Gln Glu Ile Leu Ser Lys
85 90 95
Ile Gly Tyr Lys Asp Asp Glu Gly Ile Ala Asn Glu Leu Ser Phe Gln
100 105 110
Met Trp Thr Asn Gln Met Gln Glu Ser Leu Asn Ser Lys Lys Gln Gly
115 120 125
Asp Leu Ala Phe Arg Ser Lys Asp Phe Thr Thr Ala Val Asp Cys Tyr
130 135 140
Thr Gln Phe Ile Asp Gly Gly Thr Met Val Ser Pro Thr Val His Ala
145 150 155 160
Arg Arg Cys Leu Ser Tyr Leu Met Asn Asp Asn Ala Gln Glu Ala Leu
165 170 175
Thr Asp Ala Leu Gln Thr Gln Val Val Ser Pro Asp Trp Pro Thr Ala
180 185 190
Leu Tyr Leu Gln Ala Ala Cys Leu Phe Lys Leu Gly Met Glu Ala Asp
195 200 205
Ala Gln Gln Ala Leu Lys Asp Gly Thr Thr Leu Glu Ala Lys Lys Ser
210 215 220
Asn Lys Arg
225

(2) INFORMATION FOR SEQ ID NO:671:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1368 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
 (A) NAME/KEY: -
 (B) LOCATION: 1..1368
 (D) OTHER INFORMATION: / Ceres Seq. ID 1498815
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:671:

```
aaaataagct tatcattctt acaaaaatat ttctgggttt ctgatattgt tcttgttctc      60
ttgaatcttt attacttgaa aaacatataa agtgatggcg gttgtggttg aagaagggtg      120
ggtgttgaat catggagggtg aagagcttgt ggatttgcca cctggtttca ggtttcatcc      180
aacagacgaa gagatcataa catgttacct taaggagaaag gttttaaaaca gccgattcac      240
ggctgtggcc atggggagaag ctgatctcaa caagtgtgag ccttgggatt tgccaatagg      300
gcaaagatgg gggagaaaga gttctacttc ttctgtcaaa gggacaggaa gtatccgact      360
gggatgagga cgaaccgtgc gacggagtca ggatactgga aagccaccgg gaaggataag      420
gagatcttca aaggcaaaag ttgtctcggt gggaatgaaga aaacacttgt gttttataga      480
ggaagagctc caaaagggtga aaagactaat tgggtcatgc atgaatatcg tcttgaaggc      540
aaatattcgt attacaatct cccaaaatct gcaagggacg aatgggtcgt gtgtagggtt      600
tttcacaaga acaatccttc taccacaacc caaccaatga cgagaatacc cgttgaagat      660
ttcacaagga tggattctct agagaacatt gatcatctcc tagacttctc atctcttctc      720
cctctcatag acccgagttt catgagtcaa accgaacaac caaacttcaa acccatcaac      780
cctccaactt acgatatctc atcaccaatc caaccccatc atttcaattc ttaccaatca      840
atctttaacc accagggtttt tggttctgct tcgggctcta cgtacaacaa caacaacgag      900
atgatcaaga tggagcaatc acttgttagt gtatctcaag aaacatgcct aagctcagat      960
gtgaacgcga acatgactac aaccacggag gtatcttcgg gtcctgtaat gaaacaagaa     1020
atggggatga tgggaatggt gaatggtagc aagtcgtatg aagatctatg tgacttgagg     1080
ggggacttgt gggacttcta attaatcatt tgactgtggt gaaagagtat atttgttggg     1140
atttaaataca tgttagttaa tacatatata tataggattt actagaggct taatcctagt     1200
taactatttt cacttcattg atattattta attagttgat tgtttaatta gtttatactt     1260
tatagtgtgg ttaaaaaaga aaagaaagga ttgtgataat ttgggatttt agtgcataag     1320
ttatatctca atgtaaactg tatttgtata catataatta gtcttctc
```

- (2) INFORMATION FOR SEQ ID NO:672:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 264 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: peptide
 (ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..264
 (D) OTHER INFORMATION: / Ceres Seq. ID 1498816
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:672:

```
Met Gly Glu Lys Glu Phe Tyr Phe Phe Cys Gln Arg Asp Arg Lys Tyr
1          5          10          15
Pro Thr Gly Met Arg Thr Asn Arg Ala Thr Glu Ser Gly Tyr Trp Lys
          20          25          30
Ala Thr Gly Lys Asp Lys Glu Ile Phe Lys Gly Lys Gly Cys Leu Val
          35          40          45
Gly Met Lys Lys Thr Leu Val Phe Tyr Arg Gly Arg Ala Pro Lys Gly
          50          55          60
Glu Lys Thr Asn Trp Val Met His Glu Tyr Arg Leu Glu Gly Lys Tyr
65          70          75          80
Ser Tyr Tyr Asn Leu Pro Lys Ser Ala Arg Asp Glu Trp Val Val Cys
          85          90          95
Arg Val Phe His Lys Asn Asn Pro Ser Thr Thr Thr Gln Pro Met Thr
          100         105         110
Arg Ile Pro Val Glu Asp Phe Thr Arg Met Asp Ser Leu Glu Asn Ile
```

115 120 125
Asp His Leu Leu Asp Phe Ser Ser Leu Pro Pro Leu Ile Asp Pro Ser
130 135 140
Phe Met Ser Gln Thr Glu Gln Pro Asn Phe Lys Pro Ile Asn Pro Pro
145 150 155 160
Thr Tyr Asp Ile Ser Ser Pro Ile Gln Pro His His Phe Asn Ser Tyr
165 170 175
Gln Ser Ile Phe Asn His Gln Val Phe Gly Ser Ala Ser Gly Ser Thr
180 185 190
Tyr Asn Asn Asn Asn Glu Met Ile Lys Met Glu Gln Ser Leu Val Ser
195 200 205
Val Ser Gln Glu Thr Cys Leu Ser Ser Asp Val Asn Ala Asn Met Thr
210 215 220
Thr Thr Thr Glu Val Ser Ser Gly Pro Val Met Lys Gln Glu Met Gly
225 230 235 240
Met Met Gly Met Val Asn Gly Ser Lys Ser Tyr Glu Asp Leu Cys Asp
245 250 255
Leu Arg Gly Asp Leu Trp Asp Phe
260

(2) INFORMATION FOR SEQ ID NO:673:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 245 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..245
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498817

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:673:

Met Arg Thr Asn Arg Ala Thr Glu Ser Gly Tyr Trp Lys Ala Thr Gly
1 5 10 15
Lys Asp Lys Glu Ile Phe Lys Gly Lys Gly Cys Leu Val Gly Met Lys
20 25 30
Lys Thr Leu Val Phe Tyr Arg Gly Arg Ala Pro Lys Gly Glu Lys Thr
35 40 45
Asn Trp Val Met His Glu Tyr Arg Leu Glu Gly Lys Tyr Ser Tyr Tyr
50 55 60
Asn Leu Pro Lys Ser Ala Arg Asp Glu Trp Val Val Cys Arg Val Phe
65 70 75 80
His Lys Asn Asn Pro Ser Thr Thr Thr Gln Pro Met Thr Arg Ile Pro
85 90 95
Val Glu Asp Phe Thr Arg Met Asp Ser Leu Glu Asn Ile Asp His Leu
100 105 110
Leu Asp Phe Ser Ser Leu Pro Pro Leu Ile Asp Pro Ser Phe Met Ser
115 120 125
Gln Thr Glu Gln Pro Asn Phe Lys Pro Ile Asn Pro Pro Thr Tyr Asp
130 135 140
Ile Ser Ser Pro Ile Gln Pro His His Phe Asn Ser Tyr Gln Ser Ile
145 150 155 160
Phe Asn His Gln Val Phe Gly Ser Ala Ser Gly Ser Thr Tyr Asn Asn
165 170 175
Asn Asn Glu Met Ile Lys Met Glu Gln Ser Leu Val Ser Val Ser Gln
180 185 190
Glu Thr Cys Leu Ser Ser Asp Val Asn Ala Asn Met Thr Thr Thr Thr
195 200 205
Glu Val Ser Ser Gly Pro Val Met Lys Gln Glu Met Gly Met Met Gly
210 215 220
Met Val Asn Gly Ser Lys Ser Tyr Glu Asp Leu Cys Asp Leu Arg Gly
225 230 235 240

Asp Leu Trp Asp Phe
245

(2) INFORMATION FOR SEQ ID NO:674:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 215 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..215
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498818

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:674:

Met Lys Lys Thr Leu Val Phe Tyr Arg Gly Arg Ala Pro Lys Gly Glu
1 5 10 15
Lys Thr Asn Trp Val Met His Glu Tyr Arg Leu Glu Gly Lys Tyr Ser
20 25 30
Tyr Tyr Asn Leu Pro Lys Ser Ala Arg Asp Glu Trp Val Val Cys Arg
35 40 45
Val Phe His Lys Asn Asn Pro Ser Thr Thr Thr Gln Pro Met Thr Arg
50 55 60
Ile Pro Val Glu Asp Phe Thr Arg Met Asp Ser Leu Glu Asn Ile Asp
65 70 75 80
His Leu Leu Asp Phe Ser Ser Leu Pro Pro Leu Ile Asp Pro Ser Phe
85 90 95
Met Ser Gln Thr Glu Gln Pro Asn Phe Lys Pro Ile Asn Pro Pro Thr
100 105 110
Tyr Asp Ile Ser Ser Pro Ile Gln Pro His His Phe Asn Ser Tyr Gln
115 120 125
Ser Ile Phe Asn His Gln Val Phe Gly Ser Ala Ser Gly Ser Thr Tyr
130 135 140
Asn Asn Asn Asn Glu Met Ile Lys Met Glu Gln Ser Leu Val Ser Val
145 150 155 160
Ser Gln Glu Thr Cys Leu Ser Ser Asp Val Asn Ala Asn Met Thr Thr
165 170 175
Thr Thr Glu Val Ser Ser Gly Pro Val Met Lys Gln Glu Met Gly Met
180 185 190
Met Gly Met Val Asn Gly Ser Lys Ser Tyr Glu Asp Leu Cys Asp Leu
195 200 205
Arg Gly Asp Leu Trp Asp Phe
210 215

(2) INFORMATION FOR SEQ ID NO:675:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1898 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1898
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498823

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:675:

aaaaaatttaa gtgatcatca cttctcctcc tttatcgaga gcttcagttt tagagcaaca	60
atgtctctat ttctgaagcc cttcctcttc ctatacgaca ccactcttag tcttctctta	120
cttctgttca atggatggag tcttgaggat acagcagcag cccaaaagag gcgtgaagca	180
gacaaaaatg ctgcagaaac tgaatggatc caactccaat acttgtggac caaaacaagg	240
agtgttgtac tacttcccg tttcaagggt ttgggtggtta tgtgtttggt tctatccatt	300
atagtgttct tcgagagttt ttacatgaac tttgtgatac tcttcgtcaa gttattttaa	360
cgtaaaccctc ataaagtgtc caaatggggag gccatgcaag aagatgttga ggttggacc	420

gataactacc	caatggttct	tatccaaata	ccaatgtaca	atgaaaaaga	ggtctttcaa	480
ttatctatag	cagcaatatg	tagtttggtc	tggccatcga	gccgtctagt	agttcaagtt	540
gtagatgatt	ctacggatcc	ggccgtaagg	gaaggtgtgg	acgtagagat	tgcaaaatgg	600
caaagccaag	gcataaacat	aaggtgtgaa	aggagagata	acaggaacgg	ctacaaagcc	660
ggagctatga	aagaagctct	tacgcagagc	tacgtcaagc	aatgcgactt	cgtagcagtc	720
ttcgatgctg	atttccaacc	cgagcccgat	tatctcatcc	gcgctgtccc	tttccttgtc	780
cacaaccctg	acgttgctct	agttcaagcc	cgatggatat	ttgttaacgc	gaacaaatgc	840
ttgatgacga	ggatgcaaga	gatgtctctc	aactatcatt	tcaaagtggg	acaagaatca	900
gggtcgacta	gacatgcttt	cttcggggtt	aatggaaccg	cgggtgtatg	gagaatatcg	960
gcaatggaag	cagcaggagg	atggaaatca	aggaccacag	tagaggacat	ggacttggct	1020
gttcgtgttg	gtcttcattg	ctggaaattt	gtctacctta	acgacctcac	ggtgagaaac	1080
gagcttccaa	gcaaatttaa	ggcctacaga	ttccagcaac	ataggtggtc	ctgtggaccg	1140
gcgaatctat	ttagaaaaat	gacgatggag	atcattttca	ataagagagt	atcaatttgg	1200
aagaagtttt	atgtgatcta	cagctttttc	ttcgtaagga	aagtggcggg	acacttcttg	1260
acattcttct	tctactgtat	aattgtgcca	acaagtgtct	tcttccctga	aatccacatc	1320
ccatcttggt	ctaccattta	cgttccctct	ttgatcagta	tcttccacac	cctggcaact	1380
ccaagatcct	tctacctcgt	gatatttttg	gtcttggtcg	agaatgtaat	ggctatgcat	1440
cgaaccaaag	gtacgtgcat	tggcctactt	gaaggaggaa	gagtaaacga	atgggttggtg	1500
accgaaaaaa	taggagatgc	tttgaagagt	aagctactct	ctcgggtagt	ccaaagaaaa	1560
tcttgttatc	aaagagtga	ttccaaggaa	gtgatgggtg	gggtatacat	attaggatgt	1620
gcactctatg	gcctgatcta	tgggcacaca	tggttacatt	tctatctttt	tcttcaggcc	1680
acagcctttt	tcgtctccgg	ttttggtttt	gtcggaacgg	cctaagaacc	ttccctgccc	1740
attattttta	gtcaccaaat	aaattctcca	tgttttagtt	cttattttaca	ctttttattta	1800
ttttgacacc	attgtacggt	ttggacccca	tatcatcatg	ttgtataagt	ataacgaata	1860
atgatttttt	gtttgtttga	atgtatgcgt	catcgcgt			

(2) INFORMATION FOR SEQ ID NO:676:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 574 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..574

(D) OTHER INFORMATION: / Ceres Seq. ID 1498824

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:676:

Lys	Lys	Leu	Ser	Asp	His	His	Phe	Ser	Ser	Phe	Ile	Glu	Ser	Phe	Ser
1			5					10						15	
Phe	Arg	Ala	Thr	Met	Ser	Leu	Phe	Leu	Lys	Pro	Phe	Leu	Phe	Leu	Tyr
			20					25					30		
Asp	Thr	Thr	Leu	Ser	Leu	Leu	Leu	Leu	Phe	Asn	Gly	Trp	Ser	Leu	
			35				40				45				
Glu	Asp	Thr	Ala	Ala	Ala	Gln	Lys	Arg	Arg	Glu	Ala	Asp	Lys	Asn	Ala
			50				55				60				
Ala	Glu	Thr	Glu	Trp	Ile	Gln	Leu	Gln	Tyr	Leu	Trp	Thr	Lys	Thr	Arg
65					70				75					80	
Ser	Val	Val	Leu	Leu	Pro	Val	Phe	Lys	Gly	Leu	Val	Val	Met	Cys	Leu
			85					90					95		
Val	Leu	Ser	Ile	Ile	Val	Phe	Phe	Glu	Ser	Phe	Tyr	Met	Asn	Phe	Val
			100					105					110		
Ile	Leu	Phe	Val	Lys	Leu	Phe	Lys	Arg	Lys	Pro	His	Lys	Val	Tyr	Lys
			115				120					125			
Trp	Glu	Ala	Met	Gln	Glu	Asp	Val	Glu	Val	Gly	Pro	Asp	Asn	Tyr	Pro
			130			135				140					
Met	Val	Leu	Ile	Gln	Ile	Pro	Met	Tyr	Asn	Glu	Lys	Glu	Val	Phe	Gln
145				150					155					160	
Leu	Ser	Ile	Ala	Ala	Ile	Cys	Ser	Leu	Val	Trp	Pro	Ser	Ser	Arg	Leu
			165					170						175	
Val	Val	Gln	Val	Val	Asp	Asp	Ser	Thr	Asp	Pro	Ala	Val	Arg	Glu	Gly
			180					185						190	

Val Asp Val Glu Ile Ala Lys Trp Gln Ser Gln Gly Ile Asn Ile Arg
195 200 205
Cys Glu Arg Arg Asp Asn Arg Asn Gly Tyr Lys Ala Gly Ala Met Lys
210 215 220
Glu Ala Leu Thr Gln Ser Tyr Val Lys Gln Cys Asp Phe Val Ala Val
225 230 235 240
Phe Asp Ala Asp Phe Gln Pro Glu Pro Asp Tyr Leu Ile Arg Ala Val
245 250 255
Pro Phe Leu Val His Asn Pro Asp Val Ala Leu Val Gln Ala Arg Trp
260 265 270
Ile Phe Val Asn Ala Asn Lys Cys Leu Met Thr Arg Met Gln Glu Met
275 280 285
Ser Leu Asn Tyr His Phe Lys Val Glu Gln Glu Ser Gly Ser Thr Arg
290 295 300
His Ala Phe Phe Gly Phe Asn Gly Thr Ala Gly Val Trp Arg Ile Ser
305 310 315 320
Ala Met Glu Ala Ala Gly Gly Trp Lys Ser Arg Thr Thr Val Glu Asp
325 330 335
Met Asp Leu Ala Val Arg Val Gly Leu His Gly Trp Lys Phe Val Tyr
340 345 350
Leu Asn Asp Leu Thr Val Arg Asn Glu Leu Pro Ser Lys Phe Lys Ala
355 360 365
Tyr Arg Phe Gln Gln His Arg Trp Ser Cys Gly Pro Ala Asn Leu Phe
370 375 380
Arg Lys Met Thr Met Glu Ile Ile Phe Asn Lys Arg Val Ser Ile Trp
385 390 395 400
Lys Lys Phe Tyr Val Ile Tyr Ser Phe Phe Phe Val Arg Lys Val Ala
405 410 415
Val His Phe Leu Thr Phe Phe Phe Tyr Cys Ile Ile Val Pro Thr Ser
420 425 430
Val Phe Phe Pro Glu Ile His Ile Pro Ser Trp Ser Thr Ile Tyr Val
435 440 445
Pro Ser Leu Ile Ser Ile Phe His Thr Leu Ala Thr Pro Arg Ser Phe
450 455 460
Tyr Leu Val Ile Phe Trp Val Leu Phe Glu Asn Val Met Ala Met His
465 470 475 480
Arg Thr Lys Gly Thr Cys Ile Gly Leu Leu Glu Gly Gly Arg Val Asn
485 490 495
Glu Trp Val Val Thr Glu Lys Leu Gly Asp Ala Leu Lys Ser Lys Leu
500 505 510
Leu Ser Arg Val Val Gln Arg Lys Ser Cys Tyr Gln Arg Val Asn Ser
515 520 525
Lys Glu Val Met Val Gly Val Tyr Ile Leu Gly Cys Ala Leu Tyr Gly
530 535 540
Leu Ile Tyr Gly His Thr Trp Leu His Phe Tyr Leu Phe Leu Gln Ala
545 550 555 560
Thr Ala Phe Phe Val Ser Gly Phe Gly Phe Val Gly Thr Ala
565 570

(2) INFORMATION FOR SEQ ID NO:677:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 554 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..554
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498825

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:677:

Met Ser Leu Phe Leu Lys Pro Phe Leu Phe Leu Tyr Asp Thr Thr Leu

1					5					10					15				
Ser	Leu	Leu	Leu	Leu	Leu	Phe	Asn	Gly	Trp	Ser	Leu	Glu	Asp	Thr	Ala				
			20					25					30						
Ala	Ala	Gln	Lys	Arg	Arg	Glu	Ala	Asp	Lys	Asn	Ala	Ala	Glu	Thr	Glu				
		35					40					45							
Trp	Ile	Gln	Leu	Gln	Tyr	Leu	Trp	Thr	Lys	Thr	Arg	Ser	Val	Val	Leu				
	50					55					60								
Leu	Pro	Val	Phe	Lys	Gly	Leu	Val	Val	Met	Cys	Leu	Val	Leu	Ser	Ile				
65					70					75					80				
Ile	Val	Phe	Phe	Glu	Ser	Phe	Tyr	Met	Asn	Phe	Val	Ile	Leu	Phe	Val				
				85					90					95					
Lys	Leu	Phe	Lys	Arg	Lys	Pro	His	Lys	Val	Tyr	Lys	Trp	Glu	Ala	Met				
			100					105					110						
Gln	Glu	Asp	Val	Glu	Val	Gly	Pro	Asp	Asn	Tyr	Pro	Met	Val	Leu	Ile				
		115					120					125							
Gln	Ile	Pro	Met	Tyr	Asn	Glu	Lys	Glu	Val	Phe	Gln	Leu	Ser	Ile	Ala				
	130					135					140								
Ala	Ile	Cys	Ser	Leu	Val	Trp	Pro	Ser	Ser	Arg	Leu	Val	Val	Gln	Val				
145				150						155					160				
Val	Asp	Asp	Ser	Thr	Asp	Pro	Ala	Val	Arg	Glu	Gly	Val	Asp	Val	Glu				
				165					170					175					
Ile	Ala	Lys	Trp	Gln	Ser	Gln	Gly	Ile	Asn	Ile	Arg	Cys	Glu	Arg	Arg				
		180						185					190						
Asp	Asn	Arg	Asn	Gly	Tyr	Lys	Ala	Gly	Ala	Met	Lys	Glu	Ala	Leu	Thr				
	195						200					205							
Gln	Ser	Tyr	Val	Lys	Gln	Cys	Asp	Phe	Val	Ala	Val	Phe	Asp	Ala	Asp				
	210				215						220								
Phe	Gln	Pro	Glu	Pro	Asp	Tyr	Leu	Ile	Arg	Ala	Val	Pro	Phe	Leu	Val				
225					230					235					240				
His	Asn	Pro	Asp	Val	Ala	Leu	Val	Gln	Ala	Arg	Trp	Ile	Phe	Val	Asn				
			245					250					255						
Ala	Asn	Lys	Cys	Leu	Met	Thr	Arg	Met	Gln	Glu	Met	Ser	Leu	Asn	Tyr				
		260						265					270						
His	Phe	Lys	Val	Glu	Gln	Glu	Ser	Gly	Ser	Thr	Arg	His	Ala	Phe	Phe				
	275						280					285							
Gly	Phe	Asn	Gly	Thr	Ala	Gly	Val	Trp	Arg	Ile	Ser	Ala	Met	Glu	Ala				
	290					295					300								
Ala	Gly	Gly	Trp	Lys	Ser	Arg	Thr	Thr	Val	Glu	Asp	Met	Asp	Leu	Ala				
305				310						315					320				
Val	Arg	Val	Gly	Leu	His	Gly	Trp	Lys	Phe	Val	Tyr	Leu	Asn	Asp	Leu				
				325					330					335					
Thr	Val	Arg	Asn	Glu	Leu	Pro	Ser	Lys	Phe	Lys	Ala	Tyr	Arg	Phe	Gln				
			340					345					350						
Gln	His	Arg	Trp	Ser	Cys	Gly	Pro	Ala	Asn	Leu	Phe	Arg	Lys	Met	Thr				
	355						360					365							
Met	Glu	Ile	Ile	Phe	Asn	Lys	Arg	Val	Ser	Ile	Trp	Lys	Lys	Phe	Tyr				
	370					375					380								
Val	Ile	Tyr	Ser	Phe	Phe	Phe	Val	Arg	Lys	Val	Ala	Val	His	Phe	Leu				
385				390						395					400				
Thr	Phe	Phe	Phe	Tyr	Cys	Ile	Ile	Val	Pro	Thr	Ser	Val	Phe	Phe	Pro				
				405				410					415						
Glu	Ile	His	Ile	Pro	Ser	Trp	Ser	Thr	Ile	Tyr	Val	Pro	Ser	Leu	Ile				
			420					425					430						
Ser	Ile	Phe	His	Thr	Leu	Ala	Thr	Pro	Arg	Ser	Phe	Tyr	Leu	Val	Ile				
	435						440					445							
Phe	Trp	Val	Leu	Phe	Glu	Asn	Val	Met	Ala	Met	His	Arg	Thr	Lys	Gly				
	450					455					460								
Thr	Cys	Ile	Gly	Leu	Leu	Glu	Gly	Gly	Arg	Val	Asn	Glu	Trp	Val	Val				
465				470					475						480				
Thr	Glu	Lys	Leu	Gly	Asp	Ala	Leu	Lys	Ser	Lys	Leu	Leu	Ser	Arg	Val				
				485					490					495					

Val Gln Arg Lys Ser Cys Tyr Gln Arg Val Asn Ser Lys Glu Val Met
500 505 510
Val Gly Val Tyr Ile Leu Gly Cys Ala Leu Tyr Gly Leu Ile Tyr Gly
515 520 525
His Thr Trp Leu His Phe Tyr Leu Phe Leu Gln Ala Thr Ala Phe Phe
530 535 540
Val Ser Gly Phe Gly Phe Val Gly Thr Ala
545 550

(2) INFORMATION FOR SEQ ID NO:678:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 481 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..481
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498826

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:678:

Met Cys Leu Val Leu Ser Ile Ile Val Phe Phe Glu Ser Phe Tyr Met
1 5 10 15
Asn Phe Val Ile Leu Phe Val Lys Leu Phe Lys Arg Lys Pro His Lys
20 25 30
Val Tyr Lys Trp Glu Ala Met Gln Glu Asp Val Glu Val Gly Pro Asp
35 40 45
Asn Tyr Pro Met Val Leu Ile Gln Ile Pro Met Tyr Asn Glu Lys Glu
50 55 60
Val Phe Gln Leu Ser Ile Ala Ala Ile Cys Ser Leu Val Trp Pro Ser
65 70 75 80
Ser Arg Leu Val Val Gln Val Val Asp Asp Ser Thr Asp Pro Ala Val
85 90 95
Arg Glu Gly Val Asp Val Glu Ile Ala Lys Trp Gln Ser Gln Gly Ile
100 105 110
Asn Ile Arg Cys Glu Arg Arg Asp Asn Arg Asn Gly Tyr Lys Ala Gly
115 120 125
Ala Met Lys Glu Ala Leu Thr Gln Ser Tyr Val Lys Gln Cys Asp Phe
130 135 140
Val Ala Val Phe Asp Ala Asp Phe Gln Pro Glu Pro Asp Tyr Leu Ile
145 150 155 160
Arg Ala Val Pro Phe Leu Val His Asn Pro Asp Val Ala Leu Val Gln
165 170 175
Ala Arg Trp Ile Phe Val Asn Ala Asn Lys Cys Leu Met Thr Arg Met
180 185 190
Gln Glu Met Ser Leu Asn Tyr His Phe Lys Val Glu Gln Glu Ser Gly
195 200 205
Ser Thr Arg His Ala Phe Phe Gly Phe Asn Gly Thr Ala Gly Val Trp
210 215 220
Arg Ile Ser Ala Met Glu Ala Ala Gly Gly Trp Lys Ser Arg Thr Thr
225 230 235 240
Val Glu Asp Met Asp Leu Ala Val Arg Val Gly Leu His Gly Trp Lys
245 250 255
Phe Val Tyr Leu Asn Asp Leu Thr Val Arg Asn Glu Leu Pro Ser Lys
260 265 270
Phe Lys Ala Tyr Arg Phe Gln Gln His Arg Trp Ser Cys Gly Pro Ala
275 280 285
Asn Leu Phe Arg Lys Met Thr Met Glu Ile Ile Phe Asn Lys Arg Val
290 295 300
Ser Ile Trp Lys Lys Phe Tyr Val Ile Tyr Ser Phe Phe Phe Val Arg
305 310 315 320
Lys Val Ala Val His Phe Leu Thr Phe Phe Phe Tyr Cys Ile Ile Val

325 330 335
Pro Thr Ser Val Phe Phe Pro Glu Ile His Ile Pro Ser Trp Ser Thr
340 345 350
Ile Tyr Val Pro Ser Leu Ile Ser Ile Phe His Thr Leu Ala Thr Pro
355 360 365
Arg Ser Phe Tyr Leu Val Ile Phe Trp Val Leu Phe Glu Asn Val Met
370 375 380
Ala Met His Arg Thr Lys Gly Thr Cys Ile Gly Leu Leu Glu Gly Gly
385 390 395 400
Arg Val Asn Glu Trp Val Val Thr Glu Lys Leu Gly Asp Ala Leu Lys
405 410 415
Ser Lys Leu Leu Ser Arg Val Val Gln Arg Lys Ser Cys Tyr Gln Arg
420 425 430
Val Asn Ser Lys Glu Val Met Val Gly Val Tyr Ile Leu Gly Cys Ala
435 440 445
Leu Tyr Gly Leu Ile Tyr Gly His Thr Trp Leu His Phe Tyr Leu Phe
450 455 460
Leu Gln Ala Thr Ala Phe Phe Val Ser Gly Phe Gly Phe Val Gly Thr
465 470 475 480
Ala

(2) INFORMATION FOR SEQ ID NO:679:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 518 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..518
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498829

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:679:

ttccaaggaa aaaaaaagtc tttaccgta aacatttttt ctccatcttc ttgatatcaa	60
caaaacacac ctcaacaaaa aaaaaaaaaa aacttcatct ctctcagatt tcgaaattga	120
cccgctcggtg attcttaatc tctcctctct gttcttctcc gatcaaacct cattccaaag	180
aaacaaacca tggatctcca accagaagag cttcaattct tgacaatacc tcaactactt	240
caagaatcaa tctcaatcaa gaaacgatct ccaagaacct tctacctcat aaccctctcc	300
ttcatcttcc ctctctcctt cgctatcctc gctcaactcac tcttcaactca accaatctta	360
gccaaactcg acaaatccga cccaccaaac tcagatcggt cacgcatga ttggactgtt	420
cttctaattc tccagttcag ttacttgatc ttctcttttg ccttctctct tctctcaacc	480
gctgcwgtwg tcttcaccgt cgcttctctt tacaccgg	

(2) INFORMATION FOR SEQ ID NO:680:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 109 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..109
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498830

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:680:

Met Asp Leu Gln Pro Glu Glu Leu Gln Phe Leu Thr Ile Pro Gln Leu
1 5 10 15
Leu Gln Glu Ser Ile Ser Ile Lys Lys Arg Ser Pro Arg Thr Phe Tyr
20 25 30
Leu Ile Thr Leu Ser Phe Ile Phe Pro Leu Ser Phe Ala Ile Leu Ala
35 40 45
His Ser Leu Phe Thr Gln Pro Ile Leu Ala Lys Leu Asp Lys Ser Asp

(2) INFORMATION FOR SEQ ID NO:681:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:681:

(2) INFORMATION FOR SEQ ID NO:682:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:682:

[illegible]

(2) INFORMATION FOR SEQ ID NO:683:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 487 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..487
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498841

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:683:

aatttaaatt tctcttttcta tctactataa aaagtgactc tctaagaact ccaaagatta	60
gaacattgaa ttgaattagc catggagaag aatactttctc aaaccatctt ctccaacttt	120
tttcttctcc ttctcctttc ttcattgtgtc tctgtctcagc tccggacagg tttctaccag	180
aactcatgtc cgaacgtgga aaccattgta cgtaacgctg tccgtcagaa attccagcag	240
actttcgtta ccgctccggc cactcttcgc ctcttcttcc acgattgctt cgttcgtgga	300
tgtgatgcgt caataatgat agcatcacca tcggagagag accatccaga tgacatgtca	360
ttggccggag acggattcga cacggtggtg aaggcgaaca agccgttgat agcaatccca	420
attgccgcaa caaagtctca tgtgctgaca ttttggtctc cgccactcgt gaagtcgtcg	480
ttttgac	

(2) INFORMATION FOR SEQ ID NO:684:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 134 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..134
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498842

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:684:

Met	Glu	Lys	Asn	Thr	Ser	Gln	Thr	Ile	Phe	Ser	Asn	Phe	Phe	Leu	Leu
1			5					10						15	
Leu	Leu	Leu	Ser	Ser	Cys	Val	Ser	Ala	Gln	Leu	Arg	Thr	Gly	Phe	Tyr
			20					25					30		
Gln	Asn	Ser	Cys	Pro	Asn	Val	Glu	Thr	Ile	Val	Arg	Asn	Ala	Val	Arg
			35				40					45			
Gln	Lys	Phe	Gln	Gln	Thr	Phe	Val	Thr	Ala	Pro	Ala	Thr	Leu	Arg	Leu
			50			55					60				
Phe	Phe	His	Asp	Cys	Phe	Val	Arg	Gly	Cys	Asp	Ala	Ser	Ile	Met	Ile
65					70				75					80	
Ala	Ser	Pro	Ser	Glu	Arg	Asp	His	Pro	Asp	Asp	Met	Ser	Leu	Ala	Gly
				85					90					95	
Asp	Gly	Phe	Asp	Thr	Val	Val	Lys	Ala	Asn	Lys	Pro	Leu	Ile	Ala	Ile
			100					105					110		
Pro	Ile	Ala	Ala	Thr	Lys	Ser	His	Val	Leu	Thr	Phe	Trp	Leu	Ser	Pro
			115				120					125			
Leu	Val	Lys	Ser	Ser	Phe										

(2) INFORMATION FOR SEQ ID NO:685:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 527 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..527

(D) OTHER INFORMATION: / Ceres Seq. ID 1498843

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:685:

aaaatccgaa	aaagaccaat	caatcctttc	tccctgaaat	ggcggcgggt	ctgcagacga	60
atatccggac	ggtcaaggtt	ccggctacgt	tcagagctgt	aagtaaacag	tcattggcac	120
cctttagagt	aagatgtgct	gttgcttccc	ctgggaaaaa	acgatacacc	atcactctcc	180
ttcccggaga	cggcatcggg	ccggagggtg	tctccattgc	caaaaatgtg	cttcagcaag	240
ctggatcttt	ggaaggtgtg	gaatttaact	tccgtgagat	gcccattgga	ggagctgctt	300
tggatttggt	cggagtgtcc	ttgccggagg	agactatctc	agctgcaaaa	gaatcagatg	360
cagtgtctct	tggagccatt	ggagggtaca	aatgggataa	caatgaaaaa	catctgaggg	420
ctgagaaggg	gttacttcag	attcgtgcag	ctctcaaagt	ctttgcaa	atctgagacctg	480
ctacagttct	cccacagtta	gtggatgctt	ccaccttaaa	gagagag		

(2) INFORMATION FOR SEQ ID NO:686:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 175 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..175

(D) OTHER INFORMATION: / Ceres Seq. ID 1498844

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:686:

Asn	Pro	Lys	Lys	Thr	Asn	Gln	Ser	Phe	Leu	Pro	Glu	Met	Ala	Ala	Ala	
1				5					10					15		
Leu	Gln	Thr	Asn	Ile	Arg	Thr	Val	Lys	Val	Pro	Ala	Thr	Phe	Arg	Ala	
			20					25					30			
Val	Ser	Lys	Gln	Ser	Leu	Ala	Pro	Phe	Arg	Val	Arg	Cys	Ala	Val	Ala	
		35					40					45				
Ser	Pro	Gly	Lys	Lys	Arg	Tyr	Thr	Ile	Thr	Leu	Leu	Pro	Gly	Asp	Gly	
	50				55					60						
Ile	Gly	Pro	Glu	Val	Val	Ser	Ile	Ala	Lys	Asn	Val	Leu	Gln	Gln	Ala	
65				70					75					80		
Gly	Ser	Leu	Glu	Gly	Val	Glu	Phe	Asn	Phe	Arg	Glu	Met	Pro	Ile	Gly	
			85					90					95			
Gly	Ala	Ala	Leu	Asp	Leu	Val	Gly	Val	Pro	Leu	Pro	Glu	Glu	Thr	Ile	
		100					105						110			
Ser	Ala	Ala	Lys	Glu	Ser	Asp	Ala	Val	Leu	Leu	Gly	Ala	Ile	Gly	Gly	
	115					120					125					
Tyr	Lys	Trp	Asp	Asn	Asn	Glu	Lys	His	Leu	Arg	Pro	Glu	Lys	Gly	Leu	
	130				135				140							
Leu	Gln	Ile	Arg	Ala	Ala	Leu	Lys	Val	Phe	Ala	Asn	Leu	Arg	Pro	Ala	
145				150					155						160	
Thr	Val	Leu	Pro	Gln	Leu	Val	Asp	Ala	Ser	Thr	Leu	Lys	Arg	Glu		
			165					170						175		

(2) INFORMATION FOR SEQ ID NO:687:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 163 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..163

(D) OTHER INFORMATION: / Ceres Seq. ID 1498845

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:687:

Met	Ala	Ala	Ala	Gln	Thr	Asn	Ile	Arg	Thr	Val	Lys	Val	Pro	Ala	
1				5					10				15		
Thr	Phe	Arg	Ala	Val	Ser	Lys	Gln	Ser	Leu	Ala	Pro	Phe	Arg	Val	Arg
			20					25					30		

Cys Ala Val Ala Ser Pro Gly Lys Lys Arg Tyr Thr Ile Thr Leu Leu
35 40 45
Pro Gly Asp Gly Ile Gly Pro Glu Val Val Ser Ile Ala Lys Asn Val
50 55 60
Leu Gln Gln Ala Gly Ser Leu Glu Gly Val Glu Phe Asn Phe Arg Glu
65 70 75 80
Met. Pro Ile Gly Gly Ala Ala Leu Asp Leu Val Gly Val Pro Leu Pro
85 90 95
Glu Glu Thr Ile Ser Ala Ala Lys Glu Ser Asp Ala Val Leu Leu Gly
100 105 110
Ala Ile Gly Gly Tyr Lys Trp Asp Asn Asn Glu Lys His Leu Arg Pro
115 120 125
Glu Lys Gly Leu Leu Gln Ile Arg Ala Ala Leu Lys Val Phe Ala Asn
130 135 140
Leu Arg Pro Ala Thr Val Leu Pro Gln Leu Val Asp Ala Ser Thr Leu
145 150 155 160
Lys Arg Glu

(2) INFORMATION FOR SEQ ID NO:688:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1356 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1356
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498846

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:688:

aaaccctaac	atttttcgat	tttccccgac	tttctccgac	gatgcatgag	cgatagcgat	60
ggtgattccg	gtgacttatg	ctccgacgat	tgacacgatc	atttgaggca	gtctcctttg	120
tccagatttt	cttcttcaac	ctctttctct	tgcttacc	ccaaattcat	catctttgaa	180
actgcttcat	ccctttcgct	ttggtgattc	tgaagactcc	gctttatacc	cattttgatc	240
tggagaagga	tatagatgaa	gtgctacagt	cgcatactgt	ttattcaa	gtttcgaaag	300
gagttcttgc	aaaatcgaaa	gacttgatga	agtcgtttgg	atcagatgat	catacgaaaa	360
tatgcatcga	tattttggag	aaaggagagc	ttcaagttgc	tggaaaagaa	agagaatcac	420
agttctcaag	ccagtttcg	gatatagcaa	cgattgttat	gcagaaaact	atcaaccctg	480
aaacacaacg	accttatacc	atcagcatgg	tagagcgctt	aatgcatgaa	attcattttg	540
ctgttgatcc	tcatagtaat	tccaagaagc	aggcacttga	tgtcatccgt	gagctgcaaa	600
agcacttccc	tataaagcgt	tctccaatga	gactgcgtct	tactgttcc	gttcaaaatt	660
tcccctcgct	tctggagaag	ctaaaagaat	gggatggtag	tgttgtctcc	aaagacgaat	720
ctggaacaca	gatgtccact	gtctgcgaga	tggaaccggg	cctattccga	gagtgtgatt	780
cccatgtgag	gagtatccag	ggaagactag	aaatactcgc	tgtatcagtt	catgcagaag	840
gtgacacaag	catggatcat	tacgatgagc	atgatgat	ggcattgcaa	accacacaagc	900
cgttgttacc	tgctgagact	gagactaagg	atttgaccga	tcccgtcggt	gaacttagca	960
agaaactgca	gaagcaagag	ataagtacta	cagataacat	aaagcaagaa	ggtggagaag	1020
aaaagaagg	gaccaagtgc	agcacttgca	acacgttcgt	tggagaggct	aagcaataca	1080
gagagcactg	taagagtgat	tggcacaac	acaaccttaa	gcgtaagact	cggaaactcc	1140
ctcctattag	tgctgacgaa	tgcatgtctg	agattgacat	ggacgactct	agagcagatt	1200
tgaaagacta	ctctttctga	aactacaatt	ttctcctttt	gtgcttttaa	ttttgtcaat	1260
gtgttaaatac	tcgtagtcat	atgtgagtat	gaatacacia	aacttgtgga	atgaaatttt	1320
gcgcaaactt	taagagtaaa	aacttgtgtt	taagag			

(2) INFORMATION FOR SEQ ID NO:689:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 297 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..297

(D) OTHER INFORMATION: / Ceres Seq. ID 1498847

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:689:

Met	Lys	Ser	Phe	Gly	Ser	Asp	Asp	His	Thr	Lys	Ile	Cys	Ile	Asp	Ile
1				5					10					15	
Leu	Glu	Lys	Gly	Glu	Leu	Gln	Val	Ala	Gly	Lys	Glu	Arg	Glu	Ser	Gln
			20					25					30		
Phe	Ser	Ser	Gln	Phe	Arg	Asp	Ile	Ala	Thr	Ile	Val	Met	Gln	Lys	Thr
		35					40					45			
Ile	Asn	Pro	Glu	Thr	Gln	Arg	Pro	Tyr	Thr	Ile	Ser	Met	Val	Glu	Arg
	50					55					60				
Leu	Met	His	Glu	Ile	His	Phe	Ala	Val	Asp	Pro	His	Ser	Asn	Ser	Lys
65					70				75					80	
Lys	Gln	Ala	Leu	Asp	Val	Ile	Arg	Glu	Leu	Gln	Lys	His	Phe	Pro	Ile
			85					90						95	
Lys	Arg	Ser	Pro	Met	Arg	Leu	Arg	Leu	Thr	Val	Pro	Val	Gln	Asn	Phe
			100					105					110		
Pro	Ser	Leu	Glu	Lys	Leu	Lys	Glu	Trp	Asp	Gly	Ser	Val	Val	Ser	
	115					120					125				
Lys	Asp	Glu	Ser	Gly	Thr	Gln	Met	Ser	Thr	Val	Cys	Glu	Met	Glu	Pro
	130					135					140				
Gly	Leu	Phe	Arg	Glu	Cys	Asp	Ser	His	Val	Arg	Ser	Ile	Gln	Gly	Arg
145					150				155					160	
Leu	Glu	Ile	Leu	Ala	Val	Ser	Val	His	Ala	Glu	Gly	Asp	Thr	Ser	Met
			165					170						175	
Asp	His	Tyr	Asp	Glu	His	Asp	Asp	Met	Ala	Leu	Gln	Thr	His	Lys	Pro
		180				185							190		
Leu	Leu	Pro	Ala	Glu	Thr	Glu	Thr	Lys	Asp	Leu	Thr	Asp	Pro	Val	Val
	195					200						205			
Glu	Leu	Ser	Lys	Lys	Leu	Gln	Lys	Gln	Glu	Ile	Ser	Thr	Thr	Asp	Asn
	210				215						220				
Ile	Lys	Gln	Glu	Gly	Gly	Glu	Glu	Lys	Lys	Gly	Thr	Lys	Cys	Ser	Thr
225				230						235				240	
Cys	Asn	Thr	Phe	Val	Gly	Glu	Ala	Lys	Gln	Tyr	Arg	Glu	His	Cys	Lys
			245					250						255	
Ser	Asp	Trp	His	Lys	His	Asn	Leu	Lys	Arg	Lys	Thr	Arg	Lys	Leu	Pro
	260					265						270			
Pro	Ile	Ser	Ala	Asp	Glu	Cys	Met	Ser	Glu	Ile	Asp	Met	Asp	Asp	Ser
	275					280						285			
Arg	Ala	Asp	Leu	Lys	Asp	Tyr	Ser	Phe							
	290				295										

(2) INFORMATION FOR SEQ ID NO:690:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 253 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..253

(D) OTHER INFORMATION: / Ceres Seq. ID 1498848

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:690:

Met	Gln	Lys	Thr	Ile	Asn	Pro	Glu	Thr	Gln	Arg	Pro	Tyr	Thr	Ile	Ser
1				5					10					15	
Met	Val	Glu	Arg	Leu	Met	His	Glu	Ile	His	Phe	Ala	Val	Asp	Pro	His
		20						25					30		
Ser	Asn	Ser	Lys	Lys	Gln	Ala	Leu	Asp	Val	Ile	Arg	Glu	Leu	Gln	Lys
		35				40						45			
His	Phe	Pro	Ile	Lys	Arg	Ser	Pro	Met	Arg	Leu	Arg	Leu	Thr	Val	Pro

50	55	60
Val Gln Asn Phe Pro Ser Leu Leu Glu Lys Leu Lys Glu Trp Asp Gly		
65	70	75
Ser Val Val Ser Lys Asp Glu Ser Gly Thr Gln Met Ser Thr Val Cys		80
	85	90
Glu Met Glu Pro Gly Leu Phe Arg Glu Cys Asp Ser His Val Arg Ser		95
	100	105
Ile Gln Gly Arg Leu Glu Ile Leu Ala Val Ser Val His Ala Glu Gly		110
	115	120
Asp Thr Ser Met Asp His Tyr Asp Glu His Asp Asp Met Ala Leu Gln		125
	130	135
Thr His Lys Pro Leu Leu Pro Ala Glu Thr Glu Thr Lys Asp Leu Thr		140
145	150	155
Asp Pro Val Val Glu Leu Ser Lys Lys Leu Gln Lys Gln Glu Ile Ser		160
	165	170
Thr Thr Asp Asn Ile Lys Gln Glu Gly Gly Glu Glu Lys Lys Gly Thr		175
	180	185
Lys Cys Ser Thr Cys Asn Thr Phe Val Gly Glu Ala Lys Gln Tyr Arg		190
	195	200
Glu His Cys Lys Ser Asp Trp His Lys His Asn Leu Lys Arg Lys Thr		205
	210	215
Arg Lys Leu Pro Pro Ile Ser Ala Asp Glu Cys Met Ser Glu Ile Asp		220
225	230	235
Met Asp Asp Ser Arg Ala Asp Leu Lys Asp Tyr Ser Phe		240
	245	250

(2) INFORMATION FOR SEQ ID NO:691:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 237 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..237

(D) OTHER INFORMATION: / Ceres Seq. ID 1498849

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:691:

Met Val Glu Arg Leu Met His Glu Ile His Phe Ala Val Asp Pro His		
1	5	10
Ser Asn Ser Lys Lys Gln Ala Leu Asp Val Ile Arg Glu Leu Gln Lys		15
	20	25
His Phe Pro Ile Lys Arg Ser Pro Met Arg Leu Arg Leu Thr Val Pro		30
	35	40
Val Gln Asn Phe Pro Ser Leu Leu Glu Lys Leu Lys Glu Trp Asp Gly		45
	50	55
Ser Val Val Ser Lys Asp Glu Ser Gly Thr Gln Met Ser Thr Val Cys		60
65	70	75
Glu Met Glu Pro Gly Leu Phe Arg Glu Cys Asp Ser His Val Arg Ser		80
	85	90
Ile Gln Gly Arg Leu Glu Ile Leu Ala Val Ser Val His Ala Glu Gly		95
	100	105
Asp Thr Ser Met Asp His Tyr Asp Glu His Asp Asp Met Ala Leu Gln		110
	115	120
Thr His Lys Pro Leu Leu Pro Ala Glu Thr Glu Thr Lys Asp Leu Thr		125
	130	135
Asp Pro Val Val Glu Leu Ser Lys Lys Leu Gln Lys Gln Glu Ile Ser		140
145	150	155
Thr Thr Asp Asn Ile Lys Gln Glu Gly Gly Glu Glu Lys Lys Gly Thr		160
	165	170
Lys Cys Ser Thr Cys Asn Thr Phe Val Gly Glu Ala Lys Gln Tyr Arg		175
	180	185
		190

Glu His Cys Lys Ser Asp Trp His Lys His Asn Leu Lys Arg Lys Thr
195 200 205
Arg Lys Leu Pro Pro Ile Ser Ala Asp Glu Cys Met Ser Glu Ile Asp
210 215 220
Met Asp Asp Ser Arg Ala Asp Leu Lys Asp Tyr Ser Phe
225 230 235

(2) INFORMATION FOR SEQ ID NO:692:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1337 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
(B) LOCATION: 1..1337
(D) OTHER INFORMATION: / Ceres Seq. ID 1498854

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:692:

atatgaacat	aaccaatct	gaagatcaat	cataacctta	aaccatctct	cataatttta	60
gtatttctat	tctcaccacc	aaaactcggt	gatacatcac	acccaactg	ttgttactca	120
tgctctacag	atcgatttac	cgcactcttc	gaccgggtact	atcatcttcg	gtacaatcct	180
ccggttttagg	aattggagga	ttcaggggac	atctcattag	ccacttgccc	aatgttcggc	240
tattgagctc	tgacacgtca	tctccggtaa	gtgggaataa	ccagccagaa	aatcctatcc	300
gaacggccga	tggtaaagt	atatccactt	attgggggtat	acctcctact	aagatcacta	360
aaccggacgg	ttcagcttgg	aagtggaaat	gttttcagcc	atgggattca	tacaaaccgg	420
atgtgtccat	tgatgtaact	aaacatcata	aaccctccaa	tttcaactgac	aaattcgcac	480
attggaccgt	tcaaactctg	aaaataccgg	ttcaactatt	ttttcagagg	aagcacatgt	540
gccatgcat	gttgctagag	acggtggctg	cggtgccggg	aatggtcggg	tggatgcttt	600
tgcacttgaa	atctctccgg	aggttcgaac	atagcggggg	atggatcaaa	gctttgctcg	660
aagaggctga	gaacgagcgt	atgcatctca	tgactttcat	cgaactttca	caaccctaat	720
ggtacgaacg	agcgattgtg	ttcacgggtc	aaggcggttt	cttcaacgca	tatttccttg	780
cttatgtaat	ttcacccaaa	cttgctcatc	gtatcactgg	atacttagaa	gaagaggctg	840
taaattctta	cactgaattt	ctcaaagaca	ttgatgccgg	aaaattcgaa	aactcgccag	900
ctccagccat	cgcaatcgat	tactggcggt	tgccctaaaga	tgcaacgctt	agggatgtgg	960
tttatgttat	acgagctgac	gaagctcacc	accgtgatat	taaccactat	gcttcggata	1020
tacaattcaa	aggacatgaa	ctcaaggaag	ctccggctcc	tattggatat	cattaaagat	1080
tatgtgacaa	agtcacaaag	ctgtgtatac	atctatgaac	atatgttggt	gtggatctcc	1140
atgatatttt	tattttatgt	tttcgattta	tttaaaactg	ttattcggtt	ttattagctc	1200
aatatggata	tttaaacat	attattttgt	tacgatttat	gaacatagta	ctactcatgt	1260
gtgtgtaaaa	gatcatactg	cctggacacg	aagcggatat	ccggaaaaat	tataatattt	1320
gttttttgat	tcgttttc					

(2) INFORMATION FOR SEQ ID NO:693:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 318 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..318
(D) OTHER INFORMATION: / Ceres Seq. ID 1498855

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:693:

Met	Ser	Tyr	Arg	Ser	Ile	Tyr	Arg	Thr	Leu	Arg	Pro	Val	Leu	Ser	Ser
1				5				10					15		
Ser	Val	Gln	Ser	Ser	Gly	Leu	Gly	Ile	Gly	Gly	Phe	Arg	Gly	His	Leu
			20					25					30		
Ile	Ser	His	Leu	Pro	Asn	Val	Arg	Leu	Leu	Ser	Ser	Asp	Thr	Ser	Ser
		35					40					45			
Pro	Val	Ser	Gly	Asn	Asn	Gln	Pro	Glu	Asn	Pro	Ile	Arg	Thr	Ala	Asp
	50					55					60				

Gly	Lys	Val	Ile	Ser	Thr	Tyr	Trp	Gly	Ile	Pro	Pro	Thr	Lys	Ile	Thr
65					70					75					80
Lys	Pro	Asp	Gly	Ser	Ala	Trp	Lys	Trp	Asn	Cys	Phe	Gln	Pro	Trp	Asp
				85					90					95	
Ser	Tyr	Lys	Pro	Asp	Val	Ser	Ile	Asp	Val	Thr	Lys	His	His	Lys	Pro
			100					105					110		
Ser	Asn	Phe	Thr	Asp	Lys	Phe	Ala	Tyr	Trp	Thr	Val	Gln	Thr	Leu	Lys
		115					120					125			
Ile	Pro	Val	Gln	Leu	Phe	Phe	Gln	Arg	Lys	His	Met	Cys	His	Ala	Met
	130					135					140				
Leu	Leu	Glu	Thr	Val	Ala	Ala	Val	Pro	Gly	Met	Val	Gly	Trp	Met	Leu
145					150					155					160
Leu	His	Leu	Lys	Ser	Leu	Arg	Arg	Phe	Glu	His	Ser	Gly	Gly	Trp	Ile
				165					170					175	
Lys	Ala	Leu	Leu	Glu	Glu	Ala	Glu	Asn	Glu	Arg	Met	His	Leu	Met	Thr
			180					185					190		
Phe	Ile	Glu	Leu	Ser	Gln	Pro	Lys	Trp	Tyr	Glu	Arg	Ala	Ile	Val	Phe
	195					200						205			
Thr	Val	Gln	Gly	Val	Phe	Phe	Asn	Ala	Tyr	Phe	Leu	Ala	Tyr	Val	Ile
	210					215					220				
Ser	Pro	Lys	Leu	Ala	His	Arg	Ile	Thr	Gly	Tyr	Leu	Glu	Glu	Glu	Ala
225					230					235					240
Val	Asn	Ser	Tyr	Thr	Glu	Phe	Leu	Lys	Asp	Ile	Asp	Ala	Gly	Lys	Phe
				245					250					255	
Glu	Asn	Ser	Pro	Ala	Pro	Ala	Ile	Ala	Ile	Asp	Tyr	Trp	Arg	Leu	Pro
			260					265					270		
Lys	Asp	Ala	Thr	Leu	Arg	Asp	Val	Tyr	Val	Ile	Arg	Ala	Asp	Glu	
			275				280				285				
Ala	His	His	Arg	Asp	Ile	Asn	His	Tyr	Ala	Ser	Asp	Ile	Gln	Phe	Lys
	290					295					300				
Gly	His	Glu	Leu	Lys	Glu	Ala	Pro	Ala	Pro	Ile	Gly	Tyr	His		
305					310					315					

(2) INFORMATION FOR SEQ ID NO:694:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 179 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..179
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498856

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:694:

Met	Cys	His	Ala	Met	Leu	Leu	Glu	Thr	Val	Ala	Ala	Val	Pro	Gly	Met
1				5					10					15	
Val	Gly	Trp	Met	Leu	Leu	His	Leu	Lys	Ser	Leu	Arg	Arg	Phe	Glu	His
			20					25					30		
Ser	Gly	Gly	Trp	Ile	Lys	Ala	Leu	Glu	Glu	Ala	Glu	Asn	Glu	Arg	
			35				40					45			
Met	His	Leu	Met	Thr	Phe	Ile	Glu	Leu	Ser	Gln	Pro	Lys	Trp	Tyr	Glu
	50					55					60				
Arg	Ala	Ile	Val	Phe	Thr	Val	Gln	Gly	Val	Phe	Phe	Asn	Ala	Tyr	Phe
65					70					75				80	
Leu	Ala	Tyr	Val	Ile	Ser	Pro	Lys	Leu	Ala	His	Arg	Ile	Thr	Gly	Tyr
				85					90					95	
Leu	Glu	Glu	Glu	Ala	Val	Asn	Ser	Tyr	Thr	Glu	Phe	Leu	Lys	Asp	Ile
			100					105					110		
Asp	Ala	Gly	Lys	Phe	Glu	Asn	Ser	Pro	Ala	Pro	Ala	Ile	Ala	Ile	Asp
		115					120					125			
Tyr	Trp	Arg	Leu	Pro	Lys	Asp	Ala	Thr	Leu	Arg	Asp	Val	Val	Tyr	Val

130	135	140
Ile Arg Ala Asp Glu	Ala His His Arg Asp	Ile Asn His Tyr Ala Ser
145	150	155
Asp Ile Gln Phe Lys	Gly His Glu Leu Lys	Glu Ala Pro Ala Pro Ile
165	170	175

Gly Tyr His

(2) INFORMATION FOR SEQ ID NO:695:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 175 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..175
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498857

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:695:

Met	Leu	Leu	Glu	Thr	Val	Ala	Ala	Val	Pro	Gly	Met	Val	Gly	Trp	Met
1			5					10						15	
Leu	Leu	His	Leu	Lys	Ser	Leu	Arg	Arg	Phe	Glu	His	Ser	Gly	Gly	Trp
			20					25					30		
Ile	Lys	Ala	Leu	Leu	Glu	Glu	Ala	Glu	Asn	Glu	Arg	Met	His	Leu	Met
			35				40					45			
Thr	Phe	Ile	Glu	Leu	Ser	Gln	Pro	Lys	Trp	Tyr	Glu	Arg	Ala	Ile	Val
			50				55				60				
Phe	Thr	Val	Gln	Gly	Val	Phe	Phe	Asn	Ala	Tyr	Phe	Leu	Ala	Tyr	Val
65					70					75				80	
Ile	Ser	Pro	Lys	Leu	Ala	His	Arg	Ile	Thr	Gly	Tyr	Leu	Glu	Glu	Glu
				85					90					95	
Ala	Val	Asn	Ser	Tyr	Thr	Glu	Phe	Leu	Lys	Asp	Ile	Asp	Ala	Gly	Lys
			100					105					110		
Phe	Glu	Asn	Ser	Pro	Ala	Pro	Ala	Ile	Ala	Ile	Asp	Tyr	Trp	Arg	Leu
			115				120					125			
Pro	Lys	Asp	Ala	Thr	Leu	Arg	Asp	Val	Val	Tyr	Val	Ile	Arg	Ala	Asp
			130				135					140			
Glu	Ala	His	His	Arg	Asp	Ile	Asn	His	Tyr	Ala	Ser	Asp	Ile	Gln	Phe
145					150					155				160	
Lys	Gly	His	Glu	Leu	Lys	Glu	Ala	Pro	Ala	Pro	Ile	Gly	Tyr	His	
				165					170					175	

(2) INFORMATION FOR SEQ ID NO:696:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1159 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1159
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498858

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:696:

atagtttggt	acttttagtgt	tgactgttga	ccgcgacgaa	tccgtcggaa	accggaatca	60
ccatggattt	tcctccgacg	aagcttgatt	atcatgtaga	catgttcaat	cttcagtctc	120
attccagatt	tctctcctta	tttaaggcgc	aagatggacg	catagctcta	atactagaat	180
caacggtgtt	tcattccaaa	gggtgtggcc	agccgtcaga	caccggttta	attgttttct	240
ccggttcgga	tttgaaattt	tccgttcaag	atgttcgatc	gaaagacgga	attgttctcc	300
attacggagt	tttcgaaggt	tcgaatcctg	aaagtggaa	tgatagttag	aaagggaaag	360
aagtttactt	aactgttgat	gaatcaaggc	gtaaactcaa	ttccagggtg	cactcagctg	420
gacacttgct	agatatgtgt	atgcagaaa	gttggttagg	acatttgtag	cctggaaaag	480

```
ggtaccattt tcctgacggt ccttttgtgg aatacaaagg aagcgtccca caggaggagt 540
ttcaggtgaa gcagaaagag ttggaggcag aagctaacga actgatatcc aaaggaggaa 600
aggtttatgc tgctatatgg ccctatgaag aggcattctgt gctctgtggg ggcagtcttc 660
ctgattatat ttccaagggc agcactcccc ggatcataaa attaggtgac agccccgggt 720
gtccatgtgg tggaacccat gtctccaatt tatctgatat cataagcatg aagatcacac 780
agatgagaac aaagaaagga atgacgaaag ttttctacac cattgcatct tgaaactctt 840
atgggttcca gtttctatac ggtagatata caataagtca aggaaggga t gatagt gag 900
gacgactgtt ttcattcagtt ggcttcaaca gcaagcagct tctcctgtgc ctcaacagcc 960
acaaatcagt atttgtgggt atttatcaat ctcttaaacy actctctcta ttattgataa 1020
gtcgtatatg atatatgata ttgatgtgat attttcttcc actcagcctc ttaattagta 1080
ttaatatatt gactcttggg attgtagaat cgtaccgggc atttggtcct agatttttat 1140
tcatgcatcg gtttgattt
```

(2) INFORMATION FOR SEQ ID NO:697:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 256 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..256
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498859

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:697:

```
Met Asp Phe Pro Thr Lys Leu Asp Tyr His Val Asp Met Phe Asn
1      5      10      15
Leu Gln Ser His Ser Arg Phe Leu Ser Leu Phe Lys Ala Gln Asp Gly
20      25      30
Arg Ile Ala Leu Ile Leu Glu Ser Thr Val Phe His Pro Gln Gly Gly
35      40      45
Gly Gln Pro Ser Asp Thr Gly Leu Ile Val Phe Ser Gly Ser Asp Leu
50      55      60
Lys Phe Ser Val Gln Asp Val Arg Ser Lys Asp Gly Ile Val Leu His
65      70      75      80
Tyr Gly Val Phe Glu Gly Ser Asn Pro Glu Ser Gly Ile Asp Ser Glu
85      90      95
Lys Gly Lys Glu Val Tyr Leu Thr Val Asp Glu Ser Arg Arg Lys Leu
100     105     110
Asn Ser Arg Leu His Ser Ala Gly His Leu Leu Asp Met Cys Met Gln
115     120     125
Lys Val Gly Leu Gly His Leu Glu Pro Gly Lys Gly Tyr His Phe Pro
130     135     140
Asp Gly Pro Phe Val Glu Tyr Lys Gly Ser Val Pro Gln Glu Glu Phe
145     150     155     160
Gln Val Lys Gln Lys Glu Leu Glu Ala Glu Ala Asn Glu Leu Ile Ser
165     170     175
Lys Gly Gly Lys Val Tyr Ala Ala Ile Leu Pro Tyr Glu Glu Ala Ser
180     185     190
Val Leu Cys Gly Gly Ser Leu Pro Asp Tyr Ile Ser Lys Gly Ser Thr
195     200     205
Pro Arg Ile Ile Lys Leu Gly Asp Ser Pro Gly Cys Pro Cys Gly Gly
210     215     220
Thr His Val Ser Asn Leu Ser Asp Ile Ile Ser Met Lys Ile Thr Gln
225     230     235     240
Met Arg Thr Lys Lys Gly Met Thr Lys Val Phe Tyr Thr Ile Ala Ser
245     250     255
```

(2) INFORMATION FOR SEQ ID NO:698:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 243 amino acids

- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..243
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1498860
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:698:

Met Phe Asn Leu Gln Ser His Ser Arg Phe Leu Ser Leu Phe Lys Ala
1 5 10 15
Gln Asp Gly Arg Ile Ala Leu Ile Leu Glu Ser Thr Val Phe His Pro
20 25 30
Gln Gly Gly Gly Gln Pro Ser Asp Thr Gly Leu Ile Val Phe Ser Gly
35 40 45
Ser Asp Leu Lys Phe Ser Val Gln Asp Val Arg Ser Lys Asp Gly Ile
50 55 60
Val Leu His Tyr Gly Val Phe Glu Gly Ser Asn Pro Glu Ser Gly Ile
65 70 75 80
Asp Ser Glu Lys Gly Lys Glu Val Tyr Leu Thr Val Asp Glu Ser Arg
85 90 95
Arg Lys Leu Asn Ser Arg Leu His Ser Ala Gly His Leu Leu Asp Met
100 105 110
Cys Met Gln Lys Val Gly Leu Gly His Leu Glu Pro Gly Lys Gly Tyr
115 120 125
His Phe Pro Asp Gly Pro Phe Val Glu Tyr Lys Gly Ser Val Pro Gln
130 135 140
Glu Glu Phe Gln Val Lys Gln Lys Glu Leu Glu Ala Glu Ala Asn Glu
145 150 155 160
Leu Ile Ser Lys Gly Gly Lys Val Tyr Ala Ala Ile Leu Pro Tyr Glu
165 170 175
Glu Ala Ser Val Leu Cys Gly Gly Ser Leu Pro Asp Tyr Ile Ser Lys
180 185 190
Gly Ser Thr Pro Arg Ile Ile Lys Leu Gly Asp Ser Pro Gly Cys Pro
195 200 205
Cys Gly Gly Thr His Val Ser Asn Leu Ser Asp Ile Ile Ser Met Lys
210 215 220
Ile Thr Gln Met Arg Thr Lys Lys Gly Met Thr Lys Val Phe Tyr Thr
225 230 235 240
Ile Ala Ser

- (2) INFORMATION FOR SEQ ID NO:699:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 132 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..132
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1498861
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:699:

Met Cys Met Gln Lys Val Gly Leu Gly His Leu Glu Pro Gly Lys Gly
1 5 10 15
Tyr His Phe Pro Asp Gly Pro Phe Val Glu Tyr Lys Gly Ser Val Pro
20 25 30
Gln Glu Glu Phe Gln Val Lys Gln Lys Glu Leu Glu Ala Glu Ala Asn
35 40 45
Glu Leu Ile Ser Lys Gly Gly Lys Val Tyr Ala Ala Ile Leu Pro Tyr
50 55 60

Glu Glu Ala Ser Val Leu Cys Gly Gly Ser Leu Pro Asp Tyr Ile Ser
65 70 75 80
Lys Gly Ser Thr Pro Arg Ile Ile Lys Leu Gly Asp Ser Pro Gly Cys
85 90 95
Pro Cys Gly Gly Thr His Val Ser Asn Leu Ser Asp Ile Ile Ser Met
100 105 110
Lys Ile Thr Gln Met Arg Thr Lys Lys Gly Met Thr Lys Val Phe Tyr
115 120 125
Thr Ile Ala Ser
130

(2) INFORMATION FOR SEQ ID NO:700:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1308 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1308
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498874

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:700:

cttcttcgta	cgtaaattaa	aatctgaaga	aacaaaatcg	tgaaatcgat	ctctttaagc	60
atcatctagg	gttcatcact	gaaatcaaaa	atgcaattaa	atctctacaa	aatctctcag	120
atctaattccc	agatcggttg	tggtttcttc	tccgtaaacc	aatcccacat	atgaattaaa	180
gattcgatct	cgaaatcggt	ggcttttggt	gttggtgcat	tcttcggtga	tggtccgac	240
tcggattcta	accagagacg	aagagcttgg	tggtatttca	gacgatgatg	attctccatc	300
gggtaaaaga	tctaaacttg	atcgcttccc	tcttagccgt	tggaactcg	ccgtttctct	360
cggtgtcttc	ctcgtcttct	cctctggact	ctgttgatc	tacatgacca	tgctgtctgc	420
tgaatttggc	aaactcaaac	ttccaagaaa	gcctcgctga	tctccgtttg	ctcaaagata	480
atctagcvaa	ttatgcgrat	gagtatccgg	cgcagttttg	ttttagggtg	ttgtgcaacg	540
tacattttta	tgcagacctt	tatgattcca	gggactatct	tcatgtcact	attagctgga	600
gctctctttg	gagtattcaa	aggtgttggt	ttggttggtt	tcaatgcaac	agcaggagct	660
acctcgtggt	tctttttgtc	gaaattgatt	ggtcgaccgt	tgattacttg	gctatggcct	720
gacaaattaa	gattctttca	agcagagatt	agtaagcgta	gagataagct	tctgaactat	780
atgttggttt	tgaggataac	accaactctg	ccaaatcttt	ttatcaatct	tgcatctcct	840
atagtcgatg	tacctttcca	tgtcttcttt	ttggcgacat	tgattggtct	cattcctgca	900
gcttatataa	ctgtcagagc	tggccttgct	acttggagat	ctcaaactcg	tgaaagatct	960
gtatgatttc	aagacattgt	cagtgtcttt	cctcatcggt	tttatctcta	ttcttccaac	1020
gatactgaaa	agaaagaaga	ttgttgaata	gccagggaga	agcatcttta	caatacacat	1080
ggcctaacct	tcaatgccat	acagagaaca	agaaatacact	taacttggtt	agaggacaca	1140
acagaacaaa	actttctgatt	cgtttacttg	tcacttgctg	taacgattcg	ttgatagttt	1200
ttttgttggt	atattttctt	actatttggc	aagtagaggt	tgagaagaaa	ttacagaaat	1260
aatacaattt	ttgtacaag	acgagagacc	atgaaatatt	ttggttct		

(2) INFORMATION FOR SEQ ID NO:701:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 157 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..157
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498875

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:701:

Met Xaa Met Ser Ile Arg Arg Ser Phe Val Leu Gly Tyr Cys Ala Thr
1 5 10 15
Tyr Ile Phe Met Gln Thr Phe Met Ile Pro Gly Thr Ile Phe Met Ser
20 25 30
Leu Leu Ala Gly Ala Leu Phe Gly Val Phe Lys Gly Val Val Leu Val

Met Gln Thr Phe Met Ile Pro Gly Thr Ile Phe Met Ser Leu Leu Ala
1 5 10 15

Gly Ala Leu Phe Gly Val Phe Lys Gly Val Val Leu Val Val Phe Asn
20 25 30
Ala Thr Ala Gly Ala Thr Ser Cys Phe Phe Leu Ser Lys Leu Ile Gly
35 40 45
Arg Pro Leu Ile Thr Trp Leu Trp Pro Asp Lys Leu Arg Phe Phe Gln
50 55 60
Ala Glu Ile Ser Lys Arg Arg Asp Lys Leu Leu Asn Tyr Met Leu Phe
65 70 75 80
Leu Arg Ile Thr Pro Thr Leu Pro Asn Leu Phe Ile Asn Leu Ala Ser
85 90 95
Pro Ile Val Asp Val Pro Phe His Val Phe Phe Leu Ala Thr Leu Ile
100 105 110
Gly Leu Ile Pro Ala Ala Tyr Ile Thr Val Arg Ala Gly Leu Ala Thr
115 120 125
Trp Arg Ser Gln Ile Gly Glu Arg Ser Val
130 135

(2) INFORMATION FOR SEQ ID NO:704:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1603 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1603
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498878

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:704:

ctttttgcga tcaatcgaaa gaaaacaaaa aatggggaaa gttccgctcgt cgttttcgtag	60
tataccggcg aattttattgg tcagaaaaaac aacaccatct cctccagcgc cgccgcgaga	120
ttttcgcaac agaaccgccg tgggaggaga ttcagccaaa cttccccaca atactcaagc	180
ccctcgcgag ccctccttga ggaatccatt caagtcacca aatctctcag acgctaaaag	240
cctcttcaat tcaatcgccg ccacttcacg aatcccactc gatctcaaat tccacaactc	300
tgttctccaa tcctatgctt caatcgccgt cgtcgacgat acggtgaaat tctttcagca	360
tattatgaaa tcgcagccta atttcaggcc gggacgttca acgttcctta tcttgctttc	420
acatgcttgt agagctcctg attcgtcgat ttcgaatgtt catagagttc ttaatctcat	480
ggttaataat ggtttagagc ctgatcaagt aactaccgat atcgcggtga ggtctctttg	540
cgaaacgggt cgggttgatg aagctaagga tttgatgaag gagctcactg agaaacactc	600
tcctccggat acatatactt ataactttct actgaagcat ttgtgcaaat gcaaagatct	660
tcattgttgt tatgagtttg ttgatgagat gagagatgat ttcgatgtta agccggatct	720
tgtagcttc actacttgta ttgataatgt ttgtaactct aagaacttga gggaggcaat	780
gtatctagtt agtaagttag gtaatgctgg gttaagccg gattgtttcc tctataacac	840
gattatgaaa ggtttttgca cactgagtaa agggagttag gcggttggtg tgtataagaa	900
aatgaaggaa gaaggtggtg agccagatca gattacttac aatactttga tatttgact	960
gtcgaaagct ggtagagttg aggaagctag gatgtatttg aaaactatgg ttgatgcggg	1020
gtatgagccg gatactgcta cttacacatc actgatgaat ggaatgtgta gaaaagggtga	1080
gtcttttaggt gcgttgagtt tgttagaaga aatggaagca agaggggtgtg ctccaaatga	1140
ttgtacttat aatactttgc ttcattgatt gtgtaaagca aggttgatgg ataaaggat	1200
ggagttatat gaaatgatga aatcaagtgg tgtaaagctt gagagtaatg gttatgctac	1260
acttgtgagg tctctggtta aaagtggcaa ggtcgcagag gcttatgaag tgtttgatta	1320
tgcagttgat agcaagagtt tgtcagatgc ttctgcgtac tctacacttg aaactacctt	1380
gaaatggttg aaaaaagcta aagaacaagg cttggttcca taaatggtat cctctagctg	1440
agctttaccg actttcttct ttatgcaagt ccatatttca tttttgaagt agtgttactc	1500
caaaagcaat gaatttggtt cgaaatatgc tgttcgattc ttaagggacc agcagtgatt	1560
tataatagta actttggttg taatattatt gtcacttgag att	

(2) INFORMATION FOR SEQ ID NO:705:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 473 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..473

(D) OTHER INFORMATION: / Ceres Seq. ID 1498879

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:705:

Phe	Leu	Arg	Ser	Ile	Glu	Arg	Lys	Gln	Lys	Met	Gly	Lys	Val	Pro	Ser
1				5				10						15	
Ser	Phe	Arg	Ser	Ile	Pro	Ala	Asn	Leu	Leu	Val	Arg	Lys	Thr	Thr	Pro
			20					25					30		
Ser	Pro	Pro	Ala	Pro	Pro	Arg	Asp	Phe	Arg	Asn	Arg	Thr	Ala	Val	Gly
		35					40					45			
Gly	Asp	Ser	Ala	Lys	Leu	Pro	His	Asn	Thr	Gln	Ala	Pro	Arg	Glu	Pro
	50					55				60					
Ser	Leu	Arg	Asn	Pro	Phe	Lys	Ser	Pro	Asn	Leu	Ser	Asp	Ala	Lys	Ser
65				70						75				80	
Leu	Phe	Asn	Ser	Ile	Ala	Ala	Thr	Ser	Arg	Ile	Pro	Leu	Asp	Leu	Lys
			85						90					95	
Phe	His	Asn	Ser	Val	Leu	Gln	Ser	Tyr	Ala	Ser	Ile	Ala	Val	Val	Asp
			100					105					110		
Asp	Thr	Val	Lys	Phe	Phe	Gln	His	Ile	Met	Lys	Ser	Gln	Pro	Asn	Phe
		115				120						125			
Arg	Pro	Gly	Arg	Ser	Thr	Phe	Leu	Ile	Leu	Leu	Ser	His	Ala	Cys	Arg
	130					135					140				
Ala	Pro	Asp	Ser	Ser	Ile	Ser	Asn	Val	His	Arg	Val	Leu	Asn	Leu	Met
145				150						155				160	
Val	Asn	Asn	Gly	Leu	Glu	Pro	Asp	Gln	Val	Thr	Thr	Asp	Ile	Ala	Val
			165						170					175	
Arg	Ser	Leu	Cys	Glu	Thr	Gly	Arg	Val	Asp	Glu	Ala	Lys	Asp	Leu	Met
		180						185					190		
Lys	Glu	Leu	Thr	Glu	Lys	His	Ser	Pro	Pro	Asp	Thr	Tyr	Thr	Tyr	Asn
	195						200					205			
Phe	Leu	Leu	Lys	His	Leu	Cys	Lys	Cys	Lys	Asp	Leu	His	Val	Val	Tyr
	210					215					220				
Glu	Phe	Val	Asp	Glu	Met	Arg	Asp	Asp	Phe	Asp	Val	Lys	Pro	Asp	Leu
225				230						235				240	
Val	Ser	Phe	Thr	Ile	Leu	Ile	Asp	Asn	Val	Cys	Asn	Ser	Lys	Asn	Leu
			245						250					255	
Arg	Glu	Ala	Met	Tyr	Leu	Val	Ser	Lys	Leu	Gly	Asn	Ala	Gly	Phe	Lys
		260						265					270		
Pro	Asp	Cys	Phe	Leu	Tyr	Asn	Thr	Ile	Met	Lys	Gly	Phe	Cys	Thr	Leu
	275						280					285			
Ser	Lys	Gly	Ser	Glu	Ala	Val	Gly	Val	Tyr	Lys	Lys	Met	Lys	Glu	Glu
	290					295					300				
Gly	Val	Glu	Pro	Asp	Gln	Ile	Thr	Tyr	Asn	Thr	Leu	Ile	Phe	Gly	Leu
305				310						315				320	
Ser	Lys	Ala	Gly	Arg	Val	Glu	Glu	Ala	Arg	Met	Tyr	Leu	Lys	Thr	Met
			325						330					335	
Val	Asp	Ala	Gly	Tyr	Glu	Pro	Asp	Thr	Ala	Thr	Tyr	Thr	Ser	Leu	Met
		340						345					350		
Asn	Gly	Met	Cys	Arg	Lys	Gly	Glu	Ser	Leu	Gly	Ala	Leu	Ser	Leu	Leu
	355						360					365			
Glu	Glu	Met	Glu	Ala	Arg	Gly	Cys	Ala	Pro	Asn	Asp	Cys	Thr	Tyr	Asn
	370					375					380				
Thr	Leu	Leu	His	Gly	Leu	Cys	Lys	Ala	Arg	Leu	Met	Asp	Lys	Gly	Met
385				390						395				400	
Glu	Leu	Tyr	Glu	Met	Met	Lys	Ser	Ser	Gly	Val	Lys	Leu	Glu	Ser	Asn
			405						410					415	
Gly	Tyr	Ala	Thr	Leu	Val	Arg	Ser	Leu	Val	Lys	Ser	Gly	Lys	Val	Ala
			420					425					430		
Glu	Ala	Tyr	Glu	Val	Phe	Asp	Tyr	Ala	Val	Asp	Ser	Lys	Ser	Leu	Ser

435 440 445
Asp Ala Ser Ala Tyr Ser Thr Leu Glu Thr Thr Leu Lys Trp Leu Lys
450 455 460
Lys Ala Lys Glu Gln Gly Leu Val Pro
465 470

(2) INFORMATION FOR SEQ ID NO:706:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 463 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..463

(D) OTHER INFORMATION: / Ceres Seq. ID 1498880

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:706:

Met Gly Lys Val Pro Ser Ser Phe Arg Ser Ile Pro Ala Asn Leu Leu
1 5 10 15
Val Arg Lys Thr Thr Pro Ser Pro Pro Ala Pro Pro Arg Asp Phe Arg
20 25 30
Asn Arg Thr Ala Val Gly Gly Asp Ser Ala Lys Leu Pro His Asn Thr
35 40 45
Gln Ala Pro Arg Glu Pro Ser Leu Arg Asn Pro Phe Lys Ser Pro Asn
50 55 60
Leu Ser Asp Ala Lys Ser Leu Phe Asn Ser Ile Ala Ala Thr Ser Arg
65 70 75 80
Ile Pro Leu Asp Leu Lys Phe His Asn Ser Val Leu Gln Ser Tyr Ala
85 90 95
Ser Ile Ala Val Val Asp Asp Thr Val Lys Phe Phe Gln His Ile Met
100 105 110
Lys Ser Gln Pro Asn Phe Arg Pro Gly Arg Ser Thr Phe Leu Ile Leu
115 120 125
Leu Ser His Ala Cys Arg Ala Pro Asp Ser Ser Ile Ser Asn Val His
130 135 140
Arg Val Leu Asn Leu Met Val Asn Asn Gly Leu Glu Pro Asp Gln Val
145 150 155 160
Thr Thr Asp Ile Ala Val Arg Ser Leu Cys Glu Thr Gly Arg Val Asp
165 170 175
Glu Ala Lys Asp Leu Met Lys Glu Leu Thr Glu Lys His Ser Pro Pro
180 185 190
Asp Thr Tyr Thr Tyr Asn Phe Leu Lys His Leu Cys Lys Cys Lys
195 200 205
Asp Leu His Val Val Tyr Glu Phe Val Asp Glu Met Arg Asp Asp Phe
210 215 220
Asp Val Lys Pro Asp Leu Val Ser Phe Thr Ile Leu Ile Asp Asn Val
225 230 235 240
Cys Asn Ser Lys Asn Leu Arg Glu Ala Met Tyr Leu Val Ser Lys Leu
245 250 255
Gly Asn Ala Gly Phe Lys Pro Asp Cys Phe Leu Tyr Asn Thr Ile Met
260 265 270
Lys Gly Phe Cys Thr Leu Ser Lys Gly Ser Glu Ala Val Gly Val Tyr
275 280 285
Lys Lys Met Lys Glu Glu Gly Val Glu Pro Asp Gln Ile Thr Tyr Asn
290 295 300
Thr Leu Ile Phe Gly Leu Ser Lys Ala Gly Arg Val Glu Glu Ala Arg
305 310 315 320
Met Tyr Leu Lys Thr Met Val Asp Ala Gly Tyr Glu Pro Asp Thr Ala
325 330 335
Thr Tyr Thr Ser Leu Met Asn Gly Met Cys Arg Lys Gly Glu Ser Leu
340 345 350

Gly Ala Leu Ser Leu Leu Glu Glu Met Glu Ala Arg Gly Cys Ala Pro
355 360 365
Asn Asp Cys Thr Tyr Asn Thr Leu Leu His Gly Leu Cys Lys Ala Arg
370 375 380
Leu Met Asp Lys Gly Met Glu Leu Tyr Glu Met Met Lys Ser Ser Gly
385 390 395 400
Val Lys Leu Glu Ser Asn Gly Tyr Ala Thr Leu Val Arg Ser Leu Val
405 410 415
Lys Ser Gly Lys Val Ala Glu Ala Tyr Glu Val Phe Asp Tyr Ala Val
420 425 430
Asp Ser Lys Ser Leu Ser Asp Ala Ser Ala Tyr Ser Thr Leu Glu Thr
435 440 445
Thr Leu Lys Trp Leu Lys Lys Ala Lys Glu Gln Gly Leu Val Pro
450 455 460

(2) INFORMATION FOR SEQ ID NO:707:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 352 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..352

(D) OTHER INFORMATION: / Ceres Seq. ID 1498881

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:707:

Met Lys Ser Gln Pro Asn Phe Arg Pro Gly Arg Ser Thr Phe Leu Ile
1 5 10 15
Leu Leu Ser His Ala Cys Arg Ala Pro Asp Ser Ser Ile Ser Asn Val
20 25 30
His Arg Val Leu Asn Leu Met Val Asn Asn Gly Leu Glu Pro Asp Gln
35 40 45
Val Thr Thr Asp Ile Ala Val Arg Ser Leu Cys Glu Thr Gly Arg Val
50 55 60
Asp Glu Ala Lys Asp Leu Met Lys Glu Leu Thr Glu Lys His Ser Pro
65 70 75 80
Pro Asp Thr Tyr Thr Tyr Asn Phe Leu Leu Lys His Leu Cys Lys Cys
85 90 95
Lys Asp Leu His Val Val Tyr Glu Phe Val Asp Glu Met Arg Asp Asp
100 105 110
Phe Asp Val Lys Pro Asp Leu Val Ser Phe Thr Ile Leu Ile Asp Asn
115 120 125
Val Cys Asn Ser Lys Asn Leu Arg Glu Ala Met Tyr Leu Val Ser Lys
130 135 140
Leu Gly Asn Ala Gly Phe Lys Pro Asp Cys Phe Leu Tyr Asn Thr Ile
145 150 155 160
Met Lys Gly Phe Cys Thr Leu Ser Lys Gly Ser Glu Ala Val Gly Val
165 170 175
Tyr Lys Lys Met Lys Glu Glu Gly Val Glu Pro Asp Gln Ile Thr Tyr
180 185 190
Asn Thr Leu Ile Phe Gly Leu Ser Lys Ala Gly Arg Val Glu Glu Ala
195 200 205
Arg Met Tyr Leu Lys Thr Met Val Asp Ala Gly Tyr Glu Pro Asp Thr
210 215 220
Ala Thr Tyr Thr Ser Leu Met Asn Gly Met Cys Arg Lys Gly Glu Ser
225 230 235 240
Leu Gly Ala Leu Ser Leu Leu Glu Glu Met Glu Ala Arg Gly Cys Ala
245 250 255
Pro Asn Asp Cys Thr Tyr Asn Thr Leu Leu His Gly Leu Cys Lys Ala
260 265 270
Arg Leu Met Asp Lys Gly Met Glu Leu Tyr Glu Met Met Lys Ser Ser

275	280	285
Gly Val Lys Leu Glu Ser Asn Gly Tyr Ala Thr Leu Val Arg Ser Leu		
290	295	300
Val Lys Ser Gly Lys Val Ala Glu Ala Tyr Glu Val Phe Asp Tyr Ala		
305	310	315
Val Asp Ser Lys Ser Leu Ser Asp Ala Ser Ala Tyr Ser Thr Leu Glu		
325	330	335
Thr Thr Leu Lys Trp Leu Lys Lys Ala Lys Glu Gln Gly Leu Val Pro		
340	345	350

(2) INFORMATION FOR SEQ ID NO:708:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 823 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..823
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498882

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:708:

taacttctgc	aaaaaaatca	atcccgatc	cgatcaagtt	ttattttccg	attcgcttcc	60
aagttcaatt	caatttcaac	cctaattttg	tttgaaaga	ttaagccatg	ggaggtcacg	120
gtggtttgaa	tattcttcca	cagaagaggt	ggaacgttta	caacttggac	agtccgaaag	180
gatgaagaag	ctgcggttag	agaagagcag	atcaaacgcg	aggacgctag	aaaaagagat	240
gctgaatctc	gtctcgaagt	gcttcgtaac	gtccgtgggt	tagcccctct	caccggaggc	300
agagaagggt	aaggatgaga	cgggtggtgt	ggcggcggct	gttggttaaat	ccacggatgt	360
tgttggtgag	agtgttgaat	cggaaaatgt	atagattggg	atatggagtt	gctggtaaag	420
gtgtgaagcg	tccttgagaa	acgtaacgat	gaaaatgata	gtgttcgagg	tgaggggtgat	480
gatggtggat	gtggtggtta	tgaagctaag	aagaagaaga	tgagtgggaa	gaagagctta	540
aaggagttga	agagggagag	ggttgagaag	gaaagagaga	gagccctttt	catgaaacag	600
agccagagag	ccggtggttt	ttcccggagg	tgagtttttg	gatgaaatta	tacgttattt	660
gcattggggt	tgtacaagtt	agtagttaac	tgttggttact	tgattcatat	ccaaagtatt	720
ggtttatttaa	cgctactcga	tgcttagtgc	tgatagaacc	atgtacatag	tttgagagtgt	780
gatagatagt	ttatcagggg	aatcaatagt	ttatcaggtc	ctc		

(2) INFORMATION FOR SEQ ID NO:709:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..33
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498883

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:709:

Thr Ser Ala Lys Lys Ser Ile Pro Ile Lys Phe Tyr Phe Pro		
1	5	10
Ile Arg Phe Gln Val Gln Phe Asn Phe Asn Pro Asn Phe Val Trp Lys		
20	25	30

Asp

(2) INFORMATION FOR SEQ ID NO:710:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..40

(D) OTHER INFORMATION: / Ceres Seq. ID 1498884

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:710:

Met Arg Arg Trp Trp Trp Arg Arg Leu Leu Leu Asn Pro Arg Met Leu
1 5 10 15
Leu Trp Arg Val Leu Asn Arg Lys Met Tyr Arg Leu Gly Tyr Gly Val
20 25 30
Ala Gly Lys Lys Gly Val Lys Arg Pro
35 40

(2) INFORMATION FOR SEQ ID NO:711:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 37 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..37

(D) OTHER INFORMATION: / Ceres Seq. ID 1498885

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:711:

Met Ser Gly Lys Lys Ser Leu Lys Glu Leu Lys Arg Glu Arg Val Glu
1 5 10 15
Lys Glu Arg Glu Arg Ala Leu Phe Met Lys Gln Ser Gln Arg Ala Gly
20 25 30
Gly Phe Ser Arg Arg
35

(2) INFORMATION FOR SEQ ID NO:712:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1517 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1517

(D) OTHER INFORMATION: / Ceres Seq. ID 1498886

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:712:

aaactaagaa	acacccaaga	aaacaaacaa	acttttttaa	aaatgtccgt	ttcaacacat	60
caccaccacg	tggtcctctt	cccttacatg	tcaaaaggcc	acatcatccc	tctcctccaa	120
ttcggtcgtc	tcctcctccg	tcaccaccgc	aaagaaccaa	ccatcaccgt	caccgttttc	180
accactccca	agaaccaacc	tttcatctca	gacttcctct	cggacacgcc	ggagatcaaa	240
gtcatctctc	tccctttccc	ggaaaacatc	accggaatcc	ctcccggcgt	cgagaacacc	300
gaaaggctcc	catccatgtc	acttttcgtc	cccttcacac	gcgccacgaa	gcttctccaa	360
cctttcttcg	aagaaacact	caagactcct	ccaaaagtgt	cgttcatggt	ctctgatgga	420
ttcctctggt	ggacatcgga	gtctgcagct	aagttcaaca	ttccaagatt	tgtctcctac	480
ggcatgaact	cttactccgc	cgctgtctcc	atctctgttt	tcaaacacga	actctttacc	540
gaaccggaaa	gtaaattctga	taccgaaccg	gtcactgtac	cagactttcc	atggatcaag	600
atcaagaagt	gtgatttcga	ccatggcact	accgagccgg	agaatcagg	tgcagccctc	660
gaactatcta	tggaccaa	caagtgcacc	accacaagcc	atgggttttt	agtcaatagc	720
ttctacgagc	tcgagtcagc	atttggtgat	tacaacaaca	actctggtga	taaaccaaa	780
tcgtggtgtg	ttgggacct	gtggttgaca	gatcctccta	aacaggggag	tgctaaaccg	840
gcttggtatt	attggttgga	tcagaagcga	gaggaagggc	gtccgggttt	gtacgtggcg	900
tttggaacgc	aggcagagat	atcgaacaag	cagcttatgg	aactagcttt	cggcttgga	960
gattcaaagg	tgaactttct	gtgggtcaca	agaaaagatg	tggaggagat	tattggagaa	1020
ggattcaacg	atagaataag	agagagtggg	atgatagtga	gagattgggt	ggaccaatgg	1080
gagatattgt	cacatgaaag	tgtcaaagga	tttttgagcc	attgtgggtg	gaactcagca	1140

caagagagca tatgtgtcgg ggtcccattg ttggcttggc cgatgatggc cgagcaaccg 1200
ctcaatgcga agatggttgt ggaggagata aaggtgggag taagagttga aacggaagat 1260
gggagtgtaa aaggttttgt gacaagagag gaactaagtg gaaagattaa agaactgatg 1320
gaaggagaaa cggggaaaaac cgcaagaaaag aatgtgaaag aatactcgaa aatggcaaaa 1380
gcggctttgg tcgaaggggac tggttcgtca tggaagaatt tagatatgat tcttaaggac 1440
ttatgtaaga gtagagattc aaacggtgct agtgagtaga gtgattaaga attgaataac 1500
tgaaccggtc tacgttt

(2) INFORMATION FOR SEQ ID NO:713:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 478 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..478

(D) OTHER INFORMATION: / Ceres Seq. ID 1498887

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:713:

Met	Ser	Val	Ser	Thr	His	His	His	His	Val	Val	Leu	Phe	Pro	Tyr	Met
1				5					10					15	
Ser	Lys	Gly	His	Ile	Ile	Pro	Leu	Leu	Gln	Phe	Gly	Arg	Leu	Leu	Leu
			20					25					30		
Arg	His	His	Arg	Lys	Glu	Pro	Thr	Ile	Thr	Val	Thr	Val	Phe	Thr	Thr
			35				40					45			
Pro	Lys	Asn	Gln	Pro	Phe	Ile	Ser	Asp	Phe	Leu	Ser	Asp	Thr	Pro	Glu
		50				55				60					
Ile	Lys	Val	Ile	Ser	Leu	Pro	Phe	Pro	Glu	Asn	Ile	Thr	Gly	Ile	Pro
65					70				75					80	
Pro	Gly	Val	Glu	Asn	Thr	Glu	Arg	Leu	Pro	Ser	Met	Ser	Leu	Phe	Val
				85					90					95	
Pro	Phe	Thr	Arg	Ala	Thr	Lys	Leu	Leu	Gln	Pro	Phe	Phe	Glu	Glu	Thr
			100					105					110		
Leu	Lys	Thr	Leu	Pro	Lys	Val	Ser	Phe	Met	Val	Ser	Asp	Gly	Phe	Leu
			115				120					125			
Trp	Trp	Thr	Ser	Glu	Ser	Ala	Ala	Lys	Phe	Asn	Ile	Pro	Arg	Phe	Val
						135					140				
Ser	Tyr	Gly	Met	Asn	Ser	Tyr	Ser	Ala	Ala	Val	Ser	Ile	Ser	Val	Phe
145				150						155				160	
Lys	His	Glu	Leu	Phe	Thr	Glu	Pro	Glu	Ser	Lys	Ser	Asp	Thr	Glu	Pro
				165					170					175	
Val	Thr	Val	Pro	Asp	Phe	Pro	Trp	Ile	Lys	Ile	Lys	Lys	Cys	Asp	Phe
			180					185					190		
Asp	His	Gly	Thr	Thr	Glu	Pro	Glu	Glu	Ser	Gly	Ala	Ala	Leu	Glu	Leu
			195				200					205			
Ser	Met	Asp	Gln	Ile	Lys	Ser	Thr	Thr	Thr	Ser	His	Gly	Phe	Leu	Val
		210				215					220				
Asn	Ser	Phe	Tyr	Glu	Leu	Glu	Ser	Ala	Phe	Val	Asp	Tyr	Asn	Asn	Asn
225				230						235				240	
Ser	Gly	Asp	Lys	Pro	Lys	Ser	Trp	Cys	Val	Gly	Pro	Leu	Cys	Leu	Thr
			245						250					255	
Asp	Pro	Pro	Lys	Gln	Gly	Ser	Ala	Lys	Pro	Ala	Trp	Ile	His	Trp	Leu
			260					265					270		
Asp	Gln	Lys	Arg	Glu	Glu	Gly	Arg	Pro	Val	Leu	Tyr	Val	Ala	Phe	Gly
		275					280					285			
Thr	Gln	Ala	Glu	Ile	Ser	Asn	Lys	Gln	Leu	Met	Glu	Leu	Ala	Phe	Gly
		290				295					300				
Leu	Glu	Asp	Ser	Lys	Val	Asn	Phe	Leu	Trp	Val	Thr	Arg	Lys	Asp	Val
305					310					315				320	
Glu	Glu	Ile	Ile	Gly	Glu	Gly	Phe	Asn	Asp	Arg	Ile	Arg	Glu	Ser	Gly
				325					330					335	

Met Ile Val Arg Asp Trp Val Asp Gln Trp Glu Ile Leu Ser His Glu
340 345 350
Ser Val Lys Gly Phe Leu Ser His Cys Gly Trp Asn Ser Ala Gln Glu
355 360 365
Ser Ile Cys Val Gly Val Pro Leu Leu Ala Trp Pro Met Met Ala Glu
370 375 380
Gln Pro Leu Asn Ala Lys Met Val Val Glu Glu Ile Lys Val Gly Val
385 390 395 400
Arg Val Glu Thr Glu Asp Gly Ser Val Lys Gly Phe Val Thr Arg Glu
405 410 415
Glu Leu Ser Gly Lys Ile Lys Glu Leu Met Glu Gly Glu Thr Gly Lys
420 425 430
Thr Ala Arg Lys Asn Val Lys Glu Tyr Ser Lys Met Ala Lys Ala Ala
435 440 445
Leu Val Glu Gly Thr Gly Ser Ser Trp Lys Asn Leu Asp Met Ile Leu
450 455 460
Lys Asp Leu Cys Lys Ser Arg Asp Ser Asn Gly Ala Ser Glu
465 470 475

(2) INFORMATION FOR SEQ ID NO:714:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 463 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..463
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498888

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:714:

Met Ser Lys Gly His Ile Ile Pro Leu Leu Gln Phe Gly Arg Leu Leu
1 5 10 15
Leu Arg His His Arg Lys Glu Pro Thr Ile Thr Val Thr Val Phe Thr
20 25 30
Thr Pro Lys Asn Gln Pro Phe Ile Ser Asp Phe Leu Ser Asp Thr Pro
35 40 45
Glu Ile Lys Val Ile Ser Leu Pro Phe Pro Glu Asn Ile Thr Gly Ile
50 55 60
Pro Pro Gly Val Glu Asn Thr Glu Arg Leu Pro Ser Met Ser Leu Phe
65 70 75 80
Val Pro Phe Thr Arg Ala Thr Lys Leu Leu Gln Pro Phe Phe Glu Glu
85 90 95
Thr Leu Lys Thr Leu Pro Lys Val Ser Phe Met Val Ser Asp Gly Phe
100 105 110
Leu Trp Trp Thr Ser Glu Ser Ala Ala Lys Phe Asn Ile Pro Arg Phe
115 120 125
Val Ser Tyr Gly Met Asn Ser Tyr Ser Ala Ala Val Ser Ile Ser Val
130 135 140
Phe Lys His Glu Leu Phe Thr Glu Pro Glu Ser Lys Ser Asp Thr Glu
145 150 155 160
Pro Val Thr Val Pro Asp Phe Pro Trp Ile Lys Ile Lys Lys Cys Asp
165 170 175
Phe Asp His Gly Thr Thr Glu Pro Glu Glu Ser Gly Ala Ala Leu Glu
180 185 190
Leu Ser Met Asp Gln Ile Lys Ser Thr Thr Thr Ser His Gly Phe Leu
195 200 205
Val Asn Ser Phe Tyr Glu Leu Glu Ser Ala Phe Val Asp Tyr Asn Asn
210 215 220
Asn Ser Gly Asp Lys Pro Lys Ser Trp Cys Val Gly Pro Leu Cys Leu
225 230 235 240
Thr Asp Pro Pro Lys Gln Gly Ser Ala Lys Pro Ala Trp Ile His Trp

Leu	Asp	Gln	Lys	Arg	Glu	Glu	Gly	Arg	Pro	Val	Leu	Tyr	Val	Ala	Phe
			260					265					270		
Gly	Thr	Gln	Ala	Glu	Ile	Ser	Asn	Lys	Gln	Leu	Met	Glu	Leu	Ala	Phe
		275					280					285			
Gly	Leu	Glu	Asp	Ser	Lys	Val	Asn	Phe	Leu	Trp	Val	Thr	Arg	Lys	Asp
	290					295				300					
Val	Glu	Glu	Ile	Ile	Gly	Glu	Gly	Phe	Asn	Asp	Arg	Ile	Arg	Glu	Ser
305					310				315					320	
Gly	Met	Ile	Val	Arg	Asp	Trp	Val	Asp	Gln	Trp	Glu	Ile	Leu	Ser	His
			325					330					335		
Glu	Ser	Val	Lys	Gly	Phe	Leu	Ser	His	Cys	Gly	Trp	Asn	Ser	Ala	Gln
		340						345					350		
Glu	Ser	Ile	Cys	Val	Gly	Val	Pro	Leu	Leu	Ala	Trp	Pro	Met	Met	Ala
	355					360				365					
Glu	Gln	Pro	Leu	Asn	Ala	Lys	Met	Val	Val	Glu	Glu	Ile	Lys	Val	Gly
	370					375				380					
Val	Arg	Val	Glu	Thr	Glu	Asp	Gly	Ser	Val	Lys	Gly	Phe	Val	Thr	Arg
385					390				395					400	
Glu	Glu	Leu	Ser	Gly	Lys	Ile	Lys	Glu	Leu	Met	Glu	Gly	Glu	Thr	Gly
			405					410					415		
Lys	Thr	Ala	Arg	Lys	Asn	Val	Lys	Glu	Tyr	Ser	Lys	Met	Ala	Lys	Ala
		420					425					430			
Ala	Leu	Val	Glu	Gly	Thr	Gly	Ser	Ser	Trp	Lys	Asn	Leu	Asp	Met	Ile
	435					440					445				
Leu	Lys	Asp	Leu	Cys	Lys	Ser	Arg	Asp	Ser	Asn	Gly	Ala	Ser	Glu	
	450				455					460					

(2) INFORMATION FOR SEQ ID NO:715:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 387 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..387
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498889

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:715:

Met	Ser	Leu	Phe	Val	Pro	Phe	Thr	Arg	Ala	Thr	Lys	Leu	Leu	Gln	Pro
1				5					10					15	
Phe	Phe	Glu	Glu	Thr	Leu	Lys	Thr	Leu	Pro	Lys	Val	Ser	Phe	Met	Val
		20						25				30			
Ser	Asp	Gly	Phe	Leu	Trp	Trp	Thr	Ser	Glu	Ser	Ala	Ala	Lys	Phe	Asn
	35					40					45				
Ile	Pro	Arg	Phe	Val	Ser	Tyr	Gly	Met	Asn	Ser	Tyr	Ser	Ala	Ala	Val
	50				55				60						
Ser	Ile	Ser	Val	Phe	Lys	His	Glu	Leu	Phe	Thr	Glu	Pro	Glu	Ser	Lys
65					70				75					80	
Ser	Asp	Thr	Glu	Pro	Val	Thr	Val	Pro	Asp	Phe	Pro	Trp	Ile	Lys	Ile
			85					90					95		
Lys	Lys	Cys	Asp	Phe	Asp	His	Gly	Thr	Thr	Glu	Pro	Glu	Glu	Ser	Gly
		100					105					110			
Ala	Ala	Leu	Glu	Leu	Ser	Met	Asp	Gln	Ile	Lys	Ser	Thr	Thr	Thr	Ser
	115					120						125			
His	Gly	Phe	Leu	Val	Asn	Ser	Phe	Tyr	Glu	Leu	Glu	Ser	Ala	Phe	Val
	130				135						140				
Asp	Tyr	Asn	Asn	Asn	Ser	Gly	Asp	Lys	Pro	Lys	Ser	Trp	Cys	Val	Gly
145				150					155					160	
Pro	Leu	Cys	Leu	Thr	Asp	Pro	Pro	Lys	Gln	Gly	Ser	Ala	Lys	Pro	Ala
			165					170						175	

Trp Ile His Trp Leu Asp Gln Lys Arg Glu Glu Gly Arg Pro Val Leu
180 185 190
Tyr Val Ala Phe Gly Thr Gln Ala Glu Ile Ser Asn Lys Gln Leu Met
195 200 205
Glu Leu Ala Phe Gly Leu Glu Asp Ser Lys Val Asn Phe Leu Trp Val
210 215 220
Thr Arg Lys Asp Val Glu Glu Ile Ile Gly Glu Gly Phe Asn Asp Arg
225 230 235 240
Ile Arg Glu Ser Gly Met Ile Val Arg Asp Trp Val Asp Gln Trp Glu
245 250 255
Ile Leu Ser His Glu Ser Val Lys Gly Phe Leu Ser His Cys Gly Trp
260 265 270
Asn Ser Ala Gln Glu Ser Ile Cys Val Gly Val Pro Leu Leu Ala Trp
275 280 285
Pro Met Met Ala Glu Gln Pro Leu Asn Ala Lys Met Val Val Glu Glu
290 295 300
Ile Lys Val Gly Val Arg Val Glu Thr Glu Asp Gly Ser Val Lys Gly
305 310 315 320
Phe Val Thr Arg Glu Glu Leu Ser Gly Lys Ile Lys Glu Leu Met Glu
325 330 335
Gly Glu Thr Gly Lys Thr Ala Arg Lys Asn Val Lys Glu Tyr Ser Lys
340 345 350
Met Ala Lys Ala Ala Leu Val Glu Gly Thr Gly Ser Ser Trp Lys Asn
355 360 365
Leu Asp Met Ile Leu Lys Asp Leu Cys Lys Ser Arg Asp Ser Asn Gly
370 375 380
Ala Ser Glu
385

(2) INFORMATION FOR SEQ ID NO:716:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1689 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1689
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498890

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:716:

atttggctct	ttatcttgct	ttgtctgat	cagtagtcac	tacatttggt	tctttcacaa	60
tctttctttt	ttgcttcata	ttgaactgca	agaccaatcc	atgaatgcaa	atataaaata	120
ttgtcttacg	gttaaccatc	tctaagtgtt	tgctagtcat	gaattgtgaa	attgtttcgc	180
ttcaaacata	gaattagttg	atttggaat	gtagacatga	atgcttatct	aaatacaata	240
aactgtgttc	ttgtttcagt	tgtgtatcag	agatgagacc	ttgactggta	atttcaatgg	300
agcataatta	aatgctaata	atacttattt	tctggttaat	gcagggaggt	tgagagtgtg	360
aagaaaccat	ttacgccacc	caggggaagt	catgttcaag	tcttgcactc	catgccacct	420
caaaagatcg	agatcttcaa	atctatggaa	aactgggccc	aggagaacct	tctgattcac	480
ctcaaggatg	tggagaagtc	ttggcaaccc	caggatttct	tgccctgacc	tgcatcagat	540
gggtttgaag	atcaggtaag	agagttaaga	gagagggcta	gagagctccc	tgatgattac	600
tttgttggtt	tggtgggga	catgatcaca	gaagaagcac	ttccgacct	tcaaactatg	660
ttgaacactt	tggatggagt	tagggatgaa	acaggtgcta	gtcctacttc	atgggctatt	720
tggaccagag	cttggactgc	agaagaaaac	cgacatggcg	atcttctgaa	taaatacctt	780
tacttgctcg	gtcgtgttga	catgaggcag	atcgaaaaga	ccattcagta	cttgattgga	840
tctggaatgg	atccgcggac	agagaataac	ccctaccttg	gcttcatcta	tacgtcattc	900
caagaaagag	cgacattcat	ctctcacgga	aacacagccc	gccaaagcaa	agagcacggg	960
gacatcaaac	tagcccaaat	atgtggcaca	atagctgcag	acgagaagcg	tcatgaaaca	1020
gcataaccca	agatagtgtg	aaagctcttt	gagattgcat	ctgatgggtac	tgatcatggct	1080
tttgcagaca	tgatgagaaa	gaaaatctca	atgcctgctc	acttgatgta	tgatggggcg	1140
aacgacaacc	tctttgacaa	cttctcttcc	gtggctcaga	ggctcgggtg	ttacaccgcc	1200
aaagactatg	cagacattct	tgagtttctg	gttggttaggt	ggaaaatcca	ggacttaacc	1260

```
gggcttttcag gtgaaggaaa caaagcacaa gactatttat gcggggttggc tccaaggatc 1320
aagagattgg atgagagagc tcaagcaaga gccaaagaaag gacccaagat tccttttcagt 1380
tggatacacg acagagaagt gcagctctaa aaggacaaag acaaaaacaa aaacctatcc 1440
tcccggttcc tcattttcatc tgtctgctct taaaattggt gtagattact atggttttct 1500
gataatgttg gtgggtctag ttacaaagtt gagatgcagt gatttagtag ctttgttttt 1560
cccagtcact atatgtttgg tctttggtcc gtttagcacac ttgtagtagt taaaacagtt 1620
taagtatggt ctgtgctcag tcttcctctt ctctgtggag ttttgtttaa gttcaggtta 1680
gttttgttt
```

(2) INFORMATION FOR SEQ ID NO:717:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 332 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..332
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498891

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:717:

```
Met Pro Pro Gln Lys Ile Glu Ile Phe Lys Ser Met Glu Asn Trp Ala
1          5          10          15
Glu Glu Asn Leu Leu Ile His Leu Lys Asp Val Glu Lys Ser Trp Gln
20          25          30
Pro Gln Asp Phe Leu Pro Asp Pro Ala Ser Asp Gly Phe Glu Asp Gln
35          40          45
Val Arg Glu Leu Arg Glu Arg Ala Arg Glu Leu Pro Asp Asp Tyr Phe
50          55          60
Val Val Leu Val Gly Asp Met Ile Thr Glu Glu Ala Leu Pro Thr Tyr
65          70          75          80
Gln Thr Met Leu Asn Thr Leu Asp Gly Val Arg Asp Glu Thr Gly Ala
85          90          95
Ser Pro Thr Ser Trp Ala Ile Trp Thr Arg Ala Trp Thr Ala Glu Glu
100         105         110
Asn Arg His Gly Asp Leu Leu Asn Lys Tyr Leu Tyr Leu Ser Gly Arg
115         120         125
Val Asp Met Arg Gln Ile Glu Lys Thr Ile Gln Tyr Leu Ile Gly Ser
130         135         140
Gly Met Asp Pro Arg Thr Glu Asn Asn Pro Tyr Leu Gly Phe Ile Tyr
145         150         155         160
Thr Ser Phe Gln Glu Arg Ala Thr Phe Ile Ser His Gly Asn Thr Ala
165         170         175
Arg Gln Ala Lys Glu His Gly Asp Ile Lys Leu Ala Gln Ile Cys Gly
180         185         190
Thr Ile Ala Ala Asp Glu Lys Arg His Glu Thr Ala Tyr Thr Lys Ile
195         200         205
Val Glu Lys Leu Phe Glu Ile Asp Pro Asp Gly Thr Val Met Ala Phe
210         215         220
Ala Asp Met Met Arg Lys Lys Ile Ser Met Pro Ala His Leu Met Tyr
225         230         235         240
Asp Gly Arg Asn Asp Asn Leu Phe Asp Asn Phe Ser Ser Val Ala Gln
245         250         255
Arg Leu Gly Val Tyr Thr Ala Lys Asp Tyr Ala Asp Ile Leu Glu Phe
260         265         270
Leu Val Gly Arg Trp Lys Ile Gln Asp Leu Thr Gly Leu Ser Gly Glu
275         280         285
Gly Asn Lys Ala Gln Asp Tyr Leu Cys Gly Leu Ala Pro Arg Ile Lys
290         295         300
Arg Leu Asp Glu Arg Ala Gln Ala Arg Ala Lys Lys Gly Pro Lys Ile
305         310         315         320
Pro Phe Ser Trp Ile His Asp Arg Glu Val Gln Leu
```

325

330

(2) INFORMATION FOR SEQ ID NO:718:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 321 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..321
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498892

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:718:

Met	Glu	Asn	Trp	Ala	Glu	Glu	Asn	Leu	Leu	Ile	His	Leu	Lys	Asp	Val
1				5					10					15	
Glu	Lys	Ser	Trp	Gln	Pro	Gln	Asp	Phe	Leu	Pro	Asp	Pro	Ala	Ser	Asp
			20					25					30		
Gly	Phe	Glu	Asp	Gln	Val	Arg	Glu	Leu	Arg	Glu	Arg	Ala	Arg	Glu	Leu
		35					40					45			
Pro	Asp	Asp	Tyr	Phe	Val	Val	Leu	Val	Gly	Asp	Met	Ile	Thr	Glu	Glu
	50					55					60				
Ala	Leu	Pro	Thr	Tyr	Gln	Thr	Met	Leu	Asn	Thr	Leu	Asp	Gly	Val	Arg
65					70					75				80	
Asp	Glu	Thr	Gly	Ala	Ser	Pro	Thr	Ser	Trp	Ala	Ile	Trp	Thr	Arg	Ala
			85						90					95	
Trp	Thr	Ala	Glu	Asn	Arg	His	Gly	Asp	Leu	Leu	Asn	Lys	Tyr	Leu	
		100					105					110			
Tyr	Leu	Ser	Gly	Arg	Val	Asp	Met	Arg	Gln	Ile	Glu	Lys	Thr	Ile	Gln
	115					120					125				
Tyr	Leu	Ile	Gly	Ser	Gly	Met	Asp	Pro	Arg	Thr	Glu	Asn	Asn	Pro	Tyr
	130				135					140					
Leu	Gly	Phe	Ile	Tyr	Thr	Ser	Phe	Gln	Glu	Arg	Ala	Thr	Phe	Ile	Ser
145					150					155				160	
His	Gly	Asn	Thr	Ala	Arg	Gln	Ala	Lys	Glu	His	Gly	Asp	Ile	Lys	Leu
			165						170					175	
Ala	Gln	Ile	Cys	Gly	Thr	Ile	Ala	Ala	Asp	Glu	Lys	Arg	His	Glu	Thr
		180					185						190		
Ala	Tyr	Thr	Lys	Ile	Val	Glu	Lys	Leu	Phe	Glu	Ile	Asp	Pro	Asp	Gly
	195					200						205			
Thr	Val	Met	Ala	Phe	Ala	Asp	Met	Met	Arg	Lys	Lys	Ile	Ser	Met	Pro
	210				215						220				
Ala	His	Leu	Met	Tyr	Asp	Gly	Arg	Asn	Asp	Asn	Leu	Phe	Asp	Asn	Phe
225				230					235					240	
Ser	Ser	Val	Ala	Gln	Arg	Leu	Gly	Val	Tyr	Thr	Ala	Lys	Asp	Tyr	Ala
			245						250					255	
Asp	Ile	Leu	Glu	Phe	Leu	Val	Gly	Arg	Trp	Lys	Ile	Gln	Asp	Leu	Thr
		260					265					270			
Gly	Leu	Ser	Gly	Glu	Gly	Asn	Lys	Ala	Gln	Asp	Tyr	Leu	Cys	Gly	Leu
	275					280						285			
Ala	Pro	Arg	Ile	Lys	Arg	Leu	Asp	Glu	Arg	Ala	Gln	Ala	Arg	Ala	Lys
	290				295						300				
Lys	Gly	Pro	Lys	Ile	Pro	Phe	Ser	Trp	Ile	His	Asp	Arg	Glu	Val	Gln
305				310						315				320	
Leu															

(2) INFORMATION FOR SEQ ID NO:719:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 262 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..262

(D) OTHER INFORMATION: / Ceres Seq. ID 1498893

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:719:

```
Met Ile Thr Glu Glu Ala Leu Pro Thr Tyr Gln Thr Met Leu Asn Thr
1          5          10          15
Leu Asp Gly Val Arg Asp Glu Thr Gly Ala Ser Pro Thr Ser Trp Ala
20          25          30
Ile Trp Thr Arg Ala Trp Thr Ala Glu Glu Asn Arg His Gly Asp Leu
35          40          45
Leu Asn Lys Tyr Leu Tyr Leu Ser Gly Arg Val Asp Met Arg Gln Ile
50          55          60
Glu Lys Thr Ile Gln Tyr Leu Ile Gly Ser Gly Met Asp Pro Arg Thr
65          70          75          80
Glu Asn Asn Pro Tyr Leu Gly Phe Ile Tyr Thr Ser Phe Gln Glu Arg
85          90          95
Ala Thr Phe Ile Ser His Gly Asn Thr Ala Arg Gln Ala Lys Glu His
100         105         110
Gly Asp Ile Lys Leu Ala Gln Ile Cys Gly Thr Ile Ala Ala Asp Glu
115         120         125
Lys Arg His Glu Thr Ala Tyr Thr Lys Ile Val Glu Lys Leu Phe Glu
130         135         140
Ile Asp Pro Asp Gly Thr Val Met Ala Phe Ala Asp Met Met Arg Lys
145         150         155         160
Lys Ile Ser Met Pro Ala His Leu Met Tyr Asp Gly Arg Asn Asp Asn
165         170         175
Leu Phe Asp Asn Phe Ser Ser Val Ala Gln Arg Leu Gly Val Tyr Thr
180         185         190
Ala Lys Asp Tyr Ala Asp Ile Leu Glu Phe Leu Val Gly Arg Trp Lys
195         200         205
Ile Gln Asp Leu Thr Gly Leu Ser Gly Glu Gly Asn Lys Ala Gln Asp
210         215         220
Tyr Leu Cys Gly Leu Ala Pro Arg Ile Lys Arg Leu Asp Glu Arg Ala
225         230         235         240
Gln Ala Arg Ala Lys Lys Gly Pro Lys Ile Pro Phe Ser Trp Ile His
245         250         255
Asp Arg Glu Val Gln Leu
260
```

(2) INFORMATION FOR SEQ ID NO:720:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1029 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1029

(D) OTHER INFORMATION: / Ceres Seq. ID 1498905

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:720:

```
aacaaagtgt gttcttaaat tatcttctct gataaccaa aaagccctat tttccgagat      60
gaatacccta gaagaagtag atgaatccac tcatatcttc aacgctttga tgagtctaata      120
gaggaaatth ttgttcagag ttctatgcgt cgggtccaatc cctactaaca tttcattcat      180
catggatgga aaccgcaggt tcgctaagaa acacaatctt ataggcctag atgcaggaca      240
tagagctggt ttcatatccg tgaaatatat tcttcaatac tgcaaagaga ttggtgtacc      300
gtacgtcaca ctccacgcgt ttggtatgga taatttcaag agaggacctg aagaagtcaa      360
gtgtgtgatg gatctaatac ttgagaaagt cgagctcgcg atcgatcaag ctgtatcagg      420
gaatatgaac ggcgtgagaa taatctttgc cgggtgatttg gattcggttaa acgagcatth      480
tagagctgcg acaaagaaac tgatggagct tacggaggag aatagagatc tgattgtggt      540
```

```
ggtttgcgtt gcttacagca caagtctcga gattgttcac gctgttcgaa aatcttgtgt 600
tagaaaaatgt acgaatggag atgatcttgt acttttggag ttgagtgatg ttgaagagtg 660
tatgtataca tcgattgtgc cggttccgga tcttgtgata agaaccggag gaggagatcg 720
gctgagtaac ttcatgacgt ggcaaacttc gaggtctctt cttcacagaa cggaggctct 780
ttggccggag ttagggctct ggcatattgg ttgggcaatt cttaaattcc aaagaatgca 840
agattacttg acgaagaaga aaaagctcga ttagatagtt tctaaagtta aaccctgcag 900
gaaagaactt ttaactcttt attacgttta atttacgtgt ttctatgact ggaaacgaga 960
aagctcacaa gcaaactctt tttattatgt attggatccg tataacaaac acgaatatac 1020
aaaacatcg
```

(2) INFORMATION FOR SEQ ID NO:721:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 290 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..290

(D) OTHER INFORMATION: / Ceres Seq. ID 1498906

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:721:

```
Thr Lys Cys Val Leu Lys Leu Ser Ser Leu Ile Thr Lys Lys Ala Leu
1      5      10      15
Phe Ser Glu Met Asn Thr Leu Glu Glu Val Asp Glu Ser Thr His Ile
      20      25      30
Phe Asn Ala Leu Met Ser Leu Met Arg Lys Phe Leu Phe Arg Val Leu
      35      40      45
Cys Val Gly Pro Ile Pro Thr Asn Ile Ser Phe Ile Met Asp Gly Asn
      50      55      60
Arg Arg Phe Ala Lys Lys His Asn Leu Ile Gly Leu Asp Ala Gly His
      65      70      75      80
Arg Ala Gly Phe Ile Ser Val Lys Tyr Ile Leu Gln Tyr Cys Lys Glu
      85      90      95
Ile Gly Val Pro Tyr Val Thr Leu His Ala Phe Gly Met Asp Asn Phe
      100     105     110
Lys Arg Gly Pro Glu Glu Val Lys Cys Val Met Asp Leu Met Leu Glu
      115     120     125
Lys Val Glu Leu Ala Ile Asp Gln Ala Val Ser Gly Asn Met Asn Gly
      130     135     140
Val Arg Ile Ile Phe Ala Gly Asp Leu Asp Ser Leu Asn Glu His Phe
      145     150     155     160
Arg Ala Ala Thr Lys Lys Leu Met Glu Leu Thr Glu Glu Asn Arg Asp
      165     170     175
Leu Ile Val Val Val Cys Val Ala Tyr Ser Thr Ser Leu Glu Ile Val
      180     185     190
His Ala Val Arg Lys Ser Cys Val Arg Lys Cys Thr Asn Gly Asp Asp
      195     200     205
Leu Val Leu Leu Glu Leu Ser Asp Val Glu Glu Cys Met Tyr Thr Ser
      210     215     220
Ile Val Pro Val Pro Asp Leu Val Ile Arg Thr Gly Gly Gly Asp Arg
      225     230     235     240
Leu Ser Asn Phe Met Thr Trp Gln Thr Ser Arg Ser Leu Leu His Arg
      245     250     255
Thr Glu Ala Leu Trp Pro Glu Leu Gly Leu Trp His Leu Val Trp Ala
      260     265     270
Ile Leu Lys Phe Gln Arg Met Gln Asp Tyr Leu Thr Lys Lys Lys Lys
      275     280     285
Leu Asp
      290
```

(2) INFORMATION FOR SEQ ID NO:722:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 271 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..271
(D) OTHER INFORMATION: / Ceres Seq. ID 1498907
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:722:

Met	Asn	Thr	Leu	Glu	Glu	Val	Asp	Glu	Ser	Thr	His	Ile	Phe	Asn	Ala
1				5					10					15	
Leu	Met	Ser	Leu	Met	Arg	Lys	Phe	Leu	Phe	Arg	Val	Leu	Cys	Val	Gly
			20					25					30		
Pro	Ile	Pro	Thr	Asn	Ile	Ser	Phe	Ile	Met	Asp	Gly	Asn	Arg	Arg	Phe
			35				40					45			
Ala	Lys	Lys	His	Asn	Leu	Ile	Gly	Leu	Asp	Ala	Gly	His	Arg	Ala	Gly
	50				55					60					
Phe	Ile	Ser	Val	Lys	Tyr	Ile	Leu	Gln	Tyr	Cys	Lys	Glu	Ile	Gly	Val
65				70					75					80	
Pro	Tyr	Val	Thr	Leu	His	Ala	Phe	Gly	Met	Asp	Asn	Phe	Lys	Arg	Gly
			85						90					95	
Pro	Glu	Glu	Val	Lys	Cys	Val	Met	Asp	Leu	Met	Leu	Glu	Lys	Val	Glu
			100					105					110		
Leu	Ala	Ile	Asp	Gln	Ala	Val	Ser	Gly	Asn	Met	Asn	Gly	Val	Arg	Ile
	115				120							125			
Ile	Phe	Ala	Gly	Asp	Leu	Asp	Ser	Leu	Asn	Glu	His	Phe	Arg	Ala	Ala
	130				135						140				
Thr	Lys	Lys	Leu	Met	Glu	Leu	Thr	Glu	Glu	Asn	Arg	Asp	Leu	Ile	Val
145					150					155				160	
Val	Val	Cys	Val	Ala	Tyr	Ser	Thr	Ser	Leu	Glu	Ile	Val	His	Ala	Val
			165						170					175	
Arg	Lys	Ser	Cys	Val	Arg	Lys	Cys	Thr	Asn	Gly	Asp	Asp	Leu	Val	Leu
			180					185					190		
Leu	Glu	Leu	Ser	Asp	Val	Glu	Glu	Cys	Met	Tyr	Thr	Ser	Ile	Val	Pro
			195				200					205			
Val	Pro	Asp	Leu	Val	Ile	Arg	Thr	Gly	Gly	Gly	Asp	Arg	Leu	Ser	Asn
	210					215					220				
Phe	Met	Thr	Trp	Gln	Thr	Ser	Arg	Ser	Leu	Leu	His	Arg	Thr	Glu	Ala
225					230					235				240	
Leu	Trp	Pro	Glu	Leu	Gly	Leu	Trp	His	Leu	Val	Trp	Ala	Ile	Leu	Lys
			245						250					255	
Phe	Gln	Arg	Met	Gln	Asp	Tyr	Leu	Thr	Lys	Lys	Lys	Lys	Leu	Asp	
			260					265						270	

(2) INFORMATION FOR SEQ ID NO:723:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 254 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..254
(D) OTHER INFORMATION: / Ceres Seq. ID 1498908
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:723:

Met	Ser	Leu	Met	Arg	Lys	Phe	Leu	Phe	Arg	Val	Leu	Cys	Val	Gly	Pro
1			5						10					15	
Ile	Pro	Thr	Asn	Ile	Ser	Phe	Ile	Met	Asp	Gly	Asn	Arg	Arg	Phe	Ala
			20					25					30		
Lys	Lys	His	Asn	Leu	Ile	Gly	Leu	Asp	Ala	Gly	His	Arg	Ala	Gly	Phe

35	40	45
Ile Ser Val Lys Tyr Ile Leu Gln Tyr Cys Lys	Glu Ile Gly Val Pro	
50	55	60
Tyr Val Thr Leu His Ala Phe Gly Met Asp Asn Phe Lys Arg Gly Pro		
65	70	75
Glu Glu Val Lys Cys Val Met Asp Leu Met Leu Glu Lys Val Glu Leu		
85	90	95
Ala Ile Asp Gln Ala Val Ser Gly Asn Met Asn Gly Val Arg Ile Ile		
100	105	110
Phe Ala Gly Asp Leu Asp Ser Leu Asn Glu His Phe Arg Ala Ala Thr		
115	120	125
Lys Lys Leu Met Glu Leu Thr Glu Glu Asn Arg Asp Leu Ile Val Val		
130	135	140
Val Cys Val Ala Tyr Ser Thr Ser Leu Glu Ile Val His Ala Val Arg		
145	150	155
Lys Ser Cys Val Arg Lys Cys Thr Asn Gly Asp Asp Leu Val Leu Leu		
165	170	175
Glu Leu Ser Asp Val Glu Glu Cys Met Tyr Thr Ser Ile Val Pro Val		
180	185	190
Pro Asp Leu Val Ile Arg Thr Gly Gly Gly Asp Arg Leu Ser Asn Phe		
195	200	205
Met Thr Trp Gln Thr Ser Arg Ser Leu Leu His Arg Thr Glu Ala Leu		
210	215	220
Trp Pro Glu Leu Gly Leu Trp His Leu Val Trp Ala Ile Leu Lys Phe		
225	230	235
Gln Arg Met Gln Asp Tyr Leu Thr Lys Lys Lys Lys Leu Asp		
245	250	

(2) INFORMATION FOR SEQ ID NO:724:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1358 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1358
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498912

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:724:

aaggaaacac	ttaaccaagc	aaacaacaaa	tggctctttc	aatcgttctt	cttccttcca	60
ttctcattct	cataccgact	tttctcagtt	cggttttcgc	cgtttcacca	ctcaaaactg	120
atacgtaaaa	accggggcag	cagctcagag	actgggagca	gttgatctct	gcggatggta	180
tcttcactct	cggattcttt	acacctaaag	actcatctac	ttccgaactc	gggtcagctg	240
gtcttagata	tcttggtatt	tggcctcaaa	gtattccaat	aaatctagtt	tgggtgggta	300
acccaaccga	atcagtttct	gattcatctg	gttctctatc	cattgacacc	aatgggggtc	360
taaagataac	acaggcaaac	gctattccaa	tcttggtgaa	ccaaagacca	gccgcgcagc	420
tttcattggt	cgggaatgtg	tctgccattt	tactcgatac	cgggaacttt	gtggtccgag	480
agatcaggcc	aggaggagtt	ccgggtcgtg	ttctatggca	aagctttgac	catcccacaa	540
acacattact	tcccgggatg	aagattgggt	ttaacctaa	aaccaagaaa	gaagtatcag	600
ttacgtcttg	gataactgac	caagtcccag	tcccaggagc	attcagacta	ggagagaccc	660
atcaggagct	aaccagttac	tcgtctggcg	ccgcggggaa	atctactggg	ccagtggaat	720
cttgacgaac	aatggaagct	ctcatttgaa	cttagaagta	tccagacact	acattgatta	780
tgaattcaag	ttcgattcaa	ataagtacat	gaagtacttc	agctactcaa	tcaagaaagc	840
taatagttcg	gtcttttcca	gctggttctt	ggatactcta	ggccaaatca	ctgtaacctt	900
ttctctcagc	agtaacaata	gcagcacctg	gatttccgaa	agcagtgaac	cctgcaagac	960
ggattttaag	aacagttcag	caatctgcac	cacggagaag	ccaacggctt	gtaggaaagg	1020
gtcagagtat	ttcgaaccca	gaagaggata	catgatggaa	aataataaccg	gttattatcc	1080
attttactat	gacgatagtt	tgagcgctgg	tcttagcgac	tgtcatggaa	cctgctggag	1140
aaactgttct	tgcatagctt	tccaagcctt	tcttgatgga	tgccaatatt	gggaaaaagg	1200
atcaaagttt	gttccttatg	atagcttcaa	ctccaattta	gtaacttatg	ttcttgattc	1260
tgtaaagtga	tgtgtggttg	taacttgaac	gagcaattat	gtaaccagac	tagtatcagt	1320

aaaggggttt attaagaaac taaagaatca agcagttc

(2) INFORMATION FOR SEQ ID NO:725:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 231 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..231

(D) OTHER INFORMATION: / Ceres Seq. ID 1498913

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:725:

Met	Ala	Leu	Ser	Ile	Val	Leu	Leu	Pro	Phe	Ile	Leu	Ile	Leu	Ile	Pro
1				5				10					15		
Thr	Phe	Leu	Ser	Ser	Val	Phe	Ala	Val	Ser	Pro	Leu	Lys	Thr	Asp	Thr
		20					25					30			
Leu	Lys	Pro	Gly	Gln	Gln	Leu	Arg	Asp	Trp	Glu	Gln	Leu	Ile	Ser	Ala
		35					40					45			
Asp	Gly	Ile	Phe	Thr	Leu	Gly	Phe	Phe	Thr	Pro	Lys	Asp	Ser	Ser	Thr
	50					55					60				
Ser	Glu	Leu	Gly	Ser	Ala	Gly	Leu	Arg	Tyr	Leu	Gly	Ile	Trp	Pro	Gln
65					70				75					80	
Ser	Ile	Pro	Ile	Asn	Leu	Val	Trp	Val	Gly	Asn	Pro	Thr	Glu	Ser	Val
				85					90					95	
Ser	Asp	Ser	Ser	Gly	Ser	Leu	Ser	Ile	Asp	Thr	Asn	Gly	Val	Leu	Lys
		100						105					110		
Ile	Thr	Gln	Ala	Asn	Ala	Ile	Pro	Ile	Leu	Val	Asn	Gln	Arg	Pro	Ala
		115					120					125			
Ala	Gln	Leu	Ser	Leu	Val	Gly	Asn	Val	Ser	Ala	Ile	Leu	Leu	Asp	Thr
	130					135					140				
Gly	Asn	Phe	Val	Val	Arg	Glu	Ile	Arg	Pro	Gly	Gly	Val	Pro	Gly	Arg
145					150					155				160	
Val	Leu	Trp	Gln	Ser	Phe	Asp	His	Pro	Thr	Asn	Thr	Leu	Leu	Pro	Gly
			165						170					175	
Met	Lys	Ile	Gly	Phe	Asn	Leu	Arg	Thr	Lys	Lys	Glu	Val	Ser	Val	Thr
		180						185					190		
Ser	Trp	Ile	Thr	Asp	Gln	Val	Pro	Val	Pro	Gly	Ala	Phe	Arg	Leu	Gly
	195					200					205				
Glu	Thr	His	Gln	Glu	Leu	Thr	Ser	Tyr	Ser	Ser	Gly	Ala	Ala	Gly	Lys
	210					215					220				
Ser	Thr	Gly	Pro	Val	Glu	Ser									
225					230										

(2) INFORMATION FOR SEQ ID NO:726:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 153 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..153

(D) OTHER INFORMATION: / Ceres Seq. ID 1498914

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:726:

Met	Lys	Tyr	Phe	Ser	Tyr	Ser	Ile	Lys	Lys	Ala	Asn	Ser	Ser	Val	Phe
1				5				10						15	
Ser	Ser	Trp	Phe	Leu	Asp	Thr	Leu	Gly	Gln	Ile	Thr	Val	Thr	Phe	Ser
		20						25					30		
Leu	Ser	Ser	Asn	Asn	Ser	Ser	Thr	Trp	Ile	Ser	Glu	Ser	Ser	Glu	Pro
		35					40						45		

Cys Lys Thr Asp Leu Lys Asn Ser Ser Ala Ile Cys Ile Thr Glu Lys
50 55 60
Pro Thr Ala Cys Arg Lys Gly Ser Glu Tyr Phe Glu Pro Arg Arg Gly
65 70 75 80
Tyr Met Met Glu Asn Asn Thr Gly Tyr Tyr Pro Phe Tyr Tyr Asp Asp
85 90 95
Ser Leu Ser Ala Gly Leu Ser Asp Cys His Gly Thr Cys Trp Arg Asn
100 105 110
Cys Ser Cys Ile Ala Phe Gln Ala Phe Pro Asp Gly Cys Gln Tyr Trp
115 120 125
Glu Lys Gly Ser Lys Phe Val Pro Tyr Asp Ser Phe Asn Ser Asn Leu
130 135 140
Val Thr Tyr Val Leu Asp Ser Val Lys
145 150

(2) INFORMATION FOR SEQ ID NO:727:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1153 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1153
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498918

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:727:

gacataactt gcaagctggt gagattttcc atcctcaata actttattct tccatatctc	60
tcccatttcg ctctctattt cacaacccca tataacataa tataaatca cacaatcat	120
ttctatatag tatttaaatgg ggagacagcc atgctgtgac aagctagggg tgaagaaagg	180
gccgtggacg gtggaggaag ataagaagct tataaaacttc atactaacca atggccattg	240
ttgctggcgt gctttgccga agctggcccg tctccgctcg tgtggaaaga gctgccgcct	300
ccggtggact aactatctcc ggcctgactt aaaacgaggc cttctctcgc atgatgaaga	360
acaacttgtc atagatcttc atgctaactct cggcaataag tggcttaaga tagcttcaag	420
attacctgga agaacagata acgaaataaa aaaccattgg aataactcata tcaagaagaa	480
acttcttaag atgggaatcg atcctatgac ccatacaacc cttaatcaag aaccttctaa	540
tatcgataat tccaaaacca ttccgtccaa tccagacgat gtctcagtgg aaccaaagac	600
aactaacacg aaatacgtgg agataagtgt cagcacaaca gaagaagaaa gtagtagcac	660
ggttactgat caaaacagtt cgatggataa tgaaaatcat ctaattgaca acatttatga	720
tgatgatgaa ttgttttagtt acttatggtc cgacgaaact acgaaagatg aggcctcttg	780
gagtgatagt aactttgggtg ttggtggaac attatatgac cacaatatct ccggcgccga	840
tgcagatttt ccgatatggt caccggaaaag aatcaatgac gagaagatgt ttttggatta	900
ttgtcaagac tttggtgttc atgatttttg gttttgactg ttcaccattg acatattggc	960
aactctatgg agatgaacac aagcattgag ttgtcatggt tacaacatag tggcatatac	1020
atataatat atgtacatta tatgtaaaca tatacacgca tacaatcat aaacatgtaa	1080
ggataataaa tccatgtaaa tcagtaagggt tgcaccatgg ttttcaagta ttattaatta	1140
gggtttggta ggt	

(2) INFORMATION FOR SEQ ID NO:728:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 266 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..266
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498919

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:728:

Met Gly Arg Gln Pro Cys Cys Asp Lys Leu Gly Val Lys Lys Gly Pro
1 5 10 15
Trp Thr Val Glu Glu Asp Lys Lys Leu Ile Asn Phe Ile Leu Thr Asn

(2) INFORMATION FOR SEQ ID NO:729:

(A) LENGTH: 148 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..148

(D) OTHER INFORMATION: / Ceres Seq. ID 1498920

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:729:

Met	Gly	Ile	Asp	Pro	Met	Thr	His	Gln	Pro	Leu	Asn	Gln	Glu	Pro	Ser
1				5					10					15	
Asn	Ile	Asp	Asn	Ser	Lys	Thr	Ile	Pro	Ser	Asn	Pro	Asp	Asp	Val	Ser
			20					25					30		
Val	Glu	Pro	Lys	Thr	Thr	Asn	Thr	Lys	Tyr	Val	Glu	Ile	Ser	Val	Thr
		35				40						45			
Thr	Thr	Glu	Glu	Glu	Ser	Ser	Ser	Thr	Val	Thr	Asp	Gln	Asn	Ser	Ser
	50					55					60				
Met	Asp	Asn	Glu	Asn	His	Leu	Ile	Asp	Asn	Ile	Tyr	Asp	Asp	Asp	Glu
65					70					75					80
Leu	Phe	Ser	Tyr	Leu	Trp	Ser	Asp	Glu	Thr	Thr	Lys	Asp	Glu	Ala	Ser
				85				90						95	
Trp	Ser	Asp	Ser	Asn	Phe	Gly	Val	Gly	Gly	Thr	Leu	Tyr	Asp	His	Asn
			100					105					110		
Ile	Ser	Gly	Ala	Asp	Ala	Asp	Phe	Pro	Ile	Trp	Ser	Pro	Glu	Arg	Ile
		115				120						125			
Asn	Asp	Glu	Lys	Met	Phe	Leu	Asp	Tyr	Cys	Gln	Asp	Phe	Gly	Val	His
	130					135					140				

Asp Phe Gly Phe

145

(2) INFORMATION FOR SEQ ID NO:730:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 143 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..143

(D) OTHER INFORMATION: / Ceres Seq. ID 1498921

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:730:

```
Met Thr His Gln Pro Leu Asn Gln Glu Pro Ser Asn Ile Asp Asn Ser
1          5          10          15
Lys Thr Ile Pro Ser Asn Pro Asp Asp Val Ser Val Glu Pro Lys Thr
          20          25          30
Thr Asn Thr Lys Tyr Val Glu Ile Ser Val Thr Thr Thr Glu Glu Glu
          35          40          45
Ser Ser Ser Thr Val Thr Asp Gln Asn Ser Ser Met Asp Asn Glu Asn
          50          55          60
His Leu Ile Asp Asn Ile Tyr Asp Asp Asp Glu Leu Phe Ser Tyr Leu
65          70          75          80
Trp Ser Asp Glu Thr Thr Lys Asp Glu Ala Ser Trp Ser Asp Ser Asn
          85          90          95
Phe Gly Val Gly Gly Thr Leu Tyr Asp His Asn Ile Ser Gly Ala Asp
          100          105          110
Ala Asp Phe Pro Ile Trp Ser Pro Glu Arg Ile Asn Asp Glu Lys Met
          115          120          125
Phe Leu Asp Tyr Cys Gln Asp Phe Gly Val His Asp Phe Gly Phe
          130          135          140
```

(2) INFORMATION FOR SEQ ID NO:731:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1202 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1202

(D) OTHER INFORMATION: / Ceres Seq. ID 1498922

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:731:

```
gaaacgtctt cggacacact ctcagtcgca cgctctttca cgcgcctttt cgatttcaca      60
ttcggatccg atttggtcac ccgccgaaga tccaccggca tcttctctaa acggctctgt      120
cgagaaggat cggcgctatt attgctggag gacgattggg tgtttacttt ttactagtaa      180
acggagtaat ttcccaagcg aaaggtttca tttttgagct ccacgttgaa cgaactaagc      240
ggtttctcgg agttctcttg cttcctctcc acccagcgca atggagaaaa cagacgaaga      300
gaggaagaag gctcagatgc tggacgctcg ggccagaaac attagccaca atgttcgctg      360
cactgagtgt ggaagtcagt ccattgaaga ctgcgaggca gatatcgcta ttctccttag      420
acagctgata cgtaatgaga taggagctgg aaaaactgac aaagagatct acagtaagct      480
ggaggatgaa tttggggaga cagtgcctta tgcccaaaa tttgatttgc agaccgcagc      540
cttggtggctc acaccggtta taattgctgg aggtaccgct gcaggaatatg tttaccagaa      600
gcacaggcta aggaaaaatg tagacatcat ggcgttgaa cttattagag gtgtaccatt      660
gactccaaaa gagagagtta ccattcttga tgttcttatt ccaccttccc ctctcctca      720
gggagttggt tcccgattga ggagatggct caaccggtag ttcccgtgtc tccttagctc      780
tcttgttctt ggctcgaatc ttgttgtgtt aacaagtaaa caatgtgttg aaaagagtga      840
gtacacattg attgtcttgg agaaacagat agggactgct ttgcatccat tacaagcaaa      900
tggtattctt tgtagaagat cttgggatga gatatgtatc gagaaagcat tattgaaagt      960
gtgatacttg ttgtacctt gctgtgtgat tgaatacaga gagcgggtcg atagttatat      1020
```

tacttttcggc acaaagattt atttctttcc aaatagtttt tgtgctaaat gagctttttt 1080
ccacatcttt atcttaataa gccgaagctc acaaaatgta ttgacctgcg tattgtatat 1140
acaagaagca atgagtaaac agaaagaaat agtcttgctc acaagaatga gactgtatgt 1200
tg

(2) INFORMATION FOR SEQ ID NO:732:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 159 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..159
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498923

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:732:

Met Glu Lys Thr Asp Glu Glu Arg Lys Lys Ala Gln Met Leu Asp Ala
1 5 10 15
Arg Ala Arg Asn Ile Ser His Asn Val Arg Cys Thr Glu Cys Gly Ser
20 25 30
Gln Ser Ile Glu Asp Ser Gln Ala Asp Ile Ala Ile Leu Leu Arg Gln
35 40 45
Leu Ile Arg Asn Glu Ile Gly Ala Gly Lys Thr Asp Lys Glu Ile Tyr
50 55 60
Ser Lys Leu Glu Asp Glu Phe Gly Glu Thr Val Leu Tyr Ala Pro Lys
65 70 75 80
Phe Asp Leu Gln Thr Ala Ala Leu Trp Leu Thr Pro Val Ile Ile Ala
85 90 95
Gly Gly Thr Ala Ala Gly Ile Val Tyr Gln Lys His Arg Leu Arg Lys
100 105 110
Asn Val Asp Ile Met Ala Leu Asn Leu Ile Arg Gly Val Pro Leu Thr
115 120 125
Pro Lys Glu Arg Val Thr Ile Leu Asp Val Leu Ile Pro Pro Ser Pro
130 135 140
Pro Pro Gln Gly Val Val Ser Arg Leu Arg Arg Trp Leu Asn Arg
145 150 155

(2) INFORMATION FOR SEQ ID NO:733:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 147 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..147
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498924

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:733:

Met Leu Asp Ala Arg Ala Arg Asn Ile Ser His Asn Val Arg Cys Thr
1 5 10 15
Glu Cys Gly Ser Gln Ser Ile Glu Asp Ser Gln Ala Asp Ile Ala Ile
20 25 30
Leu Leu Arg Gln Leu Ile Arg Asn Glu Ile Gly Ala Gly Lys Thr Asp
35 40 45
Lys Glu Ile Tyr Ser Lys Leu Glu Asp Glu Phe Gly Glu Thr Val Leu
50 55 60
Tyr Ala Pro Lys Phe Asp Leu Gln Thr Ala Ala Leu Trp Leu Thr Pro
65 70 75 80
Val Ile Ile Ala Gly Gly Thr Ala Ala Gly Ile Val Tyr Gln Lys His
85 90 95
Arg Leu Arg Lys Asn Val Asp Ile Met Ala Leu Asn Leu Ile Arg Gly

100 105 110
Val Pro Leu Thr Pro Lys Glu Arg Val Thr Ile Leu Asp Val Leu Ile
115 120 125
Pro Pro Ser Pro Pro Pro Gln Gly Val Val Ser Arg Leu Arg Arg Trp
130 135 140
Leu Asn Arg
145

(2) INFORMATION FOR SEQ ID NO:734:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1931 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1931
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498925

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:734:

aattttttcac	tttctatttc	tctatatcta	tttttttata	gatatatatt	ttgtcttggt	60
tggattttgt	tctcgtgggt	tacttacttg	agagaacctc	gagacctgtc	ttgtctttat	120
gcttcagaag	caaatcaaag	catctctcca	agatttgaag	ctccatctat	ggctgcccctt	180
cttctccttt	tccttttcct	cttcgcaagc	tctgctctct	ctcaagattc	tttgatcggt	240
gtgaatattg	gtactgaagt	gacaaacatg	ccaagtccaa	cacaagtagt	agcactcctc	300
aaatcacaga	acatcaaccg	cgtccgcctc	tatgacgcag	accgctcaat	gcttctcgcg	360
tttgctcaca	ccgggggttca	agttataatc	tcagtacctc	acgaccagct	tctcgggtatc	420
agccaatcaa	atgcaaccgc	agccaattgg	gtgactagaa	atgtagctgc	atattaccct	480
gcgaccaaca	ttaccacaat	tgctgtcgga	tcagaagtc	taaccagcct	aacaaacgca	540
gcttctgtcc	ttgtctcagc	cctcaaatac	atacaagctg	ctctcgtcac	ggccaatctc	600
gaccgtcaga	tcaaagtatc	gacaccgcac	tcttcaacca	tcattcttga	ttctttccct	660
ccttcgcaag	ctttcttcaa	caagacttgg	gatccagtta	ttgtccctct	cctcaaattc	720
ctacagtcca	caggatcgcc	attgctgctc	aacgtttacc	cgtatttcga	ctatgttcag	780
tccaatggag	ttataccgct	tgactacgcg	cttttccagc	ctctccaagc	caacaaagaa	840
gctgtagacg	ccaacacatt	gttacattac	acaaacgttt	ttgatgcaat	cgtagacgct	900
gcttattttg	caatgtctta	tcttaacttc	accaacattc	caatcgtggg	cacagaatct	960
ggatggccat	ctaaaggagg	cccttctgag	cacgacgcaa	cggtagagaa	tgcaaacact	1020
tacaatagca	atttgatcca	gcattgtgac	aacaagactg	gaacgccaaa	acaccggga	1080
actgcagtta	ctacatacat	ctacgagctt	tacaacgagg	atacgaggcc	aggaccggta	1140
tctgagaaga	actgggggct	gtttttatca	aacgggactc	cgggtttacac	attgcgttta	1200
gcgggtgcag	gggcgattct	ggcaaatgat	actacaaacc	agacattttg	tatagcgaag	1260
gaaaagggtg	atagaaagat	gcttcaagca	gctcttgact	gggcttgccg	tccaggggaag	1320
gtcgattgct	cggcactgat	gcagggagag	tcatgttatg	aacccgacga	tgtgggttgca	1380
cattctactt	atgcgtttta	tgcttattac	cagaagatgg	gaaaagcttc	aggaagctgt	1440
gatttcaaag	gagttgctac	agtcaccacc	actgatccaa	gtcgagggaac	atgcgtgttc	1500
cctggaagtg	caaaaagcaa	tcagacactt	ggaaacaaca	cctcggcggt	ggccccctca	1560
gcgaactcta	caacctctgg	atgtatccca	aagtactatc	atcacccctca	cgcactcttc	1620
ggtgacttaa	cattactctc	ccttctactg	atcattgcct	tagtattctt	gtagaaactc	1680
tgaaaagaac	aacaactctc	aattcttggt	tctctaaatt	ttaacttctt	tctttgcaac	1740
acttgagaca	aaagagctcg	gtgggtttgt	tctctctgtg	tctagtgtgc	taccagtttt	1800
tgttgatcat	ctccttttaa	catggagttc	attgagggta	gcagttaggt	tcgggttcaa	1860
gatcatggat	gattgtaact	aatttcctgt	gttgaaagct	tgattctttc	ttttttatgg	1920
ctgaatattt	c					

(2) INFORMATION FOR SEQ ID NO:735:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 557 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide

(B) LOCATION: 1..557

(D) OTHER INFORMATION: / Ceres Seq. ID 1498926

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:735:

Asn	Phe	Ser	Leu	Ser	Ile	Ser	Leu	Tyr	Leu	Phe	Phe	Tyr	Arg	Tyr	Ile
1			5					10						15	
Phe	Cys	Leu	Gly	Trp	Ile	Leu	Phe	Ser	Trp	Val	Thr	Tyr	Leu	Arg	Glu
		20						25					30		
Pro	Arg	Asp	Leu	Ser	Cys	Leu	Tyr	Ala	Ser	Glu	Ala	Asn	Gln	Ser	Ile
		35					40					45			
Ser	Pro	Arg	Phe	Glu	Ala	Pro	Ser	Met	Ala	Ala	Leu	Leu	Leu	Leu	Phe
	50					55					60				
Leu	Phe	Leu	Phe	Ala	Ser	Ser	Ala	Leu	Ser	Gln	Asp	Ser	Leu	Ile	Gly
65					70					75					80
Val	Asn	Ile	Gly	Thr	Glu	Val	Thr	Asn	Met	Pro	Ser	Pro	Thr	Gln	Val
			85					90						95	
Val	Ala	Leu	Leu	Lys	Ser	Gln	Asn	Ile	Asn	Arg	Val	Arg	Leu	Tyr	Asp
			100					105					110		
Ala	Asp	Arg	Ser	Met	Leu	Leu	Ala	Phe	Ala	His	Thr	Gly	Val	Gln	Val
		115					120					125			
Ile	Ile	Ser	Val	Pro	Asn	Asp	Gln	Leu	Leu	Gly	Ile	Ser	Gln	Ser	Asn
	130					135					140				
Ala	Thr	Ala	Ala	Asn	Trp	Val	Thr	Arg	Asn	Val	Ala	Ala	Tyr	Tyr	Pro
145					150					155					160
Ala	Thr	Asn	Ile	Thr	Thr	Ile	Ala	Val	Gly	Ser	Glu	Val	Leu	Thr	Ser
			165					170						175	
Leu	Thr	Asn	Ala	Ser	Val	Leu	Val	Ser	Ala	Leu	Lys	Tyr	Ile	Gln	
		180					185					190			
Ala	Ala	Leu	Val	Thr	Ala	Asn	Leu	Asp	Arg	Gln	Ile	Lys	Val	Ser	Thr
		195					200					205			
Pro	His	Ser	Ser	Thr	Ile	Ile	Leu	Asp	Ser	Phe	Pro	Pro	Ser	Gln	Ala
	210					215					220				
Phe	Phe	Asn	Lys	Thr	Trp	Asp	Pro	Val	Ile	Val	Pro	Leu	Leu	Lys	Phe
225					230					235					240
Leu	Gln	Ser	Thr	Gly	Ser	Pro	Leu	Leu	Leu	Asn	Val	Tyr	Pro	Tyr	Phe
			245						250					255	
Asp	Tyr	Val	Gln	Ser	Asn	Gly	Val	Ile	Pro	Leu	Asp	Tyr	Ala	Leu	Phe
		260					265						270		
Gln	Pro	Leu	Gln	Ala	Asn	Lys	Glu	Ala	Val	Asp	Ala	Asn	Thr	Leu	Leu
		275					280					285			
His	Tyr	Thr	Asn	Val	Phe	Asp	Ala	Ile	Val	Asp	Ala	Ala	Tyr	Phe	Ala
	290					295					300				
Met	Ser	Tyr	Leu	Asn	Phe	Thr	Asn	Ile	Pro	Ile	Val	Val	Thr	Glu	Ser
305					310					315					320
Gly	Trp	Pro	Ser	Lys	Gly	Gly	Pro	Ser	Glu	His	Asp	Ala	Thr	Val	Glu
			325						330					335	
Asn	Ala	Asn	Thr	Tyr	Asn	Ser	Asn	Leu	Ile	Gln	His	Val	Ile	Asn	Lys
			340					345					350		
Thr	Gly	Thr	Pro	Lys	His	Pro	Gly	Thr	Ala	Val	Thr	Thr	Tyr	Ile	Tyr
		355					360					365			
Glu	Leu	Tyr	Asn	Glu	Asp	Thr	Arg	Pro	Gly	Pro	Val	Ser	Glu	Lys	Asn
	370					375					380				
Trp	Gly	Leu	Phe	Tyr	Thr	Asn	Gly	Thr	Pro	Val	Tyr	Thr	Leu	Arg	Leu
385					390					395					400
Ala	Gly	Ala	Gly	Ala	Ile	Leu	Ala	Asn	Asp	Thr	Thr	Asn	Gln	Thr	Phe
			405						410					415	
Cys	Ile	Ala	Lys	Glu	Lys	Val	Asp	Arg	Lys	Met	Leu	Gln	Ala	Ala	Leu
		420						425					430		
Asp	Trp	Ala	Cys	Gly	Pro	Gly	Lys	Val	Asp	Cys	Ser	Ala	Leu	Met	Gln
		435					440					445			
Gly	Glu	Ser	Cys	Tyr	Glu	Pro	Asp	Asp	Val	Val	Ala	His	Ser	Thr	Tyr
	450						455					460			

Ala	Phe	Asn	Ala	Tyr	Tyr	Gln	Lys	Met	Gly	Lys	Ala	Ser	Gly	Ser	Cys
465					470					475					480
Asp	Phe	Lys	Gly	Val	Ala	Thr	Val	Thr	Thr	Thr	Asp	Pro	Ser	Arg	Gly
			485						490					495	
Thr	Cys	Val	Phe	Pro	Gly	Ser	Ala	Lys	Ser	Asn	Gln	Thr	Leu	Gly	Asn
		500						505					510		
Asn	Thr	Ser	Ala	Leu	Ala	Pro	Ser	Ala	Asn	Ser	Thr	Thr	Ser	Gly	Cys
		515					520					525			
Ile	Pro	Lys	Tyr	Tyr	His	His	Pro	His	Ala	Ser	Phe	Gly	Asp	Leu	Thr
	530					535					540				
Leu	Leu	Ser	Leu	Leu	Leu	Ile	Ile	Ala	Leu	Val	Phe	Leu			
545					550					555					

(2) INFORMATION FOR SEQ ID NO:736:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 501 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..501

(D) OTHER INFORMATION: / Ceres Seq. ID 1498927

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:736:

Met	Ala	Ala	Leu	Leu	Leu	Leu	Phe	Leu	Phe	Leu	Phe	Ala	Ser	Ser	Ala
1			5					10					15		
Leu	Ser	Gln	Asp	Ser	Leu	Ile	Gly	Val	Asn	Ile	Gly	Thr	Glu	Val	Thr
		20					25					30			
Asn	Met	Pro	Ser	Pro	Thr	Gln	Val	Val	Ala	Leu	Leu	Lys	Ser	Gln	Asn
		35				40						45			
Ile	Asn	Arg	Val	Arg	Leu	Tyr	Asp	Ala	Asp	Arg	Ser	Met	Leu	Leu	Ala
	50					55					60				
Phe	Ala	His	Thr	Gly	Val	Gln	Val	Ile	Ile	Ser	Val	Pro	Asn	Asp	Gln
65				70					75					80	
Leu	Leu	Gly	Ile	Ser	Gln	Ser	Asn	Ala	Thr	Ala	Ala	Asn	Trp	Val	Thr
			85					90					95		
Arg	Asn	Val	Ala	Ala	Tyr	Tyr	Pro	Ala	Thr	Asn	Ile	Thr	Thr	Ile	Ala
		100						105					110		
Val	Gly	Ser	Glu	Val	Leu	Thr	Ser	Leu	Thr	Asn	Ala	Ala	Ser	Val	Leu
		115				120						125			
Val	Ser	Ala	Leu	Lys	Tyr	Ile	Gln	Ala	Ala	Leu	Val	Thr	Ala	Asn	Leu
	130					135					140				
Asp	Arg	Gln	Ile	Lys	Val	Ser	Thr	Pro	His	Ser	Ser	Thr	Ile	Ile	Leu
145				150						155					160
Asp	Ser	Phe	Pro	Pro	Ser	Gln	Ala	Phe	Phe	Asn	Lys	Thr	Trp	Asp	Pro
			165					170					175		
Val	Ile	Val	Pro	Leu	Leu	Lys	Phe	Leu	Gln	Ser	Thr	Gly	Ser	Pro	Leu
		180						185					190		
Leu	Leu	Asn	Val	Tyr	Pro	Tyr	Phe	Asp	Tyr	Val	Gln	Ser	Asn	Gly	Val
		195					200					205			
Ile	Pro	Leu	Asp	Tyr	Ala	Leu	Phe	Gln	Pro	Leu	Gln	Ala	Asn	Lys	Glu
	210					215					220				
Ala	Val	Asp	Ala	Asn	Thr	Leu	Leu	His	Tyr	Thr	Asn	Val	Phe	Asp	Ala
225					230					235				240	
Ile	Val	Asp	Ala	Ala	Tyr	Phe	Ala	Met	Ser	Tyr	Leu	Asn	Phe	Thr	Asn
			245					250					255		
Ile	Pro	Ile	Val	Thr	Glu	Ser	Gly	Trp	Pro	Ser	Lys	Gly	Gly	Pro	
		260					265					270			
Ser	Glu	His	Asp	Ala	Thr	Val	Glu	Asn	Ala	Asn	Thr	Tyr	Asn	Ser	Asn
	275						280					285			
Leu	Ile	Gln	His	Val	Ile	Asn	Lys	Thr	Gly	Thr	Pro	Lys	His	Pro	Gly

290		295		300											
Thr	Ala	Val	Thr	Thr	Tyr	Ile	Tyr	Glu	Leu	Tyr	Asn	Glu	Asp	Thr	Arg
305					310					315					320
Pro	Gly	Pro	Val	Ser	Glu	Lys	Asn	Trp	Gly	Leu	Phe	Tyr	Thr	Asn	Gly
				325					330						335
Thr	Pro	Val	Tyr	Thr	Leu	Arg	Leu	Ala	Gly	Ala	Gly	Ala	Ile	Leu	Ala
			340					345					350		
Asn	Asp	Thr	Thr	Asn	Gln	Thr	Phe	Cys	Ile	Ala	Lys	Glu	Lys	Val	Asp
	355						360					365			
Arg	Lys	Met	Leu	Gln	Ala	Ala	Leu	Asp	Trp	Ala	Cys	Gly	Pro	Gly	Lys
	370					375					380				
Val	Asp	Cys	Ser	Ala	Leu	Met	Gln	Gly	Glu	Ser	Cys	Tyr	Glu	Pro	Asp
385					390					395					400
Asp	Val	Val	Ala	His	Ser	Thr	Tyr	Ala	Phe	Asn	Ala	Tyr	Tyr	Gln	Lys
				405					410					415	
Met	Gly	Lys	Ala	Ser	Gly	Ser	Cys	Asp	Phe	Lys	Gly	Val	Ala	Thr	Val
			420					425					430		
Thr	Thr	Thr	Asp	Pro	Ser	Arg	Gly	Thr	Cys	Val	Phe	Pro	Gly	Ser	Ala
		435					440					445			
Lys	Ser	Asn	Gln	Thr	Leu	Gly	Asn	Asn	Thr	Ser	Ala	Leu	Ala	Pro	Ser
	450					455					460				
Ala	Asn	Ser	Thr	Thr	Ser	Gly	Cys	Ile	Pro	Lys	Tyr	Tyr	His	His	Pro
465					470					475					480
His	Ala	Ser	Phe	Gly	Asp	Leu	Thr	Leu	Leu	Ser	Leu	Leu	Leu	Ile	Ile
				485				490						495	
Ala	Leu	Val	Phe	Leu											
				500											

(2) INFORMATION FOR SEQ ID NO:737:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 468 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..468
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498928

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:737:

Met	Pro	Ser	Pro	Thr	Gln	Val	Val	Ala	Leu	Leu	Lys	Ser	Gln	Asn	Ile
1				5					10					15	
Asn	Arg	Val	Arg	Leu	Tyr	Asp	Ala	Asp	Arg	Ser	Met	Leu	Leu	Ala	Phe
		20						25					30		
Ala	His	Thr	Gly	Val	Gln	Val	Ile	Ile	Ser	Val	Pro	Asn	Asp	Gln	Leu
	35					40						45			
Leu	Gly	Ile	Ser	Gln	Ser	Asn	Ala	Thr	Ala	Ala	Asn	Trp	Val	Thr	Arg
	50					55					60				
Asn	Val	Ala	Ala	Tyr	Tyr	Pro	Ala	Thr	Asn	Ile	Thr	Thr	Ile	Ala	Val
65				70					75					80	
Gly	Ser	Glu	Val	Leu	Thr	Ser	Leu	Thr	Asn	Ala	Ala	Ser	Val	Leu	Val
			85						90					95	
Ser	Ala	Leu	Lys	Tyr	Ile	Gln	Ala	Ala	Leu	Val	Thr	Ala	Asn	Leu	Asp
			100					105					110		
Arg	Gln	Ile	Lys	Val	Ser	Thr	Pro	His	Ser	Ser	Thr	Ile	Ile	Leu	Asp
	115						120					125			
Ser	Phe	Pro	Pro	Ser	Gln	Ala	Phe	Phe	Asn	Lys	Thr	Trp	Asp	Pro	Val
	130					135					140				
Ile	Val	Pro	Leu	Leu	Lys	Phe	Leu	Gln	Ser	Thr	Gly	Ser	Pro	Leu	Leu
145					150					155				160	
Leu	Asn	Val	Tyr	Pro	Tyr	Phe	Asp	Tyr	Val	Gln	Ser	Asn	Gly	Val	Ile
				165					170					175	

Pro Leu Asp Tyr Ala Leu Phe Gln Pro Leu Gln Ala Asn Lys Glu Ala
180 185 190
Val Asp Ala Asn Thr Leu Leu His Tyr Thr Asn Val Phe Asp Ala Ile
195 200 205
Val Asp Ala Ala Tyr Phe Ala Met Ser Tyr Leu Asn Phe Thr Asn Ile
210 215 220
Pro Ile Val Val Thr Glu Ser Gly Trp Pro Ser Lys Gly Gly Pro Ser
225 230 235 240
Glu His Asp Ala Thr Val Glu Asn Ala Asn Thr Tyr Asn Ser Asn Leu
245 250 255
Ile Gln His Val Ile Asn Lys Thr Gly Thr Pro Lys His Pro Gly Thr
260 265 270
Ala Val Thr Thr Tyr Ile Tyr Glu Leu Tyr Asn Glu Asp Thr Arg Pro
275 280 285
Gly Pro Val Ser Glu Lys Asn Trp Gly Leu Phe Tyr Thr Asn Gly Thr
290 295 300
Pro Val Tyr Thr Leu Arg Leu Ala Gly Ala Gly Ala Ile Leu Ala Asn
305 310 315 320
Asp Thr Thr Asn Gln Thr Phe Cys Ile Ala Lys Glu Lys Val Asp Arg
325 330 335
Lys Met Leu Gln Ala Ala Leu Asp Trp Ala Cys Gly Pro Gly Lys Val
340 345 350
Asp Cys Ser Ala Leu Met Gln Gly Glu Ser Cys Tyr Glu Pro Asp Asp
355 360 365
Val Val Ala His Ser Thr Tyr Ala Phe Asn Ala Tyr Tyr Gln Lys Met
370 375 380
Gly Lys Ala Ser Gly Ser Cys Asp Phe Lys Gly Val Ala Thr Val Thr
385 390 395 400
Thr Thr Asp Pro Ser Arg Gly Thr Cys Val Phe Pro Gly Ser Ala Lys
405 410 415
Ser Asn Gln Thr Leu Gly Asn Asn Thr Ser Ala Leu Ala Pro Ser Ala
420 425 430
Asn Ser Thr Thr Ser Gly Cys Ile Pro Lys Tyr Tyr His His Pro His
435 440 445
Ala Ser Phe Gly Asp Leu Thr Leu Leu Ser Leu Leu Ile Ile Ala
450 455 460
Leu Val Phe Leu
465

(2) INFORMATION FOR SEQ ID NO:738:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 673 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..673
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498929

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:738:

gcctataaag	tgatccttgt	gatgccttca	actatgagct	tagagagaag	aatcattctg	60
agggcactag	gtgcagacct	tcatcwmtcg	gaccagcgca	taggccttaa	aggaatgttg	120
gagaaaactg	aagcgatttt	aagcaaaact	cctggtgggt	acattccaca	acaatttgaa	180
aatcctgcaa	accccgagat	tcattaccga	accacgggac	cggaatatg	gagagattca	240
gccgggaaag	tagatatatt	ggtcgctggc	gtagggactg	gtggaactgc	tactggagta	300
gggaagttcc	tcaaggagca	gaacaaagac	atcaaggttt	gtgtggtgga	accagtagaa	360
agtccggtac	ttagcggagg	tcaaccaggt	ccacatttga	ttcagggaat	tggctctggt	420
atcgtcccat	tcaatttgga	cttaaccatt	gttgatgaaa	ttattcaagt	ggcaggtgaa	480
gaggctattg	aaacagccaa	gcttcttgcc	ctcaaagaag	gattactggt	gggaatatcc	540
tctggagccg	cagcagcggc	tgcgttaaag	gttgcaaagc	ggccagaaaa	cgcggggaaa	600
ctcattgkgg	tggtttttcc	tagtgaggagga	gaacgttatt	tatcgactaa	actgttcgat	660

tcgattagat atg

(2) INFORMATION FOR SEQ ID NO:739:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 224 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..224
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498930

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:739:

Ala	Tyr	Lys	Val	Ile	Leu	Val	Met	Pro	Ser	Thr	Met	Ser	Leu	Glu	Arg
1				5				10						15	
Arg	Ile	Ile	Leu	Arg	Ala	Leu	Gly	Ala	Asp	Leu	His	Xaa	Ser	Asp	Gln
			20					25					30		
Arg	Ile	Gly	Leu	Lys	Gly	Met	Leu	Glu	Lys	Thr	Glu	Ala	Ile	Leu	Ser
		35					40					45			
Lys	Thr	Pro	Gly	Gly	Tyr	Ile	Pro	Gln	Gln	Phe	Glu	Asn	Pro	Ala	Asn
		50				55					60				
Pro	Glu	Ile	His	Tyr	Arg	Thr	Thr	Gly	Pro	Glu	Ile	Trp	Arg	Asp	Ser
65					70					75				80	
Ala	Gly	Lys	Val	Asp	Ile	Leu	Val	Ala	Gly	Val	Gly	Thr	Gly	Gly	Thr
			85						90					95	
Ala	Thr	Gly	Val	Gly	Lys	Phe	Leu	Lys	Glu	Gln	Asn	Lys	Asp	Ile	Lys
			100					105					110		
Val	Cys	Val	Val	Glu	Pro	Val	Glu	Ser	Pro	Val	Leu	Ser	Gly	Gly	Gln
			115				120					125			
Pro	Gly	Pro	His	Leu	Ile	Gln	Gly	Ile	Gly	Ser	Gly	Ile	Val	Pro	Phe
		130				135					140				
Asn	Leu	Asp	Leu	Thr	Ile	Val	Asp	Glu	Ile	Ile	Gln	Val	Ala	Gly	Glu
145					150					155					160
Glu	Ala	Ile	Glu	Thr	Ala	Lys	Leu	Leu	Ala	Leu	Lys	Glu	Gly	Leu	Leu
			165						170					175	
Val	Gly	Ile	Ser	Ser	Gly	Ala	Ala	Ala	Ala	Ala	Ala	Leu	Lys	Val	Ala
			180					185					190		
Lys	Arg	Pro	Glu	Asn	Ala	Gly	Lys	Leu	Ile	Xaa	Val	Val	Phe	Pro	Ser
		195				200						205			
Gly	Gly	Glu	Arg	Tyr	Leu	Ser	Thr	Lys	Leu	Phe	Asp	Ser	Ile	Arg	Tyr
		210				215					220				

(2) INFORMATION FOR SEQ ID NO:740:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 217 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..217
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498931

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:740:

Met	Pro	Ser	Thr	Met	Ser	Leu	Glu	Arg	Arg	Ile	Ile	Leu	Arg	Ala	Leu
1					5					10				15	
Gly	Ala	Asp	Leu	His	Xaa	Ser	Asp	Gln	Arg	Ile	Gly	Leu	Lys	Gly	Met
			20					25					30		
Leu	Glu	Lys	Thr	Glu	Ala	Ile	Leu	Ser	Lys	Thr	Pro	Gly	Gly	Tyr	Ile
		35					40					45			

Pro Gln Gln Phe Glu Asn Pro Ala Asn Pro Glu Ile His Tyr Arg Thr
50 55 60
Thr Gly Pro Glu Ile Trp Arg Asp Ser Ala Gly Lys Val Asp Ile Leu
65 70 75 80
Val Ala Gly Val Gly Thr Gly Gly Thr Ala Thr Gly Val Gly Lys Phe
85 90 95
Leu Lys Glu Gln Asn Lys Asp Ile Lys Val Cys Val Val Glu Pro Val
100 105 110
Glu Ser Pro Val Leu Ser Gly Gly Gln Pro Gly Pro His Leu Ile Gln
115 120 125
Gly Ile Gly Ser Gly Ile Val Pro Phe Asn Leu Asp Leu Thr Ile Val
130 135 140
Asp Glu Ile Ile Gln Val Ala Gly Glu Glu Ala Ile Glu Thr Ala Lys
145 150 155 160
Leu Leu Ala Leu Lys Glu Gly Leu Leu Val Gly Ile Ser Ser Gly Ala
165 170 175
Ala Ala Ala Ala Ala Leu Lys Val Ala Lys Arg Pro Glu Asn Ala Gly
180 185 190
Lys Leu Ile Xaa Val Val Phe Pro Ser Gly Gly Glu Arg Tyr Leu Ser
195 200 205
Thr Lys Leu Phe Asp Ser Ile Arg Tyr
210 215

(2) INFORMATION FOR SEQ ID NO:741:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 213 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..213
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498932

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:741:

Met Ser Leu Glu Arg Arg Ile Ile Leu Arg Ala Leu Gly Ala Asp Leu
1 5 10 15
His Xaa Ser Asp Gln Arg Ile Gly Leu Lys Gly Met Leu Glu Lys Thr
20 25 30
Glu Ala Ile Leu Ser Lys Thr Pro Gly Gly Tyr Ile Pro Gln Gln Phe
35 40 45
Glu Asn Pro Ala Asn Pro Glu Ile His Tyr Arg Thr Thr Gly Pro Glu
50 55 60
Ile Trp Arg Asp Ser Ala Gly Lys Val Asp Ile Leu Val Ala Gly Val
65 70 75 80
Gly Thr Gly Gly Thr Ala Thr Gly Val Gly Lys Phe Leu Lys Glu Gln
85 90 95
Asn Lys Asp Ile Lys Val Cys Val Val Glu Pro Val Glu Ser Pro Val
100 105 110
Leu Ser Gly Gly Gln Pro Gly Pro His Leu Ile Gln Gly Ile Gly Ser
115 120 125
Gly Ile Val Pro Phe Asn Leu Asp Leu Thr Ile Val Asp Glu Ile Ile
130 135 140
Gln Val Ala Gly Glu Glu Ala Ile Glu Thr Ala Lys Leu Leu Ala Leu
145 150 155 160
Lys Glu Gly Leu Leu Val Gly Ile Ser Ser Gly Ala Ala Ala Ala Ala
165 170 175
Ala Leu Lys Val Ala Lys Arg Pro Glu Asn Ala Gly Lys Leu Ile Xaa
180 185 190
Val Val Phe Pro Ser Gly Gly Glu Arg Tyr Leu Ser Thr Lys Leu Phe
195 200 205
Asp Ser Ile Arg Tyr

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(2) INFORMATION FOR SEQ ID NO:742:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1334 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1334
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498933

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:742:

```
ccccgggaag agagagacta ttgaatattc ttcttccttc actttggctg agagagcgac      60
gacgatggcg gaatctcgca gcaacagagc ggcggttcag gctactaacg acgatgcac      120
cgccagtaaa ttgtcttggt tcaaaaaggg atatatgaaa gacgactatg ttcatctctt      180
tgtgaaaaga cctgttcgaa gatctcccat cattaatcga ggttactttt cccgttgggc      240
tgccttccga aagcttatgt ctcaagcttct tctaagcggg acaagttcta agaaacagat      300
actgtcactc ggagctgggt ttgatactac ctattttcag ttgctggatg aggggaatgg      360
gcccattctc tatgtggaac ttgattttta gtaggtgact agcaagaagg ctgctgttat      420
acaaaactcc agccaactca gggacaactc aggcgccaat gcactctattt ctattgacga      480
aggaaaagtt ctcaagtcat attacaagtt acttccagtt gacctgcgcg atataccaaa      540
attaagagat gttatatcct ttgcagatat ggatctaagt ctgccgacgt ttattattgc      600
agaatgtggt ttgattttatc tggaccccgga ttcaagccgt gccatcgtca attggctcgtc      660
aaaaacgttt tcaactgcag tatttttctt atatgagcag atccatccag atgatgcatt      720
tgggcatcaa atgattagaa atttggagag tcggggatgt gcactcttaa gcattgatgc      780
atcaccaact ttacttgcaa aggagagatt gtttcttgat aatggatggc agagagctgt      840
tgcctgggac atgctaaaag tgtatggtag ttttgttgat actcaagaaa aacgcaggat      900
cgagcgattg gagttggttg acgaatttga agagtggcac atgatgcagg aacattactg      960
tgtcacatat gctgtcaatg atgcaatggg aatatttggg gatttcggtt tcacaagaga     1020
agggggcggt gaaagaatga gctcatcagc gtcacacct tgaaaaggag gaggggtgtgt     1080
attgcattga atccccggaa cttgcaactg gaatgatgat tgattgcaca aagttagaaa     1140
ggcctttctc tgggtgctga gcagaaaacg aaggaaacac gaacttgtct gcgttatctg     1200
tgcttttgat ttagtttagg ctcatggctg agatatgtgg gccgggcctc cccttgtttt     1260
atttttggtt gtattttcta ataattgtgc aaaacaaaga aacctcacct cgggtcaagaa     1320
acgctctgaa atct
```

(2) INFORMATION FOR SEQ ID NO:743:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 130 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..130
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498934

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:743:

```
Pro Gly Lys Arg Glu Thr Ile Glu Tyr Ser Ser Ser Phe Thr Leu Ala
1          5          10          15
Glu Arg Ala Thr Thr Met Ala Glu Ser Arg Ser Asn Arg Ala Ala Val
20          25          30
Gln Ala Thr Asn Asp Asp Ala Ser Ala Ser Lys Leu Ser Cys Val Lys
35          40          45
Lys Gly Tyr Met Lys Asp Asp Tyr Val His Leu Phe Val Lys Arg Pro
50          55          60
Val Arg Arg Ser Pro Ile Ile Asn Arg Gly Tyr Phe Ser Arg Trp Ala
65          70          75          80
Ala Phe Arg Lys Leu Met Ser Gln Phe Leu Leu Ser Gly Thr Ser Ser
85          90          95
Lys Lys Gln Ile Leu Ser Leu Gly Ala Gly Phe Asp Thr Thr Tyr Phe
```

100 105 110
Gln Leu Leu Asp Glu Gly Asn Gly Pro Asn Leu Tyr Val Glu Leu Asp
115 120 125
Phe Lys
130

(2) INFORMATION FOR SEQ ID NO:744:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 164 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..164

(D) OTHER INFORMATION: / Ceres Seq. ID 1498935

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:744:

Met Asp Leu Ser Leu Pro Thr Phe Ile Ile Ala Glu Cys Val Leu Ile
1 5 10 15
Tyr Leu Asp Pro Asp Ser Ser Arg Ala Ile Val Asn Trp Ser Ser Lys
20 25 30
Thr Phe Ser Thr Ala Val Phe Phe Leu Tyr Glu Gln Ile His Pro Asp
35 40 45
Asp Ala Phe Gly His Gln Met Ile Arg Asn Leu Glu Ser Arg Gly Cys
50 55 60
Ala Leu Leu Ser Ile Asp Ala Ser Pro Thr Leu Leu Ala Lys Glu Arg
65 70 75 80
Leu Phe Leu Asp Asn Gly Trp Gln Arg Ala Val Ala Trp Asp Met Leu
85 90 95
Lys Val Tyr Gly Ser Phe Val Asp Thr Gln Glu Lys Arg Arg Ile Glu
100 105 110
Arg Leu Glu Leu Phe Asp Glu Phe Glu Glu Trp His Met Met Gln Glu
115 120 125
His Tyr Cys Val Thr Tyr Ala Val Asn Asp Ala Met Gly Ile Phe Gly
130 135 140
Asp Phe Gly Phe Thr Arg Glu Gly Gly Gly Glu Arg Met Ser Ser Ser
145 150 155 160
Ala Ser Ser Pro

(2) INFORMATION FOR SEQ ID NO:745:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 110 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..110

(D) OTHER INFORMATION: / Ceres Seq. ID 1498936

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:745:

Met Ile Arg Asn Leu Glu Ser Arg Gly Cys Ala Leu Leu Ser Ile Asp
1 5 10 15
Ala Ser Pro Thr Leu Leu Ala Lys Glu Arg Leu Phe Leu Asp Asn Gly
20 25 30
Trp Gln Arg Ala Val Ala Trp Asp Met Leu Lys Val Tyr Gly Ser Phe
35 40 45
Val Asp Thr Gln Glu Lys Arg Arg Ile Glu Arg Leu Glu Leu Phe Asp
50 55 60
Glu Phe Glu Glu Trp His Met Met Gln Glu His Tyr Cys Val Thr Tyr
65 70 75 80

Ala Val Asn Asp Ala Met Gly Ile Phe Gly Asp Phe Gly Phe Thr Arg
85 90 95
Glu Gly Gly Gly Glu Arg Met Ser Ser Ser Ala Ser Ser Pro
100 105 110

(2) INFORMATION FOR SEQ ID NO:746:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 855 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..855
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498937

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:746:

aaaaatcaag	aaatatggcc	acaagagcct	ctacatctag	cagagtctct	ccagctttca	60
ctttcctcgt	catcttcttc	ctcttatctc	tcactgcttc	agtagaagct	gctggctcgtg	120
gagttaacaa	tgacaagaaa	ggcggcggat	taggagcttc	tttcatattc	ggagattctc	180
tagtcgatgc	cggaaataat	aattatctat	cgacgttgtc	tagggctaata	atgaagccta	240
atggtattga	tttcaaagct	tccggaggaa	ctcctaccgg	ccgggttcacc	aatggacgga	300
ccatcggtga	tatcgttggg	gaagaactcg	gatcagcgaa	ctacgcgata	ccgttcttgg	360
caccagacgc	gaagggaaaa	gctttattag	ccggagtga	ctatgcatct	ggaggaggag	420
gaatcatgaa	tgccaccggg	agaatctttg	tgaatagatt	aggtatggat	gtacaagttg	480
atttcttcaa	cactacacgg	aaacagtttg	atgatctact	tggaaaagag	aaagcaaaag	540
attacatagc	caagaaatcg	atattctcaa	tcactatagg	agcaaatgat	ttcctcaaca	600
attatctatt	cccactactc	tcggtagcat	tcatgattcc	tcctcctggt	ccaatgcatt	660
agagagagaa	aagaaagtcc	ctcaaaagtc	gaagacaaag	aaagatgttt	aatctctctc	720
tttattttctc	ttagctctgt	tttttaaagt	ttggaacact	tgtacttggt	tccaaaagat	780
gttttttttaa	ggataaaacc	atttgagaaa	tgtattagaa	gctcttgatt	tctctatcta	840
tgtctctctc	tcgcc					

(2) INFORMATION FOR SEQ ID NO:747:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 219 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..219
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498938

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:747:

Lys	Ser	Arg	Asn	Met	Ala	Thr	Arg	Ala	Ser	Thr	Ser	Ser	Arg	Val	Ser	
1			5					10					15			
Pro	Ala	Phe	Thr	Phe	Leu	Val	Ile	Phe	Phe	Leu	Leu	Ser	Leu	Thr	Ala	
			20					25					30			
Ser	Val	Glu	Ala	Ala	Gly	Arg	Gly	Val	Asn	Asn	Asp	Lys	Lys	Gly	Gly	
		35				40						45				
Gly	Leu	Gly	Ala	Ser	Phe	Ile	Phe	Gly	Asp	Ser	Leu	Val	Asp	Ala	Gly	
	50					55					60					
Asn	Asn	Asn	Tyr	Leu	Ser	Thr	Leu	Ser	Arg	Ala	Asn	Met	Lys	Pro	Asn	
65				70					75					80		
Gly	Ile	Asp	Phe	Lys	Ala	Ser	Gly	Gly	Thr	Pro	Thr	Gly	Arg	Phe	Thr	
			85					90						95		
Asn	Gly	Arg	Thr	Ile	Gly	Asp	Ile	Val	Gly	Glu	Glu	Leu	Gly	Ser	Ala	
			100					105					110			
Asn	Tyr	Ala	Ile	Pro	Phe	Leu	Ala	Pro	Asp	Ala	Lys	Gly	Lys	Ala	Leu	
		115					120					125				
Leu	Ala	Gly	Val	Asn	Tyr	Ala	Ser	Gly	Gly	Gly	Gly	Ile	Met	Asn	Ala	
	130						135					140				

Thr Gly Arg Ile Phe Val Asn Arg Leu Gly Met Asp Val Gln Val Asp
145 150 155 160
Phe Phe Asn Thr Thr Arg Lys Gln Phe Asp Asp Leu Leu Gly Lys Glu
165 170 175
Lys Ala Lys Asp Tyr Ile Ala Lys Lys Ser Ile Phe Ser Ile Thr Ile
180 185 190
Gly Ala Asn Asp Phe Leu Asn Asn Tyr Leu Phe Pro Leu Leu Ser Val
195 200 205
Ala Phe Met Ile Pro Pro Pro Gly Pro Met His
210 215

(2) INFORMATION FOR SEQ ID NO:748:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 215 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..215
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498939

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:748:

Met Ala Thr Arg Ala Ser Thr Ser Ser Arg Val Ser Pro Ala Phe Thr
1 5 10 15
Phe Leu Val Ile Phe Phe Leu Leu Ser Leu Thr Ala Ser Val Glu Ala
20 25 30
Ala Gly Arg Gly Val Asn Asn Asp Lys Lys Gly Gly Gly Leu Gly Ala
35 40 45
Ser Phe Ile Phe Gly Asp Ser Leu Val Asp Ala Gly Asn Asn Asn Tyr
50 55 60
Leu Ser Thr Leu Ser Arg Ala Asn Met Lys Pro Asn Gly Ile Asp Phe
65 70 75 80
Lys Ala Ser Gly Gly Thr Pro Thr Gly Arg Phe Thr Asn Gly Arg Thr
85 90 95
Ile Gly Asp Ile Val Gly Glu Glu Leu Gly Ser Ala Asn Tyr Ala Ile
100 105 110
Pro Phe Leu Ala Pro Asp Ala Lys Gly Lys Ala Leu Leu Ala Gly Val
115 120 125
Asn Tyr Ala Ser Gly Gly Gly Gly Ile Met Asn Ala Thr Gly Arg Ile
130 135 140
Phe Val Asn Arg Leu Gly Met Asp Val Gln Val Asp Phe Phe Asn Thr
145 150 155 160
Thr Arg Lys Gln Phe Asp Asp Leu Leu Gly Lys Glu Lys Ala Lys Asp
165 170 175
Tyr Ile Ala Lys Lys Ser Ile Phe Ser Ile Thr Ile Gly Ala Asn Asp
180 185 190
Phe Leu Asn Asn Tyr Leu Phe Pro Leu Leu Ser Val Ala Phe Met Ile
195 200 205
Pro Pro Pro Gly Pro Met His
210 215

(2) INFORMATION FOR SEQ ID NO:749:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 143 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..143
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498940

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:749:

Met	Lys	Pro	Asn	Gly	Ile	Asp	Phe	Lys	Ala	Ser	Gly	Gly	Thr	Pro	Thr
1			5					10						15	
Gly	Arg	Phe	Thr	Asn	Gly	Arg	Thr	Ile	Gly	Asp	Ile	Val	Gly	Glu	Glu
			20					25					30		
Leu	Gly	Ser	Ala	Asn	Tyr	Ala	Ile	Pro	Phe	Leu	Ala	Pro	Asp	Ala	Lys
			35					40				45			
Gly	Lys	Ala	Leu	Leu	Ala	Gly	Val	Asn	Tyr	Ala	Ser	Gly	Gly	Gly	Gly
			50					55				60			
Ile	Met	Asn	Ala	Thr	Gly	Arg	Ile	Phe	Val	Asn	Arg	Leu	Gly	Met	Asp
65						70				75					80
Val	Gln	Val	Asp	Phe	Phe	Asn	Thr	Thr	Arg	Lys	Gln	Phe	Asp	Asp	Leu
						85				90				95	
Leu	Gly	Lys	Glu	Lys	Ala	Lys	Asp	Tyr	Ile	Ala	Lys	Lys	Ser	Ile	Phe
						100				105				110	
Ser	Ile	Thr	Ile	Gly	Ala	Asn	Asp	Phe	Leu	Asn	Asn	Tyr	Leu	Phe	Pro
						115				120				125	
Leu	Leu	Ser	Val	Ala	Phe	Met	Ile	Pro	Pro	Pro	Gly	Pro	Met	His	
						130				135				140	

(2) INFORMATION FOR SEQ ID NO:750:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1982 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1982
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498941

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:750:

aaacttaata	aagcctcgta	ctgagagatc	aaaacaaaac	aaaacaaaac	ccaaacactt	60
accaaataca	tcaattatcg	agaatcttcc	ttcctttaat	cctcaaaaaa	aacaaaaaac	120
tttcttcacc	tcctttcctt	gattcatcct	ctaggttaat	gggtgttttc	tcgaatcttc	180
gaggaccag	agccggagct	acccacgatg	aatttccggc	gaccaatggc	tctccttcgt	240
cttcttcttc	tccatcttca	tcaatcaagc	gaaaattatc	gaatttggtt	ccactctgcg	300
ttgctctggt	agttatcgct	gagatcgggt	ttctgggtcg	gctcgataaa	gtcgtcttgg	360
ttgatacggt	gactgatttc	ttcacccagt	ctccgtcact	ctcgcagtct	ccaccggcga	420
gatccgatcg	gaagaagatc	ggattatttt	ctgataggag	ctgcgaggag	tggttgatga	480
gagaagattc	agttacttac	tctagagatt	ttactaaaga	tccaattttt	atctcttggt	540
gtgaaaagga	ctttcaatgg	tgttctgtgg	attgtacatt	tggagatagt	tcagggaaaa	600
caccagatgc	tgcgtttgga	ttaggtcaga	aacctggaac	tcttagtata	atacgttcca	660
tggaatcagc	acagtattat	ccaaaaaatg	atcttgcaca	ggcacgacgg	tgggagaggt	720
tatgatatag	tgatgaccac	tagtctatca	tcagatgttc	ctggttgata	tttttcgtgg	780
gcggagtatg	atattatgtc	tccggtacag	ccaaaaactg	agagagctat	tgcagctgct	840
tttattttcta	attgtggtgc	tcggaatttt	cgtctacaag	cacttgaggc	attgatgaaa	900
actaacatta	agattgattc	ttatggtggt	tgatcatcgaa	accgggatgg	gaaagttgac	960
aagggtgaag	ctcttaagcg	atacaaatcc	agtttggtct	ttgagaatac	taacgaggaa	1020
gattatgtca	ccgagaagtt	ctttcaatcc	ttaggtgctg	gggtccgtccc	cgtggtagtt	1080
gggtcctcaa	atatagaaga	atttgcgcct	gcttcggact	cattccttca	cattaagact	1140
atggaagatg	tagagccagt	tgcaaaagaga	atgaagtatc	tcgcagctaa	ccctgctgct	1200
tataatcaga	cactaagatg	gaaatacgag	ggctccttcag	attctttcaa	ggcacttggt	1260
gatatggctg	ctgtacactc	ttcttgccgt	ctctgcattt	tcctggccac	gagggtccga	1320
gaacaagaag	aggaaaagccc	taatttcaag	aaacgaccgt	gcaaagttag	caggggagga	1380
tcagacacag	ttttgttagt	ttttgttaga	gaaagaggcc	ggtttgaaat	ggaatcagtc	1440
tttttgaggg	gtaaaaagtgt	gactcaggaa	gctctagaat	ctgcagttct	cgccaagttc	1500
aagtcttttaa	aacatgaggc	agtgtggaag	aaggaaaggc	ctggaaaactt	aaaaggagac	1560
aaagagctta	aaatacatcg	gatttaccgc	cttggcctaa	cgcaacgaca	ggctttgtac	1620
aacttcaaat	tcgagggaaa	ttcgagtcta	agtagtcaca	ttcaaaacaa	cccttggtgct	1680
aaatttgagg	ttgtcttcgt	ctagtttcat	tcctctggat	ctgtcacagg	tatcatctca	1740
gctaagaaga	catttctctg	tgctagaatc	gcaaagtgct	aaacaaaccg	attagatgaa	1800

acaaaagggtt aatagtcatg agattgggtga actcattttg tttaggcagt gtatctgtaa 1860
atcgttctga cattgcagac gatgtgttct tgatagctgg atgcataaat gtttgaagat 1920
ttagagcaat ttgatagttt tgaatctctt gagagtgtgt taattaatct ttaaattttt 1980
cc

(2) INFORMATION FOR SEQ ID NO:751:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 338 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..338

(D) OTHER INFORMATION: / Ceres Seq. ID 1498942

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:751:

Met Ile Leu His Arg His Asp Gly Gly Arg Gly Tyr Asp Ile Val Met
1 5 10 15
Thr Thr Ser Leu Ser Ser Asp Val Pro Val Gly Tyr Phe Ser Trp Ala
20 25 30
Glu Tyr Asp Ile Met Ser Pro Val Gln Pro Lys Thr Glu Arg Ala Ile
35 40 45
Ala Ala Ala Phe Ile Ser Asn Cys Gly Ala Arg Asn Phe Arg Leu Gln
50 55 60
Ala Leu Glu Ala Leu Met Lys Thr Asn Ile Lys Ile Asp Ser Tyr Gly
65 70 75 80
Gly Cys His Arg Asn Arg Asp Gly Lys Val Asp Lys Val Glu Ala Leu
85 90 95
Lys Arg Tyr Lys Phe Ser Leu Ala Phe Glu Asn Thr Asn Glu Glu Asp
100 105 110
Tyr Val Thr Glu Lys Phe Phe Gln Ser Leu Val Ala Gly Ser Val Pro
115 120 125
Val Val Val Gly Pro Pro Asn Ile Glu Glu Phe Ala Pro Ala Ser Asp
130 135 140
Ser Phe Leu His Ile Lys Thr Met Glu Asp Val Glu Pro Val Ala Lys
145 150 155 160
Arg Met Lys Tyr Leu Ala Ala Asn Pro Ala Ala Tyr Asn Gln Thr Leu
165 170 175
Arg Trp Lys Tyr Glu Gly Pro Ser Asp Ser Phe Lys Ala Leu Val Asp
180 185 190
Met Ala Ala Val His Ser Ser Cys Arg Leu Cys Ile Phe Leu Ala Thr
195 200 205
Arg Val Arg Glu Gln Glu Glu Glu Ser Pro Asn Phe Lys Lys Arg Pro
210 215 220
Cys Lys Cys Ser Arg Gly Gly Ser Asp Thr Val Tyr His Val Phe Val
225 230 235 240
Arg Glu Arg Gly Arg Phe Glu Met Glu Ser Val Phe Leu Arg Gly Lys
245 250 255
Ser Val Thr Gln Glu Ala Leu Glu Ser Ala Val Leu Ala Lys Phe Lys
260 265 270
Ser Leu Lys His Glu Ala Val Trp Lys Lys Glu Arg Pro Gly Asn Leu
275 280 285
Lys Gly Asp Lys Glu Leu Lys Ile His Arg Ile Tyr Pro Leu Gly Leu
290 295 300
Thr Gln Arg Gln Ala Leu Tyr Asn Phe Lys Phe Glu Gly Asn Ser Ser
305 310 315 320
Leu Ser Ser His Ile Gln Asn Asn Pro Cys Ala Lys Phe Glu Val Val
325 330 335
Phe Val

(2) INFORMATION FOR SEQ ID NO:752:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 323 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..323
 (D) OTHER INFORMATION: / Ceres Seq. ID 1498943
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:752:

Met Thr Thr Ser Leu Ser Ser Asp Val Pro Val Gly Tyr Phe Ser Trp
1 5 10 15
Ala Glu Tyr Asp Ile Met Ser Pro Val Gln Pro Lys Thr Glu Arg Ala
 20 25 30
Ile Ala Ala Ala Phe Ile Ser Asn Cys Gly Ala Arg Asn Phe Arg Leu
 35 40 45
Gln Ala Leu Glu Ala Leu Met Lys Thr Asn Ile Lys Ile Asp Ser Tyr
50 55 60
Gly Gly Cys His Arg Asn Arg Asp Gly Lys Val Asp Lys Val Glu Ala
65 70 75 80
Leu Lys Arg Tyr Lys Phe Ser Leu Ala Phe Glu Asn Thr Asn Glu Glu
 85 90 95
Asp Tyr Val Thr Glu Lys Phe Phe Gln Ser Leu Val Ala Gly Ser Val
 100 105 110
Pro Val Val Val Gly Pro Pro Asn Ile Glu Glu Phe Ala Pro Ala Ser
 115 120 125
Asp Ser Phe Leu His Ile Lys Thr Met Glu Asp Val Glu Pro Val Ala
130 135 140
Lys Arg Met Lys Tyr Leu Ala Ala Asn Pro Ala Ala Tyr Asn Gln Thr
145 150 155 160
Leu Arg Trp Lys Tyr Glu Gly Pro Ser Asp Ser Phe Lys Ala Leu Val
 165 170 175
Asp Met Ala Ala Val His Ser Ser Cys Arg Leu Cys Ile Phe Leu Ala
 180 185 190
Thr Arg Val Arg Glu Gln Glu Glu Ser Pro Asn Phe Lys Lys Arg
 195 200 205
Pro Cys Lys Cys Ser Arg Gly Gly Ser Asp Thr Val Tyr His Val Phe
210 215 220
Val Arg Glu Arg Gly Arg Phe Glu Met Glu Ser Val Phe Leu Arg Gly
225 230 235 240
Lys Ser Val Thr Gln Glu Ala Leu Glu Ser Ala Val Leu Ala Lys Phe
 245 250 255
Lys Ser Leu Lys His Glu Ala Val Trp Lys Lys Glu Arg Pro Gly Asn
 260 265 270
Leu Lys Gly Asp Lys Glu Leu Lys Ile His Arg Ile Tyr Pro Leu Gly
 275 280 285
Leu Thr Gln Arg Gln Ala Leu Tyr Asn Phe Lys Phe Glu Gly Asn Ser
290 295 300
Ser Leu Ser Ser His Ile Gln Asn Asn Pro Cys Ala Lys Phe Glu Val
305 310 315 320
Val Phe Val

- (2) INFORMATION FOR SEQ ID NO:753:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 302 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: peptide
 (ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..302

(D) OTHER INFORMATION: / Ceres Seq. ID 1498944

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:753:

Met	Ser	Pro	Val	Gln	Pro	Lys	Thr	Glu	Arg	Ala	Ile	Ala	Ala	Ala	Phe	
1				5				10						15		
Ile	Ser	Asn	Cys	Gly	Ala	Arg	Asn	Phe	Arg	Leu	Gln	Ala	Leu	Glu	Ala	
		20						25					30			
Leu	Met	Lys	Thr	Asn	Ile	Lys	Ile	Asp	Ser	Tyr	Gly	Gly	Cys	His	Arg	
		35					40					45				
Asn	Arg	Asp	Gly	Lys	Val	Asp	Lys	Val	Glu	Ala	Leu	Lys	Arg	Tyr	Lys	
		50					55				60					
Phe	Ser	Leu	Ala	Phe	Glu	Asn	Thr	Asn	Glu	Glu	Asp	Tyr	Val	Thr	Glu	
65					70				75					80		
Lys	Phe	Phe	Gln	Ser	Leu	Val	Ala	Gly	Ser	Val	Pro	Val	Val	Val	Gly	
			85					90						95		
Pro	Pro	Asn	Ile	Glu	Glu	Phe	Ala	Pro	Ala	Ser	Asp	Ser	Phe	Leu	His	
		100						105					110			
Ile	Lys	Thr	Met	Glu	Asp	Val	Glu	Pro	Val	Ala	Lys	Arg	Met	Lys	Tyr	
		115					120					125				
Leu	Ala	Ala	Asn	Pro	Ala	Ala	Tyr	Asn	Gln	Thr	Leu	Arg	Trp	Lys	Tyr	
		130				135					140					
Glu	Gly	Pro	Ser	Asp	Ser	Phe	Lys	Ala	Leu	Val	Asp	Met	Ala	Ala	Val	
145					150					155					160	
His	Ser	Ser	Cys	Arg	Leu	Cys	Ile	Phe	Leu	Ala	Thr	Arg	Val	Arg	Glu	
			165					170						175		
Gln	Glu	Glu	Glu	Ser	Pro	Asn	Phe	Lys	Lys	Arg	Pro	Cys	Lys	Cys	Ser	
			180					185					190			
Arg	Gly	Gly	Ser	Asp	Thr	Val	Tyr	His	Val	Phe	Val	Arg	Glu	Arg	Gly	
		195				200						205				
Arg	Phe	Glu	Met	Glu	Ser	Val	Phe	Leu	Arg	Gly	Lys	Ser	Val	Thr	Gln	
		210				215					220					
Glu	Ala	Leu	Glu	Ser	Ala	Val	Leu	Ala	Lys	Phe	Lys	Ser	Leu	Lys	His	
225					230					235					240	
Glu	Ala	Val	Trp	Lys	Lys	Glu	Arg	Pro	Gly	Asn	Leu	Lys	Gly	Asp	Lys	
			245						250					255		
Glu	Leu	Lys	Ile	His	Arg	Ile	Tyr	Pro	Leu	Gly	Leu	Thr	Gln	Arg	Gln	
		260					265						270			
Ala	Leu	Tyr	Asn	Phe	Lys	Phe	Glu	Gly	Asn	Ser	Ser	Leu	Ser	Ser	His	
		275					280						285			
Ile	Gln	Asn	Asn	Pro	Cys	Ala	Lys	Phe	Glu	Val	Val	Phe	Val			
		290				295					300					

(2) INFORMATION FOR SEQ ID NO:754:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1299 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1299

(D) OTHER INFORMATION: / Ceres Seq. ID 1498949

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:754:

cttttagaca	aaactagtgg	cagactgaaa	aatgaacgca	gcgcttgcaa	caaccaccgc	60
cacaactccc	gcactccgcc	gtgagacgcc	tcttattcat	tattgttctc	tcacaacaaa	120
atcgccgggt	taccaaata	acagagttag	attcggatct	tgctgtgcaa	cagtcagcaa	180
gaaattcttg	aaaatctcgg	cgagctctca	gagcgcttca	gcggcggtca	atatcacggc	240
ggatgcttcg	attccgaaag	agatgaaggc	gtgggtgtat	agtgactacg	gcggagttga	300
tgttttgaaa	ctggagagta	acattgctgt	gccggagatt	aaagaagatc	aggttctgat	360
taaagtgtgt	gcggcgggtc	ttaatcccg	cgatgctaag	agacggcagg	ggaaatttaa	420

```
agccactgat tcgcctctcc cgactgttcc gggatacgac gttgccggag tgggtggtgaa 480
agtgggaagt gcggtgaagg atttcaaaga aggagatgaa gtttatgcta acgtgagcga 540
gaaagcattg gaaggtccaa agcaattcgg ttcttttagcg gagtacacgg ccgtggaaga 600
gaagttatta gctttaaaac ctaaaaacat cgatttcgcg caagctgcag ggcttccggt 660
ggcgatagaa accgctgatg aagggttagt taggactgaa ttctccgccg gaaagtccat 720
tcttgttctt aatggtgccg gaggagtagg gagtcttatg attcagttgg cgaagcacgt 780
gtatggagct tcaaaagtgg ctgcaacagc gagtacaggg aagctggagc tagtgagaag 840
cttaggtgct gatttagcta ttgattacac aaaggagaat atagaagact tgcctgacaa 900
gtacgatgtt gtctttgacg ccattgggat gtgtgataag gcagtgaagg tgattaagga 960
aggagggaaa gttgtggcat tgactggagc tgtcacgcct cctggttttc gattcgttgt 1020
tacatctaata ggcgatgttt tgaagaaact taaccatat attgagagtg ggaaggtgaa 1080
gcctgtggtt gatcccaaag gaccgttccc attctcacgc gttgctgatg ctttttcata 1140
cttagaaacg aaccatgcca caggaaggt cgttgtttat cccattcctt aaggggctgg 1200
cttgagtgtg gtagccttta tctatctatg tgtataagca tagcaagtgt tatcttctct 1260
ttgtattaat gagggtgga ataaaagtaa atgctcttt
```

(2) INFORMATION FOR SEQ ID NO:755:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 386 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..386

(D) OTHER INFORMATION: / Ceres Seq. ID 1498950

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:755:

```
Met Asn Ala Ala Leu Ala Thr Thr Thr Ala Thr Thr Pro Ala Leu Arg
1          5          10          15
Arg Glu Thr Pro Leu Ile His Tyr Cys Ser Leu Thr Thr Lys Ser Pro
20          25          30
Val Tyr Gln Ile Asn Arg Val Arg Phe Gly Ser Cys Val Gln Thr Val
35          40          45
Ser Lys Lys Phe Leu Lys Ile Ser Ala Ser Ser Gln Ser Ala Ser Ala
50          55          60
Ala Val Asn Ile Thr Ala Asp Ala Ser Ile Pro Lys Glu Met Lys Ala
65          70          75          80
Trp Val Tyr Ser Asp Tyr Gly Gly Val Asp Val Leu Lys Leu Glu Ser
85          90          95
Asn Ile Ala Val Pro Glu Ile Lys Glu Asp Gln Val Leu Ile Lys Val
100          105          110
Val Ala Ala Gly Leu Asn Pro Val Asp Ala Lys Arg Arg Gln Gly Lys
115          120          125
Phe Lys Ala Thr Asp Ser Pro Leu Pro Thr Val Pro Gly Tyr Asp Val
130          135          140
Ala Gly Val Val Val Lys Val Gly Ser Ala Val Lys Asp Phe Lys Glu
145          150          155          160
Gly Asp Glu Val Tyr Ala Asn Val Ser Glu Lys Ala Leu Glu Gly Pro
165          170          175
Lys Gln Phe Gly Ser Leu Ala Glu Tyr Thr Ala Val Glu Glu Lys Leu
180          185          190
Leu Ala Leu Lys Pro Lys Asn Ile Asp Phe Ala Gln Ala Ala Gly Leu
195          200          205
Pro Leu Ala Ile Glu Thr Ala Asp Glu Gly Leu Val Arg Thr Glu Phe
210          215          220
Ser Ala Gly Lys Ser Ile Leu Val Leu Asn Gly Ala Gly Gly Val Gly
225          230          235          240
Ser Leu Met Ile Gln Leu Ala Lys His Val Tyr Gly Ala Ser Lys Val
245          250          255
Ala Ala Thr Ala Ser Thr Gly Lys Leu Glu Leu Val Arg Ser Leu Gly
260          265          270
```

Ala Asp Leu Ala Ile Asp Tyr Thr Lys Glu Asn Ile Glu Asp Leu Pro
275 280 285
Asp Lys Tyr Asp Val Val Phe Asp Ala Ile Gly Met Cys Asp Lys Ala
290 295 300
Val Lys Val Ile Lys Glu Gly Gly Lys Val Val Ala Leu Thr Gly Ala
305 310 315 320
Val Thr Pro Pro Gly Phe Arg Phe Val Val Thr Ser Asn Gly Asp Val
325 330 335
Leu Lys Lys Leu Asn Pro Tyr Ile Glu Ser Gly Lys Val Lys Pro Val
340 345 350
Val Asp Pro Lys Gly Pro Phe Pro Phe Ser Arg Val Ala Asp Ala Phe
355 360 365
Ser Tyr Leu Glu Thr Asn His Ala Thr Gly Lys Val Val Val Tyr Pro
370 375 380
Ile Pro
385

(2) INFORMATION FOR SEQ ID NO:756:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 309 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..309

(D) OTHER INFORMATION: / Ceres Seq. ID 1498951

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:756:

Met Lys Ala Trp Val Tyr Ser Asp Tyr Gly Gly Val Asp Val Leu Lys
1 5 10 15
Leu Glu Ser Asn Ile Ala Val Pro Glu Ile Lys Glu Asp Gln Val Leu
20 25 30
Ile Lys Val Val Ala Ala Gly Leu Asn Pro Val Asp Ala Lys Arg Arg
35 40 45
Gln Gly Lys Phe Lys Ala Thr Asp Ser Pro Leu Pro Thr Val Pro Gly
50 55 60
Tyr Asp Val Ala Gly Val Val Val Lys Val Gly Ser Ala Val Lys Asp
65 70 75 80
Phe Lys Glu Gly Asp Glu Val Tyr Ala Asn Val Ser Glu Lys Ala Leu
85 90 95
Glu Gly Pro Lys Gln Phe Gly Ser Leu Ala Glu Tyr Thr Ala Val Glu
100 105 110
Glu Lys Leu Leu Ala Leu Lys Pro Lys Asn Ile Asp Phe Ala Gln Ala
115 120 125
Ala Gly Leu Pro Leu Ala Ile Glu Thr Ala Asp Glu Gly Leu Val Arg
130 135 140
Thr Glu Phe Ser Ala Gly Lys Ser Ile Leu Val Leu Asn Gly Ala Gly
145 150 155 160
Gly Val Gly Ser Leu Met Ile Gln Leu Ala Lys His Val Tyr Gly Ala
165 170 175
Ser Lys Val Ala Ala Thr Ala Ser Thr Gly Lys Leu Glu Leu Val Arg
180 185 190
Ser Leu Gly Ala Asp Leu Ala Ile Asp Tyr Thr Lys Glu Asn Ile Glu
195 200 205
Asp Leu Pro Asp Lys Tyr Asp Val Val Phe Asp Ala Ile Gly Met Cys
210 215 220
Asp Lys Ala Val Lys Val Ile Lys Glu Gly Gly Lys Val Val Ala Leu
225 230 235 240
Thr Gly Ala Val Thr Pro Pro Gly Phe Arg Phe Val Val Thr Ser Asn
245 250 255
Gly Asp Val Leu Lys Lys Leu Asn Pro Tyr Ile Glu Ser Gly Lys Val

260 265 270
Lys Pro Val Val Asp Pro Lys Gly Pro Phe Pro Phe Ser Arg Val Ala
275 280 285
Asp Ala Phe Ser Tyr Leu Glu Thr Asn His Ala Thr Gly Lys Val Val
290 295 300
Val Tyr Pro Ile Pro
305

(2) INFORMATION FOR SEQ ID NO:757:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1347 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1347
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498952

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:757:

```
acgaataaga aaagaagaga aacatcaaac atcttttggtt tgcttccctc gtaccggttc      60
ttcatacaag tatgatcatc tgctgtctct atatatagacat acatacaaaa aaaacttgta      120
taagatttga aactaaaata ttaaatttat cctctatttt gcaggcacgc ctttaattat      180
ggattgtcat agaaagtcgt tcttggtgaa gtttttggtgc gtggcatttc tgttaaacta      240
cagcaatgtt ggctttgtag acgcagcaac aaacattggc ttgaactacg gcctccttgg      300
agacaacctc ccgcctccat ctgaagttat caacctctac aagtccttaa gtgttaccaa      360
tattcggatc ttcgacacga ctacggatgt ccttaacgcc tttcgaggga atcgcgatat      420
tggagttatg gtaggcgtga agaaccaaga cttagaggct ctttcggtca gcgaagacgc      480
tgtaaacacc tggttcgtga caaacattga gccttactta gctgatgtca acatcacggt      540
cattgctgtc gggaacgaag tcatcccagg ggaaatcggc tcttatgtgc taccgcgtcat      600
gaaatctctc accaaccattg tcaagtcgag gagtctcccg atcttgatca gcaccacggt      660
ggctatgacc aaccttggcc agtcgtatcc accttcggcc ggagatttca tacctcaagc      720
gcgtgaacaa cttaccccggt tgctgaagtt tttgtctcaa acaaatacgc ctatcctcgt      780
caacatctac cctacattcg catatgctgc tgatcctatc aacattcagc ttgattatgc      840
catcttcaac accaacaagg ttgtggtcca agttatataca acatggttca tgtgatattt      900
gatgctttcg tatgggcaat ggagaaagag ggcgtgaagg atttaccat ggtggttaaca      960
gagaccggat ggccatctgc tggtaacgga aacttaacaa ctccagatat cgcattctata      1020
tacaatacca attttggttaa acatgtggaa agcggtaaag ggacgcaaaa gagaccaaaag      1080
agtggcatta gtggatttct atttgcgacg ttcaatgaga atcaaaaagcc agcgggaacc      1140
gaacaaaatt ttgggttata taatccaaca gatatgaagc ccattctacaa gatgttttga      1200
tttttagatt cttgatttta tagacaatcc caaatcatta gtaaattaat gatgctctaa      1260
tagttgtaat agagcgggat aaaatcaaga tctacaacaa cattcatttt atatgtttga      1320
tgatcttctt aaataaaaaa acttaag
```

(2) INFORMATION FOR SEQ ID NO:758:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 238 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..238
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498953

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:758:

Met Asp Cys His Arg Lys Ser Phe Leu Leu Lys Phe Leu Cys Val Ala
1 5 10 15
Phe Leu Leu Asn Tyr Ser Asn Val Gly Phe Val Asp Ala Ala Thr Asn
20 25 30
Ile Gly Leu Asn Tyr Gly Leu Leu Gly Asp Asn Leu Pro Pro Pro Ser
35 40 45
Glu Val Ile Asn Leu Tyr Lys Ser Leu Ser Val Thr Asn Ile Arg Ile

50		55		60											
Phe	Asp	Thr	Thr	Thr	Asp	Val	Leu	Asn	Ala	Phe	Arg	Gly	Asn	Arg	Asp
65					70					75					80
Ile	Gly	Val	Met	Val	Gly	Val	Lys	Asn	Gln	Asp	Leu	Glu	Ala	Leu	Ser
				85					90					95	
Val	Ser	Glu	Asp	Ala	Val	Asn	Thr	Trp	Phe	Val	Thr	Asn	Ile	Glu	Pro
			100				105						110		
Tyr	Leu	Ala	Asp	Val	Asn	Ile	Thr	Phe	Ile	Ala	Val	Gly	Asn	Glu	Val
		115					120					125			
Ile	Pro	Gly	Glu	Ile	Gly	Ser	Tyr	Val	Leu	Pro	Val	Met	Lys	Ser	Leu
	130					135					140				
Thr	Asn	Ile	Val	Lys	Ser	Arg	Ser	Leu	Pro	Ile	Leu	Ile	Ser	Thr	Thr
145					150					155					160
Val	Ala	Met	Thr	Asn	Leu	Gly	Gln	Ser	Tyr	Pro	Pro	Ser	Ala	Gly	Asp
				165					170					175	
Phe	Ile	Pro	Gln	Ala	Arg	Glu	Gln	Leu	Thr	Pro	Val	Leu	Lys	Phe	Leu
			180					185					190		
Ser	Gln	Thr	Asn	Thr	Pro	Ile	Leu	Val	Asn	Ile	Tyr	Pro	Tyr	Phe	Ala
		195				200						205			
Tyr	Ala	Ala	Asp	Pro	Ile	Asn	Ile	Gln	Leu	Asp	Tyr	Ala	Ile	Phe	Asn
	210					215				220					
Thr	Asn	Lys	Val	Val	Val	Gln	Val	Ile	Gln	Thr	Cys	Ser	Met		
225					230					235					

(2) INFORMATION FOR SEQ ID NO:759:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 155 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..155

(D) OTHER INFORMATION: / Ceres Seq. ID 1498954

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:759:

Met	Val	Gly	Val	Lys	Asn	Gln	Asp	Leu	Glu	Ala	Leu	Ser	Val	Ser	Glu
1				5					10					15	
Asp	Ala	Val	Asn	Thr	Trp	Phe	Val	Thr	Asn	Ile	Glu	Pro	Tyr	Leu	Ala
			20					25					30		
Asp	Val	Asn	Ile	Thr	Phe	Ile	Ala	Val	Gly	Asn	Glu	Val	Ile	Pro	Gly
		35				40						45			
Glu	Ile	Gly	Ser	Tyr	Val	Leu	Pro	Val	Met	Lys	Ser	Leu	Thr	Asn	Ile
	50					55				60					
Val	Lys	Ser	Arg	Ser	Leu	Pro	Ile	Leu	Ile	Ser	Thr	Thr	Val	Ala	Met
65					70					75					80
Thr	Asn	Leu	Gly	Gln	Ser	Tyr	Pro	Pro	Ser	Ala	Gly	Asp	Phe	Ile	Pro
			85						90					95	
Gln	Ala	Arg	Glu	Gln	Leu	Thr	Pro	Val	Leu	Lys	Phe	Leu	Ser	Gln	Thr
			100					105					110		
Asn	Thr	Pro	Ile	Leu	Val	Asn	Ile	Tyr	Pro	Tyr	Phe	Ala	Tyr	Ala	Ala
		115					120					125			
Asp	Pro	Ile	Asn	Ile	Gln	Leu	Asp	Tyr	Ala	Ile	Phe	Asn	Thr	Asn	Lys
	130					135					140				
Val	Val	Val	Gln	Val	Ile	Gln	Thr	Cys	Ser	Met					
145					150					155					

(2) INFORMATION FOR SEQ ID NO:760:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1453 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1453

(D) OTHER INFORMATION: / Ceres Seq. ID 1498958

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:760:

```
aaaagaaaat tgtcaatttc gaaaaatggt gagcacaagc tctgatcttc atggccgtct      60
tctccgatta tcagaaccaa tagcagagat tcttagacgt acacagtaca caccgcaaga      120
gagcagcaaa gtatccacca aagatatact cttgtccttg ttaccaaaca cttcgtcttc      180
tcgtctcgcc aatgaagaat cgvtcaaaag tctcgcgctt gcttgtgccc ttctcgcttc      240
ttcacgttca tccactcacg aacttctctc atggatttcc agaaaacctc tctgtcatgg      300
gggaatctac attttgggag atttcaaggg attgtttcag tgatttttct agcaacagta      360
atgctgagaa gcttgtggaa ttggtagagg atagttagaa gatcgaaatg ttgccgatag      420
ttttgccgga gttaaaagat ggaatcgaaa agagttcact tggtaaaggc agtgatgcag      480
aggatgtttc agctgcaatg gctagaacac ctggttggtta tgctatactt gctgctcacc      540
agctcagggtg gtttgttact caggttaaaa aaccgaattt ggtgaaattt tgtaacttgg      600
tggttccttg tgctttgaca gcacttgatc attggtctcc tgaagtcaaa gggcagggtg      660
tgataacctt tgttcatctt gctaaaaatg tgagttccgg tgatcttggt ttgtatggag      720
atgtggttct tgatgcgtgt tgccagaata tagcttccga tgatgagatt tggatacatg      780
tggttagagtt atctgtgctt cttgttacta aaatccaccc aaataatcct cgaagcccgt      840
ggtatgagaa gatcatgaat gagatgctcg ggcatttgga acgccaacca agaaataagg      900
agcgacgtat cacttggtta agatttggtg agccactctt gaactctcta gggcttttct      960
tacttgctca ttttcgacgt atcttccctc ttttctttca gtggatgcat tcagacgacg      1020
ccgaaacagt tctggttggt cttgagagac tggagacagt tgtgaggttg acgtggatta      1080
gacactcacc tgtgttccca agatttggtg atgagcttgt ttccttgtag aaagagtcat      1140
cgatgcgtaa ggatcgcgat gatattagac ctcttatcct ccgtatcttg atgctactcc      1200
gccagtgcaa aggtctacgg tttgagtcag cgtggagtca ataccaggag gatccaaatc      1260
tgagtactgt tagtcaacat atatggacta gttcaagttg atctcaagag cgtatgtttg      1320
actaaaacag ccattttttt tctaattttc gatattagtt tgggtctaggc ctagtgatgc      1380
aagtaattac tggcgaatcc tcgaattttt gtaagcattt ggctcttgac tcttcttaag      1440
ctaattctgat ttg
```

(2) INFORMATION FOR SEQ ID NO:761:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 369 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..369

(D) OTHER INFORMATION: / Ceres Seq. ID 1498959

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:761:

```
Met Lys Asn Xaa Ser Lys Val Ser Arg Leu Leu Val Pro Phe Ser Leu
1          5          10          15
Leu His Val His Pro Leu Thr Asn Phe Ser His Gly Xaa Pro Glu Asn
20          25          30
Leu Ser Val Met Gly Glu Ser Thr Phe Trp Glu Ile Ser Arg Asp Cys
35          40          45
Phe Ser Asp Phe Ser Ser Asn Ser Asn Ala Glu Lys Leu Val Glu Leu
50          55          60
Val Glu Asp Ser Glu Lys Ile Glu Met Leu Pro Ile Val Leu Pro Glu
65          70          75          80
Leu Lys Asp Gly Ile Glu Lys Ser Ser Leu Gly Lys Gly Ser Asp Ala
85          90          95
Glu Asp Val Ser Ala Ala Met Ala Arg Thr Pro Val Gly Tyr Ala Ile
100         105         110
Leu Ala Ala His Gln Leu Arg Trp Phe Val Thr Gln Val Lys Lys Pro
115         120         125
Asn Leu Val Lys Phe Cys Asn Leu Val Val Pro Cys Ala Leu Thr Ala
130         135         140
```

Leu Asp His Trp Ser Pro Glu Val Lys Gly Gln Gly Met Ile Thr Phe
145 150 155 160
Val His Leu Ala Lys Asn Val Ser Ser Gly Asp Leu Gly Leu Tyr Gly
165 170 175
Asp Val Val Leu Asp Ala Cys Cys Gln Asn Ile Ala Ser Asp Asp Glu
180 185 190
Ile Trp Ile His Val Val Glu Leu Ser Val Leu Leu Val Thr Lys Ile
195 200 205
His Pro Asn Asn Pro Arg Ser Pro Trp Tyr Glu Lys Ile Met Asn Glu
210 215 220
Met Leu Gly His Leu Glu Arg Gln Pro Arg Asn Lys Glu Arg Arg Ile
225 230 235 240
Thr Trp Leu Arg Phe Val Glu Pro Leu Leu Asn Ser Leu Gly Leu Phe
245 250 255
Leu Leu Ala His Phe Arg Arg Ile Phe Pro Leu Phe Phe Gln Trp Met
260 265 270
His Ser Asp Asp Ala Glu Thr Val Leu Leu Val Leu Glu Arg Leu Glu
275 280 285
Thr Val Val Arg Leu Thr Trp Ile Arg His Ser Pro Val Phe Pro Arg
290 295 300
Leu Val Asp Glu Leu Val Ser Leu Tyr Lys Glu Ser Ser Met Arg Lys
305 310 315 320
Asp Arg Asp Asp Ile Arg Pro Leu Ile Leu Arg Ile Leu Met Leu Leu
325 330 335
Arg Gln Cys Lys Gly Leu Arg Phe Glu Ser Ala Trp Ser Gln Tyr Gln
340 345 350
Glu Asp Pro Asn Leu Ser Thr Val Ser Gln His Ile Trp Thr Ser Ser
355 360 365
Ser

(2) INFORMATION FOR SEQ ID NO:762:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 334 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..334

(D) OTHER INFORMATION: / Ceres Seq. ID 1498960

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:762:

Met Gly Glu Ser Thr Phe Trp Glu Ile Ser Arg Asp Cys Phe Ser Asp
1 5 10 15
Phe Ser Ser Asn Ser Asn Ala Glu Lys Leu Val Glu Leu Val Glu Asp
20 25 30
Ser Glu Lys Ile Glu Met Leu Pro Ile Val Leu Pro Glu Leu Lys Asp
35 40 45
Gly Ile Glu Lys Ser Ser Leu Gly Lys Gly Ser Asp Ala Glu Asp Val
50 55 60
Ser Ala Ala Met Ala Arg Thr Pro Val Gly Tyr Ala Ile Leu Ala Ala
65 70 75 80
His Gln Leu Arg Trp Phe Val Thr Gln Val Lys Lys Pro Asn Leu Val
85 90 95
Lys Phe Cys Asn Leu Val Val Pro Cys Ala Leu Thr Ala Leu Asp His
100 105 110
Trp Ser Pro Glu Val Lys Gly Gln Gly Met Ile Thr Phe Val His Leu
115 120 125
Ala Lys Asn Val Ser Ser Gly Asp Leu Gly Leu Tyr Gly Asp Val Val
130 135 140
Leu Asp Ala Cys Cys Gln Asn Ile Ala Ser Asp Asp Glu Ile Trp Ile

145		150		155		160									
His	Val	Val	Glu	Leu	Ser	Val	Leu	Leu	Val	Thr	Lys	Ile	His	Pro	Asn
			165						170					175	
Asn	Pro	Arg	Ser	Pro	Trp	Tyr	Glu	Lys	Ile	Met	Asn	Glu	Met	Leu	Gly
			180					185					190		
His	Leu	Glu	Arg	Gln	Pro	Arg	Asn	Lys	Glu	Arg	Arg	Ile	Thr	Trp	Leu
		195					200					205			
Arg	Phe	Val	Glu	Pro	Leu	Leu	Asn	Ser	Leu	Gly	Leu	Phe	Leu	Leu	Ala
	210					215					220				
His	Phe	Arg	Arg	Ile	Phe	Pro	Leu	Phe	Phe	Gln	Trp	Met	His	Ser	Asp
225					230					235					240
Asp	Ala	Glu	Thr	Val	Leu	Leu	Val	Leu	Glu	Arg	Leu	Glu	Thr	Val	Val
			245						250					255	
Arg	Leu	Thr	Trp	Ile	Arg	His	Ser	Pro	Val	Phe	Pro	Arg	Leu	Val	Asp
		260						265					270		
Glu	Leu	Val	Ser	Leu	Tyr	Lys	Glu	Ser	Ser	Met	Arg	Lys	Asp	Arg	Asp
	275					280						285			
Asp	Ile	Arg	Pro	Leu	Ile	Leu	Arg	Ile	Leu	Met	Leu	Leu	Arg	Gln	Cys
290					295						300				
Lys	Gly	Leu	Arg	Phe	Glu	Ser	Ala	Trp	Ser	Gln	Tyr	Gln	Glu	Asp	Pro
305				310						315					320
Asn	Leu	Ser	Thr	Val	Ser	Gln	His	Ile	Trp	Thr	Ser	Ser	Ser		
			325						330						

(2) INFORMATION FOR SEQ ID NO:763:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 297 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..297

(D) OTHER INFORMATION: / Ceres Seq. ID 1498961

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:763:

Met	Leu	Pro	Ile	Val	Leu	Pro	Glu	Leu	Lys	Asp	Gly	Ile	Glu	Lys	Ser
1				5					10					15	
Ser	Leu	Gly	Lys	Gly	Ser	Asp	Ala	Glu	Asp	Val	Ser	Ala	Ala	Met	Ala
		20						25					30		
Arg	Thr	Pro	Val	Gly	Tyr	Ala	Ile	Leu	Ala	Ala	His	Gln	Leu	Arg	Trp
		35				40						45			
Phe	Val	Thr	Gln	Val	Lys	Lys	Pro	Asn	Leu	Val	Lys	Phe	Cys	Asn	Leu
50					55						60				
Val	Val	Pro	Cys	Ala	Leu	Thr	Ala	Leu	Asp	His	Trp	Ser	Pro	Glu	Val
65				70					75					80	
Lys	Gly	Gln	Gly	Met	Ile	Thr	Phe	Val	His	Leu	Ala	Lys	Asn	Val	Ser
			85					90					95		
Ser	Gly	Asp	Leu	Gly	Leu	Tyr	Gly	Asp	Val	Val	Leu	Asp	Ala	Cys	Cys
		100					105						110		
Gln	Asn	Ile	Ala	Ser	Asp	Asp	Glu	Ile	Trp	Ile	His	Val	Val	Glu	Leu
		115				120						125			
Ser	Val	Leu	Leu	Val	Thr	Lys	Ile	His	Pro	Asn	Asn	Pro	Arg	Ser	Pro
	130					135					140				
Trp	Tyr	Glu	Lys	Ile	Met	Asn	Glu	Met	Leu	Gly	His	Leu	Glu	Arg	Gln
145				150					155					160	
Pro	Arg	Asn	Lys	Glu	Arg	Arg	Ile	Thr	Trp	Leu	Arg	Phe	Val	Glu	Pro
			165						170					175	
Leu	Leu	Asn	Ser	Leu	Gly	Leu	Phe	Leu	Leu	Ala	His	Phe	Arg	Arg	Ile
		180					185						190		
Phe	Pro	Leu	Phe	Phe	Gln	Trp	Met	His	Ser	Asp	Asp	Ala	Glu	Thr	Val
		195				200						205			

(2) INFORMATION FOR SEQ ID NO:764:

(A) LENGTH: 637 base pairs

(B) TYPE: nucleic acid

```
(C) STRANDEDNESS: single
```

(D) TOPOLOGY: linear

MOLECULE TYPE: DNA (g

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..637

(D) OTHER INFORMATION: / Ceres Seq. ID 1498962

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:764:

rgaattycac	cgcattgtatc	gtgcattggc	tgaacgttat	gatcaagcta	gtggtgagct	60
acagaagaac	catacatctg	agatccagtc	acagagctct	cttgagttat	catctcctac	120
caaagagaag	ttgagtcgcc	gtcaatctgg	ccataaagaa	gaggaagatt	catcatcttt	180
gacagattcc	ggttctgatt	ctgatcattc	ctctgccaat	gatgaagacg	gtgacgaggc	240
attgatccgt	agaatggctg	aacttgagct	tgagcttcaa	gagacgaaac	agaagctcct	300
tctccagcag	gaaagtgttg	atggtgacaa	caatgttgat	ctccttcaca	aaattactac	360
atatgagggg	gagcttaaag	aagctaataa	gaagatgcga	atgcacgaag	acgagattgc	420
taatctgaag	aatcagcttc	agagctgcat	gtcctttgac	gcagaggatc	aacttggtac	480
tgcagaaaag	agtcttgatt	tggataaaga	ggacactgaa	gcagatgcag	aagctacaaa	540
agtgcctagc	ttggagggaag	agctgagtat	cgcgaaagag	aagcttcagc	actttgagaa	600
agagacttat	tctctqaaaa	atgaqctcga	qattaagt			

(2) INFORMATION FOR SEQ ID NO:765:

(A) LENGTH: 212 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

MOLECULE TYPE: peptid

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..212

(D) OTHER INFORMATION: / Ceres Seq. ID 1498963

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:765:

Glu 1	Xaa	His	Arg	Met 5	Tyr	Arg	Ala	Leu 10	Ala	Glu	Arg	Tyr	Asp	Gln 15	Ala
Ser	Gly	Glu	Leu 20	Gln	Lys	Asn	His	Thr 25	Ser	Glu	Ile	Gln	Ser	Gln	Ser
Ser	Leu	Glu	Leu 35	Ser	Ser	Pro	Thr 40	Lys	Glu	Lys	Leu	Ser	Arg	Arg	Gln
Ser	Gly 50	His	Lys	Glu	Glu	Glu 55	Asp	Ser	Ser	Ser	Leu 60	Thr	Asp	Ser	Gly
Ser 65	Asp	Ser	Asp	His	Ser	Ser	Ala	Asn	Asp	Glu 75	Asp	Gly	Asp	Glu	Ala 80
Leu	Ile	Arg	Arg	Met 85	Ala	Glu	Leu	Glu	Leu 90	Glu	Leu	Gln	Glu	Thr	Lys
Gln	Lys	Leu	Leu 100	Gln	Gln	Glu	Ser	Val	Val 105	Asp	Gly	Asp	Asn	Asn	Val

Asp Leu Leu His Lys Ile Thr Thr Tyr Glu Gly Glu Leu Lys Glu Ala
115 120 125
Asn Glu Lys Met Arg Met His Glu Asp Glu Ile Ala Asn Leu Lys Asn
130 135 140
Gln Leu Gln Ser Cys Met Ser Phe Asp Ala Glu Asp Gln Leu Gly Thr
145 150 155 160
Ala Glu Lys Ser Leu Asp Leu Asp Lys Glu Asp Thr Glu Ala Asp Ala
165 170 175
Glu Ala Thr Lys Val Leu Ala Leu Glu Glu Glu Leu Ser Ile Ala Lys
180 185 190
Glu Lys Leu Gln His Phe Glu Lys Glu Thr Tyr Ser Leu Lys Asn Glu
195 200 205
Leu Glu Ile Ser
210

(2) INFORMATION FOR SEQ ID NO:766:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 208 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..208

(D) OTHER INFORMATION: / Ceres Seq. ID 1498964

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:766:

Met Tyr Arg Ala Leu Ala Glu Arg Tyr Asp Gln Ala Ser Gly Glu Leu
1 5 10 15
Gln Lys Asn His Thr Ser Glu Ile Gln Ser Gln Ser Ser Leu Glu Leu
20 25 30
Ser Ser Pro Thr Lys Glu Lys Leu Ser Arg Arg Gln Ser Gly His Lys
35 40 45
Glu Glu Glu Asp Ser Ser Ser Leu Thr Asp Ser Gly Ser Asp Ser Asp
50 55 60
His Ser Ser Ala Asn Asp Glu Asp Gly Asp Glu Ala Leu Ile Arg Arg
65 70 75 80
Met Ala Glu Leu Glu Leu Glu Leu Gln Glu Thr Lys Gln Lys Leu Leu
85 90 95
Leu Gln Gln Glu Ser Val Asp Gly Asp Asn Asn Val Asp Leu Leu His
100 105 110
Lys Ile Thr Thr Tyr Glu Gly Glu Leu Lys Glu Ala Asn Glu Lys Met
115 120 125
Arg Met His Glu Asp Glu Ile Ala Asn Leu Lys Asn Gln Leu Gln Ser
130 135 140
Cys Met Ser Phe Asp Ala Glu Asp Gln Leu Gly Thr Ala Glu Lys Ser
145 150 155 160
Leu Asp Leu Asp Lys Glu Asp Thr Glu Ala Asp Ala Glu Ala Thr Lys
165 170 175
Val Leu Ala Leu Glu Glu Glu Leu Ser Ile Ala Lys Glu Lys Leu Gln
180 185 190
His Phe Glu Lys Glu Thr Tyr Ser Leu Lys Asn Glu Leu Glu Ile Ser
195 200 205

(2) INFORMATION FOR SEQ ID NO:767:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 128 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..128

(D) OTHER INFORMATION: / Ceres Seq. ID 1498965

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:767:

Met	Ala	Glu	Leu	Glu	Leu	Glu	Leu	Gln	Glu	Thr	Lys	Gln	Lys	Leu	Leu
1				5					10					15	
Leu	Gln	Gln	Glu	Ser	Val	Asp	Gly	Asp	Asn	Asn	Val	Asp	Leu	Leu	His
			20					25					30		
Lys	Ile	Thr	Thr	Tyr	Glu	Gly	Glu	Leu	Lys	Glu	Ala	Asn	Glu	Lys	Met
		35					40					45			
Arg	Met	His	Glu	Asp	Glu	Ile	Ala	Asn	Leu	Lys	Asn	Gln	Leu	Gln	Ser
	50					55					60				
Cys	Met	Ser	Phe	Asp	Ala	Glu	Asp	Gln	Leu	Gly	Thr	Ala	Glu	Lys	Ser
65					70					75				80	
Leu	Asp	Leu	Asp	Lys	Glu	Asp	Thr	Glu	Ala	Asp	Ala	Glu	Ala	Thr	Lys
				85				90						95	
Val	Leu	Ala	Leu	Glu	Glu	Glu	Leu	Ser	Ile	Ala	Lys	Glu	Lys	Leu	Gln
			100					105						110	
His	Phe	Glu	Lys	Glu	Thr	Tyr	Ser	Leu	Lys	Asn	Glu	Leu	Glu	Ile	Ser
		115					120							125	

(2) INFORMATION FOR SEQ ID NO:768:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1513 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1513

(D) OTHER INFORMATION: / Ceres Seq. ID 1498966

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:768:

aaaacaaact	ctcgccttc	gcacgttg	ttctccaaa	ccagttttca	ctctctattg	60
ccgattctcg	tttcgtttg	tatcttagg	atctataaac	aaaggcatgg	gttcagttat	120
ctgttgattt	tctcaatcaa	tttctcagc	attttcagtc	ttaaggtctt	gggtccatggg	180
ttgctcgaga	aaatgtggaa	aaagtgtgg	tctgagtact	taatcgtaaa	atgcaaatac	240
aaagcttttg	tgggtttatt	aaagttggta	acttttgata	gaattttgag	gactcttact	300
tgtttgctta	catgcctgcg	tagtgtttgt	ttaaagtcct	gtgagaaata	cttttttagtg	360
aaaagctctt	tttttttttt	tttgtttagt	gttcgtttta	gtagatatgt	aatgtgaaac	420
taatttctga	atctctgttt	tgagtactgt	agagttatga	aattgggtatt	ttgctaattgc	480
atgtctacat	tgtgtccaga	ttcttataaa	aacagaaaact	ttgatcttat	cttatggatg	540
aattacttta	ggttactgat	gatgatttgt	ataacctaga	tgttcgtttc	agagaaaaaac	600
ctggaaaatta	ctgtctactt	ccttttcctt	tctctgtgat	ctttcagttt	tgatttttttc	660
cagagtcctt	ctcatatctt	tcctttgaga	agaatgtgat	gatagtaaag	tatttctatt	720
ctctggatca	atgatgatag	ctatgtgaca	ttgctttgat	ttggttttga	agggtgaaca	780
atgtttctca	aagtccaatt	accatggaac	gtgatgattc	cagctgaaaa	catggatgcc	840
aaagggtctga	tgttgaagag	agctatacta	gtagagttac	tagaggcggt	cgcttccaag	900
aaagcaacca	aggagcttgg	ctactacgtg	gcagtcacaa	ctttggacaa	gattggagaa	960
ggcaaaatca	gggagcacac	cggtgaagtt	ttgttcccgg	taatgttcag	cggaatgact	1020
ttcaagatct	tcaaaggaga	gataattcac	ggtgtgggtg	acaaggtgtt	gaagcacggt	1080
gtcttcatga	ggtgtggtcc	aatcgagaat	gtttacctct	cctacacgaa	gatgccggat	1140
tacaagtata	tccctggaga	gaaccgcatc	ttcatgaatg	agaagacgtc	taggattccag	1200
gttgagacta	cagtggaggt	tggtgtgatt	gggataaagt	ggatggaaat	agagagggag	1260
tttcaggcgt	tggctagctt	ggaaggtgac	tatcttggac	cattatctga	agagtgtatc	1320
gcttgatttc	ttcatgtgat	ggcgtttttg	ggcaatctct	tatgtctata	taactcggct	1380
ttagttcatg	tttggtagta	actagtaact	actctctagc	tgtgcaaata	atgaaaacat	1440
tgatctttga	atgtaatgaa	atcctccacc	ttcaagagga	aagattgggtc	taatttaggt	1500
tttttgtatt	ggc					

(2) INFORMATION FOR SEQ ID NO:769:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 178 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..178
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498967

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:769:

Met Phe Leu Lys Val Gln Leu Pro Trp Asn Val Met Ile Pro Ala Glu
1 5 10 15
Asn Met Asp Ala Lys Gly Leu Met Leu Lys Arg Ala Ile Leu Val Glu
20 25 30
Leu Leu Glu Ala Phe Ala Ser Lys Lys Ala Thr Lys Glu Leu Gly Tyr
35 40 45
Tyr Val Ala Val Thr Thr Leu Asp Lys Ile Gly Glu Gly Lys Ile Arg
50 55 60
Glu His Thr Gly Glu Val Leu Phe Pro Val Met Phe Ser Gly Met Thr
65 70 75 80
Phe Lys Ile Phe Lys Gly Glu Ile Ile His Gly Val Val His Lys Val
85 90 95
Leu Lys His Gly Val Phe Met Arg Cys Gly Pro Ile Glu Asn Val Tyr
100 105 110
Leu Ser Tyr Thr Lys Met Pro Asp Tyr Lys Tyr Ile Pro Gly Glu Asn
115 120 125
Pro Ile Phe Met Asn Glu Lys Thr Ser Arg Ile Gln Val Glu Thr Thr
130 135 140
Val Arg Val Val Val Ile Gly Ile Lys Trp Met Glu Val Glu Arg Glu
145 150 155 160
Phe Gln Ala Leu Ala Ser Leu Glu Gly Asp Tyr Leu Gly Pro Leu Ser
165 170 175
Glu Glu

(2) INFORMATION FOR SEQ ID NO:770:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 167 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..167
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498968

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:770:

Met Ile Pro Ala Glu Asn Met Asp Ala Lys Gly Leu Met Leu Lys Arg
1 5 10 15
Ala Ile Leu Val Glu Leu Leu Glu Ala Phe Ala Ser Lys Lys Ala Thr
20 25 30
Lys Glu Leu Gly Tyr Tyr Val Ala Val Thr Thr Leu Asp Lys Ile Gly
35 40 45
Glu Gly Lys Ile Arg Glu His Thr Gly Glu Val Leu Phe Pro Val Met
50 55 60
Phe Ser Gly Met Thr Phe Lys Ile Phe Lys Gly Glu Ile Ile His Gly
65 70 75 80
Val Val His Lys Val Leu Lys His Gly Val Phe Met Arg Cys Gly Pro
85 90 95
Ile Glu Asn Val Tyr Leu Ser Tyr Thr Lys Met Pro Asp Tyr Lys Tyr

100 105 110
Ile Pro Gly Glu Asn Pro Ile Phe Met Asn Glu Lys Thr Ser Arg Ile
115 120 125
Gln Val Glu Thr Thr Val Arg Val Val Ile Gly Ile Lys Trp Met
130 135 140
Glu Val Glu Arg Glu Phe Gln Ala Leu Ala Ser Leu Glu Gly Asp Tyr
145 150 155 160
Leu Gly Pro Leu Ser Glu Glu
165

(2) INFORMATION FOR SEQ ID NO:771:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 161 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..161

(D) OTHER INFORMATION: / Ceres Seq. ID 1498969

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:771:

Met Asp Ala Lys Gly Leu Met Leu Lys Arg Ala Ile Leu Val Glu Leu
1 5 10 15
Leu Glu Ala Phe Ala Ser Lys Lys Ala Thr Lys Glu Leu Gly Tyr Tyr
20 25 30
Val Ala Val Thr Thr Leu Asp Lys Ile Gly Glu Gly Lys Ile Arg Glu
35 40 45
His Thr Gly Glu Val Leu Phe Pro Val Met Phe Ser Gly Met Thr Phe
50 55 60
Lys Ile Phe Lys Gly Glu Ile Ile His Gly Val Val His Lys Val Leu
65 70 75 80
Lys His Gly Val Phe Met Arg Cys Gly Pro Ile Glu Asn Val Tyr Leu
85 90 95
Ser Tyr Thr Lys Met Pro Asp Tyr Lys Tyr Ile Pro Gly Glu Asn Pro
100 105 110
Ile Phe Met Asn Glu Lys Thr Ser Arg Ile Gln Val Glu Thr Thr Val
115 120 125
Arg Val Val Val Ile Gly Ile Lys Trp Met Glu Val Glu Arg Glu Phe
130 135 140
Gln Ala Leu Ala Ser Leu Glu Gly Asp Tyr Leu Gly Pro Leu Ser Glu
145 150 155 160
Glu

(2) INFORMATION FOR SEQ ID NO:772:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 695 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..695

(D) OTHER INFORMATION: / Ceres Seq. ID 1498970

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:772:

caactsgagt gttatggcat ggaatccgta tttagggcwg acgaaattga ttcaaccaag 60
aaaaaaactc cacagatatg acaagtttgc tcttggatac gacaacaacc gtaaccacaa 120
aattttgagg tttctttatg aggggagtc aagaaacgtc attattgatg ttacgattt 180
tagctctgat tcatggaggg ttcttgatat tgatatagat tggcatgaac tgtttagtca 240
cwwtagcsys tswwtgmcgg gaaatactta cttttttggt cgawagggac cacktttgcc 300
tatgctgttt aaacctcywt ctcgctcgtt tgaatatttg actctatctt gtgtagaaa 360

tgagaaactc gctgtgttat acagccacct caacagattt ggcacaatag agatttgtat 420
ttcgactaag attgatccca gtgcagtatc atggaccact tttttgagaa ttgatatgac 480
actaatcaat ggttttaccgg ataacttttt tgttcactct tatgctwcga gctttttctt 540
ckaygakgag aaraakgtcg ytgwkctttt cggkacaaac agatatagag gacgtgagac 600
ctgtcagtac taccagagag cttgcatcgt tggagatagt ggatacttca aagctgtcaa 660
catcgaacta gttttcaatt cacagctgca atctt

(2) INFORMATION FOR SEQ ID NO:773:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 231 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..231

(D) OTHER INFORMATION: / Ceres Seq. ID 1498971

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:773:

Asn Xaa Ser Val Met Ala Trp Asn Pro Tyr Leu Gly Xaa Thr Lys Leu
1 5 10 15
Ile Gln Pro Arg Lys Lys Leu His Arg Tyr Asp Lys Phe Ala Leu Gly
20 25 30
Tyr Asp Asn Asn Arg Asn His Lys Ile Leu Arg Phe Leu Tyr Glu Gly
35 40 45
Ser Pro Arg Asn Val Ile Ile Asp Val Tyr Asp Phe Ser Ser Asp Ser
50 55 60
Trp Arg Val Leu Asp Ile Asp Ile Asp Trp His Glu Leu Phe Ser His
65 70 75 80
Xaa Ser Xaa Xaa Xaa Xaa Gly Asn Thr Tyr Phe Phe Gly Arg Xaa Gly
85 90 95
Pro Xaa Leu Pro Met Leu Phe Lys Pro Xaa Ser Arg Arg Phe Glu Tyr
100 105 110
Leu Thr Leu Ser Cys Val Arg Asn Glu Lys Leu Ala Val Leu Tyr Ser
115 120 125
His Leu Asn Arg Phe Gly Thr Ile Glu Ile Cys Ile Ser Thr Lys Ile
130 135 140
Asp Pro Ser Ala Val Ser Trp Thr Thr Phe Leu Arg Ile Asp Met Thr
145 150 155 160
Leu Ile Asn Gly Leu Pro Asp Asn Phe Phe Val His Ser Tyr Ala Xaa
165 170 175
Ser Phe Phe Phe Xaa Xaa Glu Xaa Xaa Val Xaa Xaa Leu Phe Xaa Thr
180 185 190
Asn Arg Tyr Arg Gly Arg Glu Thr Cys Gln Tyr Tyr Gln Arg Ala Cys
195 200 205
Ile Val Gly Asp Ser Gly Tyr Phe Lys Ala Val Asn Ile Glu Leu Val
210 215 220
Phe Asn Ser Gln Leu Gln Ser
225 230

(2) INFORMATION FOR SEQ ID NO:774:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 227 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..227

(D) OTHER INFORMATION: / Ceres Seq. ID 1498972

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:774:

Met Ala Trp Asn Pro Tyr Leu Gly Xaa Thr Lys Leu Ile Gln Pro Arg

(2) INFORMATION FOR SEQ ID NO:775:

(A) LENGTH: 131 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..131

(D) OTHER INFORMATION: / Ceres Seq. ID 1498973

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:775:

(2) INFORMATION FOR SEQ ID NO:776:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1266 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
(A) NAME/KEY: -
(B) LOCATION: 1..1266
(D) OTHER INFORMATION: / Ceres Seq. ID 1498974
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:776:

```
gaaaatggaa taatgcttgt gagcagagag agagagcgag cgaggaggct agagaatcga      60
gaatcgatct tcgccgaacc accttgtctt ctcttagctc atcgaatctc tccgtcgcgc      120
tcgattcttc ccgccgaaga ggagggtcatg gacgtttctg ctagaaagtc acaaaaagct      180
gggcgcgaaa agttgaggag ggaaaaactg aatgagcatt ttgttgaact gggaaatgta      240
ctcgatccag agagacccaa gaatgacaaa gccacgattc tgactgatac tgttcagttg      300
ttgaaagagc tcacatctga agtcaacaaa ctgaaatctg agtacaccgc attgacagat      360
gagtcgccgc agttgacaca ggagaaaaaac gacctgagag aagaaaagac atcgctgaaa      420
tcagatatag agaattctcaa tcttcaatac cagcagagat taaggtcaat gtctccatgg      480
ggagctgcga tggatcacac agtcatgatg gctccaccac cctcctttcc ataccctatg      540
cctattgcta tgcctcccggt gtcaatccca atgcatccat caatgccatc ttacacatac      600
tttggaacc agaaccctag catgatccca gctccatgtc ctacatacat gccctacatg      660
cctcctaata cagtcgttga gcaacaatcc gtgcacattc cacagaaccc cggtaaccgt      720
tctcgggaac ctagagcaaa ggtttcaaga gagagcagat ctgagaaagc agaggactcc      780
aacgaagttg caacacaact cgaattaaaa acccctggat ctacttctga taaggatata      840
ttgcaaaggc cagagaagac aaagagatgt aagagaaaca acaacaacaa ctcaatagaa      900
gaaagctctc attctagcaa gtgttcatct tctccgagcg tacgagacca cagttcttcc      960
agtagcgtag ctggtggcca aaaacctgat gatgcaaaat gattcgaaag aatctgatgt     1020
tgatcatctc aagtatccaa gtatcgtttc gatgagtact gtatatagtg cgagtacaaa     1080
atgcacttag ctgtttaaag cagtgttttg atgcaccgtg gcattcgttt tcctcggata     1140
gtcatttctc agatgatttt catccttaat aggtctgctt tagttctaaa actcggatga     1200
tttgtaattt ccagtgtcca aatctactaa ttttattaat cctataaatt aaacaaactt     1260
atatcc
```

(2) INFORMATION FOR SEQ ID NO:777:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 333 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..333
(D) OTHER INFORMATION: / Ceres Seq. ID 1498975
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:777:

```
Glu Asn Gly Ile Met Leu Val Ser Arg Glu Arg Glu Arg Ala Arg Arg
1           5           10          15
Leu Glu Asn Arg Glu Ser Ile Phe Ala Glu Pro Pro Cys Leu Leu Leu
20          25          30
Ala His Arg Ile Ser Pro Ser Pro Ser Ile Leu Pro Ala Glu Glu Glu
35          40          45
Val Met Asp Val Ser Ala Arg Lys Ser Gln Lys Ala Gly Arg Glu Lys
50          55          60
Leu Arg Arg Glu Lys Leu Asn Glu His Phe Val Glu Leu Gly Asn Val
65          70          75          80
Leu Asp Pro Glu Arg Pro Lys Asn Asp Lys Ala Thr Ile Leu Thr Asp
85          90          95
Thr Val Gln Leu Leu Lys Glu Leu Thr Ser Glu Val Asn Lys Leu Lys
100         105         110
Ser Glu Tyr Thr Ala Leu Thr Asp Glu Ser Arg Glu Leu Thr Gln Glu
115         120         125
Lys Asn Asp Leu Arg Glu Glu Lys Thr Ser Leu Lys Ser Asp Ile Glu
```

130	135	140
Asn Leu Asn Leu Gln Tyr Gln Gln Arg Leu Arg Ser Met Ser Pro Trp		
145	150	155
Gly Ala Ala Met Asp His Thr Val Met Met Ala Pro Pro Pro Ser Phe		160
	165	170
Pro Tyr Pro Met Pro Ile Ala Met Pro Pro Gly Ser Ile Pro Met His		175
	180	185
Pro Ser Met Pro Ser Tyr Thr Tyr Phe Gly Asn Gln Asn Pro Ser Met		190
	195	200
Ile Pro Ala Pro Cys Pro Thr Tyr Met Pro Tyr Met Pro Pro Asn Thr		205
	210	215
Val Val Glu Gln Gln Ser Val His Ile Pro Gln Asn Pro Gly Asn Arg		220
225	230	235
Ser Arg Glu Pro Arg Ala Lys Val Ser Arg Glu Ser Arg Ser Glu Lys		240
	245	250
Ala Glu Asp Ser Asn Glu Val Ala Thr Gln Leu Glu Leu Lys Thr Pro		255
	260	265
Gly Ser Thr Ser Asp Lys Asp Thr Leu Gln Arg Pro Glu Lys Thr Lys		270
	275	280
Arg Cys Lys Arg Asn Asn Asn Asn Ser Ile Glu Glu Ser Ser His		285
	290	295
Ser Ser Lys Cys Ser Ser Ser Pro Ser Val Arg Asp His Ser Ser Ser		300
305	310	315
Ser Ser Val Ala Gly Gly Gln Lys Pro Asp Asp Ala Lys		320
	325	330

(2) INFORMATION FOR SEQ ID NO:778:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 329 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..329

(D) OTHER INFORMATION: / Ceres Seq. ID 1498976

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:778:

Met Leu Val Ser Arg Glu Arg Glu Arg Ala Arg Arg Leu Glu Asn Arg		
1	5	10
Glu Ser Ile Phe Ala Glu Pro Pro Cys Leu Leu Leu Ala His Arg Ile		15
	20	25
Ser Pro Ser Pro Ser Ile Leu Pro Ala Glu Glu Glu Val Met Asp Val		30
	35	40
Ser Ala Arg Lys Ser Gln Lys Ala Gly Arg Glu Lys Leu Arg Arg Glu		45
	50	55
Lys Leu Asn Glu His Phe Val Glu Leu Gly Asn Val Leu Asp Pro Glu		60
65	70	75
Arg Pro Lys Asn Asp Lys Ala Thr Ile Leu Thr Asp Thr Val Gln Leu		80
	85	90
Leu Lys Glu Leu Thr Ser Glu Val Asn Lys Leu Lys Ser Glu Tyr Thr		95
	100	105
Ala Leu Thr Asp Glu Ser Arg Glu Leu Thr Gln Glu Lys Asn Asp Leu		110
	115	120
Arg Glu Glu Lys Thr Ser Leu Lys Ser Asp Ile Glu Asn Leu Asn Leu		125
	130	135
Gln Tyr Gln Gln Arg Leu Arg Ser Met Ser Pro Trp Gly Ala Ala Met		140
145	150	155
Asp His Thr Val Met Met Ala Pro Pro Pro Ser Phe Pro Tyr Pro Met		160
	165	170
Pro Ile Ala Met Pro Pro Gly Ser Ile Pro Met His Pro Ser Met Pro		175
	180	185
		190

Ser Tyr Thr Tyr Phe Gly Asn Gln Asn Pro Ser Met Ile Pro Ala Pro
195 200 205
Cys Pro Thr Tyr Met Pro Tyr Met Pro Pro Asn Thr Val Val Glu Gln
210 215 220
Gln Ser Val His Ile Pro Gln Asn Pro Gly Asn Arg Ser Arg Glu Pro
225 230 235 240
Arg Ala Lys Val Ser Arg Glu Ser Arg Ser Glu Lys Ala Glu Asp Ser
245 250 255
Asn Glu Val Ala Thr Gln Leu Glu Leu Lys Thr Pro Gly Ser Thr Ser
260 265 270
Asp Lys Asp Thr Leu Gln Arg Pro Glu Lys Thr Lys Arg Cys Lys Arg
275 280 285
Asn Asn Asn Asn Ser Ile Glu Glu Ser Ser His Ser Ser Lys Cys
290 295 300
Ser Ser Ser Pro Ser Val Arg Asp His Ser Ser Ser Ser Val Ala
305 310 315 320
Gly Gly Gln Lys Pro Asp Asp Ala Lys
325

(2) INFORMATION FOR SEQ ID NO:779:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 284 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..284

(D) OTHER INFORMATION: / Ceres Seq. ID 1498977

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:779:

Met Asp Val Ser Ala Arg Lys Ser Gln Lys Ala Gly Arg Glu Lys Leu
1 5 10 15
Arg Arg Glu Lys Leu Asn Glu His Phe Val Glu Leu Gly Asn Val Leu
20 25 30
Asp Pro Glu Arg Pro Lys Asn Asp Lys Ala Thr Ile Leu Thr Asp Thr
35 40 45
Val Gln Leu Leu Lys Glu Leu Thr Ser Glu Val Asn Lys Leu Lys Ser
50 55 60
Glu Tyr Thr Ala Leu Thr Asp Glu Ser Arg Glu Leu Thr Gln Glu Lys
65 70 75 80
Asn Asp Leu Arg Glu Lys Thr Ser Leu Lys Ser Asp Ile Glu Asn
85 90 95
Leu Asn Leu Gln Tyr Gln Gln Arg Leu Arg Ser Met Ser Pro Trp Gly
100 105 110
Ala Ala Met Asp His Thr Val Met Met Ala Pro Pro Pro Ser Phe Pro
115 120 125
Tyr Pro Met Pro Ile Ala Met Pro Pro Gly Ser Ile Pro Met His Pro
130 135 140
Ser Met Pro Ser Tyr Thr Tyr Phe Gly Asn Gln Asn Pro Ser Met Ile
145 150 155 160
Pro Ala Pro Cys Pro Thr Tyr Met Pro Tyr Met Pro Pro Asn Thr Val
165 170 175
Val Glu Gln Gln Ser Val His Ile Pro Gln Asn Pro Gly Asn Arg Ser
180 185 190
Arg Glu Pro Arg Ala Lys Val Ser Arg Glu Ser Arg Ser Glu Lys Ala
195 200 205
Glu Asp Ser Asn Glu Val Ala Thr Gln Leu Glu Leu Lys Thr Pro Gly
210 215 220
Ser Thr Ser Asp Lys Asp Thr Leu Gln Arg Pro Glu Lys Thr Lys Arg
225 230 235 240
Cys Lys Arg Asn Asn Asn Asn Asn Ser Ile Glu Glu Ser Ser His Ser

245 250 255
Ser Lys Cys Ser Ser Ser Pro Ser Val Arg Asp His Ser Ser Ser Ser
260 265 270
Ser Val Ala Gly Gly Gln Lys Pro Asp Asp Ala Lys
275 280

(2) INFORMATION FOR SEQ ID NO:780:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1239 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1239

(D) OTHER INFORMATION: / Ceres Seq. ID 1498978

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:780:

```
gtcaaagcaa ccaaacacat aaaagagaga tttaatacaa aagaaagaga aaaaagaaag      60
atatggcagg actcatcaac aagatcggag acgcactcca cattggagga ggcaacaagg      120
aaggtgagca caagaaggaa gaggaacaca agaaacacgt tgacgagcac aagartggtg      180
agcacaaaga aggtattggt gacaagatca aagacaagat ccacggtggt gaaggtaaaa      240
gccacgacgg agaaggcaaa agccacgacg gtgagaagaa aaagaagaag gacaagaagg      300
agaagaaaca tcatgatgat ggtcaccaca gcagcagcag tgacagcgac agcgagttaa      360
ggtgaggaag tgaggaggat cgcttgaata aaacagatct ggttctggct attattaatt      420
aatgttgctg tatgttctta tcatcttaga gagagggtta agacaggaga accgtgcatc      480
tatctttgat cttgtcaaca ataccttctt tgtgctcacc actcttatga actcttttct      540
ctttaattgc ggtctcattc tcctctgttg tatcagtggt attcaattct gcgccactgc      600
atttgatat tatgtcaag ccaccgccgc tcaggagata tttggccaca ctttgcagtc      660
ccttcgcggt attaatgacc tctacaagta caatgtgttc cagatcgggt ttgttgcct      720
cgctggattg acctttttat attacattgc ctttggatgg agaagaaaaa agccgagcgg      780
cagattccag ctctctacct aatgtaaatc tcttcttttg attttatcgt ttatgtttcc      840
tcgtctctgg gatcgatcgc gtgccactga ggattgctgt gtccacaatt ataccgagat      900
tgggtctcatg atctgtgcaa gtggtcttat atcataagaa caagcacctg cccaaaaagc      960
ttctctttct tctgctcttc tttgctgttg aggtttggtt tcatttcact tgaatgtaaa     1020
attattcttc tttttctctt atcttttctc ctgtatctat tgctttattt ttgtttgatt     1080
aattacaaga aagatctctt tgtcgccgtc ttctcatggc ctattgaatg atttcgaata     1140
ctttcttgta accattactt ggttgagagt ttagactgtc agaacaaatt cagggttttg      1200
agttatttgt gtgtatagtg tgatgacaag agacttcat
```

(2) INFORMATION FOR SEQ ID NO:781:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 119 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..119

(D) OTHER INFORMATION: / Ceres Seq. ID 1498979

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:781:

```
Val Lys Ala Thr Lys His Ile Lys Glu Arg Phe Asn Thr Lys Glu Arg
1 5 10 15
Glu Lys Arg Lys Ile Trp Gln Asp Ser Ser Thr Arg Ser Glu Thr His
20 25 30
Ser Thr Leu Glu Glu Ala Thr Arg Lys Val Ser Thr Arg Arg Lys Arg
35 40 45
Asn Thr Arg Asn Thr Leu Thr Ser Thr Arg Xaa Val Ser Thr Lys Lys
50 55 60
Val Leu Leu Thr Arg Ser Lys Thr Arg Ser Thr Val Val Lys Val Lys
65 70 75 80
Ala Thr Thr Glu Lys Ala Lys Ala Thr Thr Val Arg Arg Lys Arg Arg
```

85 90 95
Arg Thr Arg Arg Arg Arg Asn Ile Met Met Met Val Thr Thr Ala Ala
100 105 110
Ala Val Thr Ala Thr Ala Ser
115

(2) INFORMATION FOR SEQ ID NO:782:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 100 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..100
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498980

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:782:

Met Ala Gly Leu Ile Asn Lys Ile Gly Asp Ala Leu His Ile Gly Gly
1 5 10 15
Gly Asn Lys Glu Gly Glu His Lys Lys Glu Glu Glu His Lys Lys His
20 25 30
Val Asp Glu His Lys Xaa Gly Glu His Lys Glu Gly Ile Val Asp Lys
35 40 45
Ile Lys Asp Lys Ile His Gly Gly Glu Gly Lys Ser His Asp Gly Glu
50 55 60
Gly Lys Ser His Asp Gly Glu Lys Lys Lys Lys Lys Asp Lys Lys Glu
65 70 75 80
Lys Lys His His Asp Asp Gly His His Ser Ser Ser Ser Asp Ser Asp
85 90 95
Ser Glu Leu Arg
100

(2) INFORMATION FOR SEQ ID NO:783:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 91 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..91
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498981

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:783:

Met Asn Ser Phe Leu Phe Asn Val Gly Leu Ile Leu Leu Cys Ser Ile
1 5 10 15
Ser Val Ile Gln Phe Cys Ala Thr Ala Phe Gly Tyr Tyr Ala Gln Ala
20 25 30
Thr Ala Ala Gln Glu Ile Phe Gly His Thr Leu Gln Ser Leu Arg Gly
35 40 45
Ile Lys Tyr Leu Tyr Lys Tyr Asn Val Phe Gln Ile Gly Phe Val Val
50 55 60
Leu Ala Gly Leu Thr Phe Leu Tyr Tyr Ile Ala Phe Gly Trp Arg Arg
65 70 75 80
Lys Lys Pro Ser Gly Arg Phe Gln Leu Ser Thr
85 90

(2) INFORMATION FOR SEQ ID NO:784:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1329 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1329

(D) OTHER INFORMATION: / Ceres Seq. ID 1498982

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:784:

```
agagctctag aatctctcaa caatggcgga atcgattttc agaaagctca gagatggtgg      60
cgaagaaggc gaactcgcac cagctctcac tatagaagaa actgtagctt cccctttcgg      120
actcgatgtc tccggctatc ttctcacaaa tctatcttct tcaatttttag ctggaaaatc      180
ctcgtcgcag ggtcttgtgt tgatcacatt ctccgcggagc cttcgttcta tttgcaattg      240
ttgaagcaaa aaggaatcgt tgtctcttca tcttctaaat ggattcgtat tttggattgt      300
tacactgata cattgggatg gattgatcaa tcttcaacta gtttttagtga aggttcaagt      360
ttgattaagt tacataagtg tgtgagtgaac ttgaaaaagc ttttttcttc aatcattgaa      420
gcaggaagag agttggttgg aactgggaag acacgtttct gcgttgccat tgattcggta      480
aatgagttgc taagacattc agcgatgcca ttagtttctg gtcttttaac agatcttcga      540
agccatgcgc aaattttccag tgtcttttgg tcattgaaca ctgaccttca ccaagagaag      600
gtcacaaatg cgcttgaata tatatccaca atgaaagcga acttagaacc tttgtgtcca      660
tcttcagatg ggcaaaggaa tgcttttagaa aacctctttt cggttcatca ggatttcggt      720
aaaggacggt ttcattgtccg gttaagctt agaaaaggac gtgtgagagt aatgtctgaa      780
gaatatcatg ttgatcaatc ggggataaac ttttcaccca tttcctctgt ggatactgtt      840
attgcagcca ctaaaagcct tttgcctaag gttcaattca atctccagtt gtctgagaaa      900
gaacgggtcg agaaagaaaa agttgtgctt ccttttgagc accaagatga tggaaaatcg      960
aacgagatct atgatgggag gagatctctt gtggatggca agattgagac aacaccattg     1020
tcgtcaatgg agttgcagac cgatgtggtt tcgtcgggta aggggtggtg gattatatat     1080
ttcagagatt cagacgatga gcattcctgat tctgatgaag atcctgatga tgatttgagc     1140
atttaagggtt cttaatttac acttgtaaga ccagagaata gctccagttt tggttttggc     1200
aatagttggg atcttagtat ccaactttgt acactaaata gaagatttga ttggttatta     1260
gatgtgtatt acagttataa ttgttacagt aatgatctca tcttctatta ttcttgagtt     1320
gtttgttgt
```

(2) INFORMATION FOR SEQ ID NO:785:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 381 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..381

(D) OTHER INFORMATION: / Ceres Seq. ID 1498983

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:785:

```
Arg Ala Leu Glu Ser Leu Asn Asn Gly Ile Asp Phe Gln Lys Ala
1      5      10      15
Gln Arg Trp Trp Arg Arg Arg Arg Thr Arg Thr Ser Ser His Tyr Arg
20     25     30
Arg Asn Cys Ser Phe Pro Phe Arg Thr Arg Cys Leu Arg Leu Ser Ser
35     40     45
His Lys Ser Ile Phe Phe Asn Phe Ser Trp Lys Ile Leu Val Ala Gly
50     55     60
Ser Cys Val Asp His Ile Leu Ala Glu Pro Ser Phe Tyr Leu Gln Leu
65     70     75     80
Leu Lys Gln Lys Gly Ile Val Val Ser Ser Ser Ser Lys Trp Ile Arg
85     90     95
Ile Leu Asp Cys Tyr Thr Asp Pro Leu Gly Trp Ile Asp Gln Ser Ser
100    105    110
Thr Ser Phe Ser Glu Gly Ser Ser Leu Ile Lys Leu His Lys Cys Val
115    120    125
Ser Asp Leu Lys Lys Leu Phe Ser Ser Ile Ile Glu Ala Gly Arg Glu
130    135    140
Leu Val Gly Thr Gly Lys Thr Arg Phe Cys Val Ala Ile Asp Ser Val
145    150    155    160
```


Asn Glu Leu Leu Arg His Ser Ala Met Pro Leu Val Ser Gly Leu Leu
165 170 175
Thr Asp Leu Arg Ser His Ala Gln Ile Ser Ser Val Phe Trp Ser Leu
180 185 190
Asn Thr Asp Leu His Gln Glu Lys Val Thr Asn Ala Leu Glu Tyr Ile
195 200 205
Ser Thr Met Lys Ala Asn Leu Glu Pro Leu Cys Pro Ser Ser Asp Gly
210 215 220
Gln Arg Asn Ala Leu Glu Asn Leu Phe Ser Val His Gln Asp Phe Gly
225 230 235 240
Lys Gly Arg Phe His Val Arg Phe Lys Leu Arg Lys Gly Arg Val Arg
245 250 255
Val Met Ser Glu Glu Tyr His Val Asp Gln Ser Gly Ile Asn Phe Ser
260 265 270
Pro Ile Ser Ser Val Asp Thr Val Ile Ala Ala Thr Lys Ser Leu Leu
275 280 285
Pro Lys Val Gln Phe Asn Leu Gln Leu Ser Glu Lys Glu Arg Val Glu
290 295 300
Lys Glu Lys Val Val Leu Pro Phe Glu His Gln Asp Asp Gly Lys Ser
305 310 315 320
Asn Glu Ile Tyr Asp Gly Arg Arg Ser Leu Val Asp Gly Lys Ile Glu
325 330 335
Thr Thr Pro Leu Ser Ser Met Glu Leu Gln Thr Asp Val Val Ser Ser
340 345 350
Gly Lys Gly Gly Glu Ile Ile Tyr Phe Arg Asp Ser Asp Asp Glu His
355 360 365
Pro Asp Ser Asp Glu Asp Pro Asp Asp Asp Leu Asp Ile
370 375 380

(2) INFORMATION FOR SEQ ID NO:786:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 213 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..213

(D) OTHER INFORMATION: / Ceres Seq. ID 1498984

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:786:

Met Pro Leu Val Ser Gly Leu Leu Thr Asp Leu Arg Ser His Ala Gln
1 5 10 15
Ile Ser Ser Val Phe Trp Ser Leu Asn Thr Asp Leu His Gln Glu Lys
20 25 30
Val Thr Asn Ala Leu Glu Tyr Ile Ser Thr Met Lys Ala Asn Leu Glu
35 40 45
Pro Leu Cys Pro Ser Ser Asp Gly Gln Arg Asn Ala Leu Glu Asn Leu
50 55 60
Phe Ser Val His Gln Asp Phe Gly Lys Gly Arg Phe His Val Arg Phe
65 70 75 80
Lys Leu Arg Lys Gly Arg Val Arg Val Met Ser Glu Glu Tyr His Val
85 90 95
Asp Gln Ser Gly Ile Asn Phe Ser Pro Ile Ser Ser Val Asp Thr Val
100 105 110
Ile Ala Ala Thr Lys Ser Leu Leu Pro Lys Val Gln Phe Asn Leu Gln
115 120 125
Leu Ser Glu Lys Glu Arg Val Glu Lys Glu Lys Val Val Leu Pro Phe
130 135 140
Glu His Gln Asp Asp Gly Lys Ser Asn Glu Ile Tyr Asp Gly Arg Arg
145 150 155 160
Ser Leu Val Asp Gly Lys Ile Glu Thr Thr Pro Leu Ser Ser Met Glu

165 170 175
Leu Gln Thr Asp Val Val Ser Ser Gly Lys Gly Gly Glu Ile Ile Tyr
180 185 190
Phe Arg Asp Ser Asp Asp Glu His Pro Asp Ser Asp Glu Asp Pro Asp
195 200 205
Asp Asp Leu Asp Ile
210

(2) INFORMATION FOR SEQ ID NO:787:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1944 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1944

(D) OTHER INFORMATION: / Ceres Seq. ID 1498985

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:787:

tttttttccc	cattttctta	ctctcttgcc	ctttcttctc	tcactctccg	gcgactgtta	60
cgagttttta	acacttccgt	cgtcttctca	gttggtgttg	ttgtttatga	caagatcttg	120
ttctatccat	taaaaccaa	gaaatggagg	aaggtcataa	agaaccattg	gtgctaagag	180
ttgaaggatc	acattgttct	ttatcagaga	tggatgattt	tgatctaact	cgggctttag	240
agaagccgag	gcagctaaag	atcgaacgga	agagatcggt	tgacgaaagg	tcgatgagcg	300
agttatcgac	tggctatgta	agacaagata	gcattttaga	aatggctcat	tctccgaagt	360
aggccaatgg	tggacactcc	tctctctgtt	aggaactctt	tcgagcctca	tccgatgggt	420
gctgaggctt	gggaagcttt	gagaaggcca	atgggtgttc	ttcgtgggtc	accggttggt	480
accattgcag	cttatgacca	tgcctccgag	gaggtcctga	actatgatca	ggtgtttgta	540
cgtgactttg	taccaagtgc	attggcggtt	ctgatgaatg	gagagcccga	tatagtgaag	600
aacttcttgc	tcaagaacct	tcagcttcaa	gggtgggaga	aacgggttga	ccggttcaag	660
cttgggggaag	gcgttatgcc	agcgagtttc	aaggtgcttc	atgatccagt	tcgtaaaacc	720
gacacaatta	ttgcggattt	tggagaaagc	gctataggaa	gagtagcacc	ggtggattca	780
ggattctggt	ggatcatact	tctccgtgct	tacacgaaat	ctacgggaga	tttgacttta	840
tctgagacac	cagagtgtca	gaggggaatg	aggcttatac	tctctctttg	cttatccgaa	900
ggttttgata	ctttccctac	gcttctttgt	gctgacgggt	gttctatggt	tgataggaga	960
atgggtggtt	atggatatcc	aatagagatt	caagctctgt	ttttcatggc	attgagatgc	1020
gccttgctga	tgcttaaac	agacgaggaa	ggtcggagatt	tcatagaaag	gattgtgaag	1080
agacttcacg	cgctgagttt	ccatatgcgc	agttactttt	ggcttgactt	tcaacaactc	1140
aacgatatct	ataggtacaa	gacagaggag	tactcacaca	ccgcggtgaa	caagttcaac	1200
gtgatgcccg	actcgatacc	agactgggtt	ttcgacttta	tgcctctccg	tggaggatat	1260
tttgctcgga	atgtaagccc	ggcccgtatg	gatttcagggt	ggttttcctt	aggaaattgt	1320
gtctccatcc	tttcttccct	ggcaactccg	gatcagtcac	tggctattat	ggacctcctc	1380
gagcaccggt	gggaggagct	agtaggcgag	atgccgctca	agatatgtta	cccttgcatc	1440
gaaagccacg	agtggcggat	tgttaccggt	tgtgatccta	aaaacacgag	gtggagttac	1500
cacaacgggtg	gatcttggcc	agtattgctg	tggacgctga	cggaggcatg	catcaagact	1560
ggacggcctc	aaatagcgag	acgtgcgatt	gatctaattg	aatcacggct	acaccgagat	1620
tgctggcccg	aatactatga	tggtaagcaa	ggaaggtacg	ttggaaaaca	agcaaggaag	1680
taccagactt	ggtcaatcgc	gggttacttg	gttgcgaaaa	tgatgcttga	agatccttca	1740
catattggaa	tgatctctct	tgaagaagac	aaacagatga	aacctgttat	caagagatct	1800
gcttcatgga	cttgctgaat	tttgtttctt	gttttgattt	ataatgtcat	ttgattaagc	1860
attcaaaaaga	cctttaatca	gcgagagagt	agttctgttt	gtatttctct	ttgatccaac	1920
tatgggtttat	tttcacttga	ggct				

(2) INFORMATION FOR SEQ ID NO:788:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 483 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..483

(D) OTHER INFORMATION: / Ceres Seq. ID 1498986

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:788:

Met	Val	Asp	Thr	Pro	Leu	Ser	Val	Arg	Asn	Ser	Phe	Glu	Pro	His	Pro
1				5					10					15	
Met	Val	Ala	Glu	Ala	Trp	Glu	Ala	Leu	Arg	Arg	Ser	Met	Val	Phe	Phe
		20						25					30		
Arg	Gly	Gln	Pro	Val	Gly	Thr	Ile	Ala	Ala	Tyr	Asp	His	Ala	Ser	Glu
		35					40					45			
Glu	Val	Leu	Asn	Tyr	Asp	Gln	Val	Phe	Val	Arg	Asp	Phe	Val	Pro	Ser
	50					55					60				
Ala	Leu	Ala	Phe	Leu	Met	Asn	Gly	Glu	Pro	Asp	Ile	Val	Lys	Asn	Phe
65					70					75					80
Leu	Leu	Lys	Thr	Leu	Gln	Leu	Gln	Gly	Trp	Glu	Lys	Arg	Val	Asp	Arg
			85						90					95	
Phe	Lys	Leu	Gly	Glu	Gly	Val	Met	Pro	Ala	Ser	Phe	Lys	Val	Leu	His
			100						105					110	
Asp	Pro	Val	Arg	Lys	Thr	Asp	Thr	Ile	Ile	Ala	Asp	Phe	Gly	Glu	Ser
		115					120					125			
Ala	Ile	Gly	Arg	Val	Ala	Pro	Val	Asp	Ser	Gly	Phe	Trp	Trp	Ile	Ile
	130					135					140				
Leu	Leu	Arg	Ala	Tyr	Thr	Lys	Ser	Thr	Gly	Asp	Leu	Thr	Leu	Ser	Glu
145						150				155					160
Thr	Pro	Glu	Cys	Gln	Arg	Gly	Met	Arg	Leu	Ile	Leu	Ser	Leu	Cys	Leu
				165					170					175	
Ser	Glu	Gly	Phe	Asp	Thr	Phe	Pro	Thr	Leu	Leu	Cys	Ala	Asp	Gly	Cys
			180					185					190		
Ser	Met	Val	Asp	Arg	Arg	Met	Gly	Val	Tyr	Gly	Tyr	Pro	Ile	Glu	Ile
		195					200					205			
Gln	Ala	Leu	Phe	Phe	Met	Ala	Leu	Arg	Cys	Ala	Leu	Ser	Met	Leu	Lys
	210					215					220				
Pro	Asp	Glu	Glu	Gly	Arg	Asp	Phe	Ile	Glu	Arg	Ile	Val	Lys	Arg	Leu
225					230					235					240
His	Ala	Leu	Ser	Phe	His	Met	Arg	Ser	Tyr	Phe	Trp	Leu	Asp	Phe	Gln
				245					250					255	
Gln	Leu	Asn	Asp	Ile	Tyr	Arg	Tyr	Lys	Thr	Glu	Glu	Tyr	Ser	His	Thr
			260					265					270		
Ala	Val	Asn	Lys	Phe	Asn	Val	Met	Pro	Asp	Ser	Ile	Pro	Asp	Trp	Val
		275					280					285			
Phe	Asp	Phe	Met	Pro	Leu	Arg	Gly	Gly	Tyr	Phe	Val	Gly	Asn	Val	Ser
	290					295					300				
Pro	Ala	Arg	Met	Asp	Phe	Arg	Trp	Phe	Ser	Leu	Gly	Asn	Cys	Val	Ser
305					310					315					320
Ile	Leu	Ser	Ser	Leu	Ala	Thr	Pro	Asp	Gln	Ser	Met	Ala	Ile	Met	Asp
				325					330					335	
Leu	Leu	Glu	His	Arg	Trp	Glu	Glu	Leu	Val	Gly	Glu	Met	Pro	Leu	Lys
			340					345					350		
Ile	Cys	Tyr	Pro	Cys	Ile	Glu	Ser	His	Glu	Trp	Arg	Ile	Val	Thr	Gly
		355					360					365			
Cys	Asp	Pro	Lys	Asn	Thr	Arg	Trp	Ser	Tyr	His	Asn	Gly	Gly	Ser	Trp
	370					375					380				
Pro	Val	Leu	Leu	Trp	Thr	Leu	Thr	Glu	Ala	Cys	Ile	Lys	Thr	Gly	Arg
385					390					395					400
Pro	Gln	Ile	Ala	Arg	Arg	Ala	Ile	Asp	Leu	Ile	Glu	Ser	Arg	Leu	His
				405					410					415	
Arg	Asp	Cys	Trp	Pro	Glu	Tyr	Tyr	Asp	Gly	Lys	Gln	Gly	Arg	Tyr	Val
			420					425					430		
Gly	Lys	Gln	Ala	Arg	Lys	Tyr	Gln	Thr	Trp	Ser	Ile	Ala	Gly	Tyr	Leu
		435					440					445			
Val	Ala	Lys	Met	Met	Leu	Glu	Asp	Pro	Ser	His	Ile	Gly	Met	Ile	Ser
	450					455						460			

Leu Glu Glu Asp Lys Gln Met Lys Pro Val Ile Lys Arg Ser Ala Ser
465 470 475 480
Trp Thr Cys

(2) INFORMATION FOR SEQ ID NO:789:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 467 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..467
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498987

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:789:

Met	Val	Ala	Glu	Ala	Trp	Glu	Ala	Leu	Arg	Arg	Ser	Met	Val	Phe	Phe
1			5					10						15	
Arg	Gly	Gln	Pro	Val	Gly	Thr	Ile	Ala	Ala	Tyr	Asp	His	Ala	Ser	Glu
			20					25					30		
Glu	Val	Leu	Asn	Tyr	Asp	Gln	Val	Phe	Val	Arg	Asp	Phe	Val	Pro	Ser
			35					40				45			
Ala	Leu	Ala	Phe	Leu	Met	Asn	Gly	Glu	Pro	Asp	Ile	Val	Lys	Asn	Phe
			50			55					60				
Leu	Leu	Lys	Thr	Leu	Gln	Leu	Gln	Gly	Trp	Glu	Lys	Arg	Val	Asp	Arg
65					70					75					80
Phe	Lys	Leu	Gly	Glu	Gly	Val	Met	Pro	Ala	Ser	Phe	Lys	Val	Leu	His
				85					90					95	
Asp	Pro	Val	Arg	Lys	Thr	Asp	Thr	Ile	Ile	Ala	Asp	Phe	Gly	Glu	Ser
			100					105					110		
Ala	Ile	Gly	Arg	Val	Ala	Pro	Val	Asp	Ser	Gly	Phe	Trp	Trp	Ile	Ile
			115				120					125			
Leu	Leu	Arg	Ala	Tyr	Thr	Lys	Ser	Thr	Gly	Asp	Leu	Thr	Leu	Ser	Glu
			130			135					140				
Thr	Pro	Glu	Cys	Gln	Arg	Gly	Met	Arg	Leu	Ile	Leu	Ser	Leu	Cys	Leu
145					150					155					160
Ser	Glu	Gly	Phe	Asp	Thr	Phe	Pro	Thr	Leu	Leu	Cys	Ala	Asp	Gly	Cys
				165					170					175	
Ser	Met	Val	Asp	Arg	Arg	Met	Gly	Val	Tyr	Gly	Tyr	Pro	Ile	Glu	Ile
			180				185						190		
Gln	Ala	Leu	Phe	Phe	Met	Ala	Leu	Arg	Cys	Ala	Leu	Ser	Met	Leu	Lys
			195				200					205			
Pro	Asp	Glu	Glu	Gly	Arg	Asp	Phe	Ile	Glu	Arg	Ile	Val	Lys	Arg	Leu
			210			215					220				
His	Ala	Leu	Ser	Phe	His	Met	Arg	Ser	Tyr	Phe	Trp	Leu	Asp	Phe	Gln
225					230					235					240
Gln	Leu	Asn	Asp	Ile	Tyr	Arg	Tyr	Lys	Thr	Glu	Glu	Tyr	Ser	His	Thr
				245					250					255	
Ala	Val	Asn	Lys	Phe	Asn	Val	Met	Pro	Asp	Ser	Ile	Pro	Asp	Trp	Val
			260					265					270		
Phe	Asp	Phe	Met	Pro	Leu	Arg	Gly	Gly	Tyr	Phe	Val	Gly	Asn	Val	Ser
			275				280					285			
Pro	Ala	Arg	Met	Asp	Phe	Arg	Trp	Phe	Ser	Leu	Gly	Asn	Cys	Val	Ser
			290			295					300				
Ile	Leu	Ser	Ser	Leu	Ala	Thr	Pro	Asp	Gln	Ser	Met	Ala	Ile	Met	Asp
305					310				315						320
Leu	Leu	Glu	His	Arg	Trp	Glu	Glu	Leu	Val	Gly	Glu	Met	Pro	Leu	Lys
				325					330					335	
Ile	Cys	Tyr	Pro	Cys	Ile	Glu	Ser	His	Glu	Trp	Arg	Ile	Val	Thr	Gly
			340				345					350			
Cys	Asp	Pro	Lys	Asn	Thr	Arg	Trp	Ser	Tyr	His	Asn	Gly	Gly	Ser	Trp

355	360	365
Pro Val Leu Leu Trp Thr	Leu Thr Glu Ala Cys Ile	Lys Thr Gly Arg
370	375	380
Pro Gln Ile Ala Arg Arg	Ala Ile Asp Leu Ile Glu	Ser Arg Leu His
385	390	395
Arg Asp Cys Trp Pro Glu Tyr Tyr	Asp Gly Lys Gln Gly Arg Tyr	Val
405	410	415
Gly Lys Gln Ala Arg Lys Tyr Gln Thr	Trp Ser Ile Ala Gly Tyr Leu	
420	425	430
Val Ala Lys Met Met Leu Glu Asp Pro	Ser His Ile Gly Met Ile Ser	
435	440	445
Leu Glu Glu Asp Lys Gln Met Lys Pro	Val Ile Lys Arg Ser Ala Ser	
450	455	460
Trp Thr Cys		
465		

(2) INFORMATION FOR SEQ ID NO:790:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 455 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..455

(D) OTHER INFORMATION: / Ceres Seq. ID 1498988

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:790:

Met Val Phe Phe Arg Gly Gln Pro Val Gly Thr Ile Ala Ala Tyr Asp	1	5	10	15
His Ala Ser Glu Glu Val Leu Asn Tyr Asp Gln Val Phe Val Arg Asp	20	25	30	
Phe Val Pro Ser Ala Leu Ala Phe Leu Met Asn Gly Glu Pro Asp Ile	35	40	45	
Val Lys Asn Phe Leu Leu Lys Thr Leu Gln Leu Gln Gly Trp Glu Lys	50	55	60	
Arg Val Asp Arg Phe Lys Leu Gly Glu Gly Val Met Pro Ala Ser Phe	65	70	75	80
Lys Val Leu His Asp Pro Val Arg Lys Thr Asp Thr Ile Ile Ala Asp	85	90	95	
Phe Gly Glu Ser Ala Ile Gly Arg Val Ala Pro Val Asp Ser Gly Phe	100	105	110	
Trp Trp Ile Ile Leu Leu Arg Ala Tyr Thr Lys Ser Thr Gly Asp Leu	115	120	125	
Thr Leu Ser Glu Thr Pro Glu Cys Gln Arg Gly Met Arg Leu Ile Leu	130	135	140	
Ser Leu Cys Leu Ser Glu Gly Phe Asp Thr Phe Pro Thr Leu Leu Cys	145	150	155	160
Ala Asp Gly Cys Ser Met Val Asp Arg Arg Met Gly Val Tyr Gly Tyr	165	170	175	
Pro Ile Glu Ile Gln Ala Leu Phe Phe Met Ala Leu Arg Cys Ala Leu	180	185	190	
Ser Met Leu Lys Pro Asp Glu Glu Gly Arg Asp Phe Ile Glu Arg Ile	195	200	205	
Val Lys Arg Leu His Ala Leu Ser Phe His Met Arg Ser Tyr Phe Trp	210	215	220	
Leu Asp Phe Gln Gln Leu Asn Asp Ile Tyr Arg Tyr Lys Thr Glu Glu	225	230	235	240
Tyr Ser His Thr Ala Val Asn Lys Phe Asn Val Met Pro Asp Ser Ile	245	250	255	
Pro Asp Trp Val Phe Asp Phe Met Pro Leu Arg Gly Gly Tyr Phe Val	260	265	270	

Gly Asn Val Ser Pro Ala Arg Met Asp Phe Arg Trp Phe Ser Leu Gly
275 280 285
Asn Cys Val Ser Ile Leu Ser Ser Leu Ala Thr Pro Asp Gln Ser Met
290 295 300
Ala Ile Met Asp Leu Leu Glu His Arg Trp Glu Glu Leu Val Gly Glu
305 310 315 320
Met Pro Leu Lys Ile Cys Tyr Pro Cys Ile Glu Ser His Glu Trp Arg
325 330 335
Ile Val Thr Gly Cys Asp Pro Lys Asn Thr Arg Trp Ser Tyr His Asn
340 345 350
Gly Gly Ser Trp Pro Val Leu Leu Trp Thr Leu Thr Glu Ala Cys Ile
355 360 365
Lys Thr Gly Arg Pro Gln Ile Ala Arg Arg Ala Ile Asp Leu Ile Glu
370 375 380
Ser Arg Leu His Arg Asp Cys Trp Pro Glu Tyr Tyr Asp Gly Lys Gln
385 390 395 400
Gly Arg Tyr Val Gly Lys Gln Ala Arg Lys Tyr Gln Thr Trp Ser Ile
405 410 415
Ala Gly Tyr Leu Val Ala Lys Met Met Leu Glu Asp Pro Ser His Ile
420 425 430
Gly Met Ile Ser Leu Glu Glu Asp Lys Gln Met Lys Pro Val Ile Lys
435 440 445
Arg Ser Ala Ser Trp Thr Cys
450 455

(2) INFORMATION FOR SEQ ID NO:791:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1454 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1454
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498993

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:791:

ctgggtgaaa	catagaaaag	tttctcttgc	tcaagttaat	gataaaaagg	tgagagcaat	60
aaacgctgat	aagccttgct	tggtccttgg	aattttgaat	tttctttttc	tatcttactt	120
atagtattgg	tagttgaggg	tgctgctgat	aagttgttgt	aggatttggt	gctctggctc	180
tggtggtagg	tctatgaaat	caaccatata	cgtgaatgga	ctgcaacatg	gtatcttcgt	240
cccagtgagg	ttgggagcat	ttgatcatgt	ccaatccgtc	aaggactgaa	gatgacagca	300
aacagctacc	tactgagtgg	gaaattgaaa	aaggtgaagg	aattgaatct	atagttccac	360
atttctcagg	ccttgagaga	gtcagtagtg	gctctgccac	cagcttctgg	cacactgctg	420
tatcgaaaag	ctcacagtcg	acctctatca	actcatcatc	tcccgaagcc	aaacgatgca	480
agcttgcatc	agaaagttcc	cctggagatt	cttgcagcaa	catagacttt	gtccagggtga	540
aggctcccac	agctctcgag	gtatccggtg	cctcagctga	atcagatctt	tgtttaaaac	600
taggaaagcg	gacatactct	gaagaatact	ggggtagaaa	caataatgaa	atttcagcgg	660
tttctatgaa	gttggttaact	ccatctgttg	tcgctgggaa	atccaaattg	tgtggtcaga	720
gcatgccagt	cccgcgttgc	caaattgatg	gctgtgaact	ggatctctca	tctgctaagg	780
gttatcatcg	taagcacaaa	gtctgcgaaa	agcattcaaa	gtgcccgaag	gttagcgtga	840
gtggcctgga	acgtcggttc	tgccaacagt	gtagcagggt	ccatgctgtc	tctgaatttg	900
atgagaagaa	acgaagctgc	cgaaaacgtc	tttctcatca	taatgcgagg	cgctcgtaagc	960
cacaaggagt	attttcaatg	aatcccgcga	gggtgtatga	tcgaagacag	catacaaata	1020
tggttgaggaa	tgggggtgtcc	cttaacgcga	gatctgaaag	aaatgtatga	atggggtaat	1080
aacacttatg	atacaaagcc	tagacaaacg	gaaaaaagct	ttactctgag	cttccagaga	1140
ggtaatggct	ctgaggacca	gctgggtgct	agtagcagcc	gtatgttctc	tacatctcaa	1200
acctcagggtg	ggttcccagc	aggaaagtcc	aagtttcaac	ttcatggcga	agatgtggga	1260
gaatactcag	gagtcctcca	tgaatctcaa	gatatccacc	gtgctctctc	tcttctgtca	1320
acctcttcgg	atcccctggc	ccaaccacat	gtgcagccat	tttctctact	ctgttcatat	1380
gatgttgtag	caaaatagat	gagtaagtaa	tgtgtaattt	gtaaacctgt	tactcagttg	1440
gtggatactt	ttcc					

(2) INFORMATION FOR SEQ ID NO:792:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 284 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..284
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498994

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:792:

Met	Asp	Cys	Asn	Met	Val	Ser	Ser	Ser	Gln	Trp	Asp	Trp	Glu	His	Leu
1				5					10					15	
Ile	Met	Ser	Asn	Pro	Ser	Arg	Thr	Glu	Asp	Asp	Ser	Lys	Gln	Leu	Pro
			20					25					30		
Thr	Glu	Trp	Glu	Ile	Glu	Lys	Gly	Glu	Gly	Ile	Glu	Ser	Ile	Val	Pro
		35					40					45			
His	Phe	Ser	Gly	Leu	Glu	Arg	Val	Ser	Ser	Gly	Ser	Ala	Thr	Ser	Phe
	50					55				60					
Trp	His	Thr	Ala	Val	Ser	Lys	Ser	Ser	Gln	Ser	Thr	Ser	Ile	Asn	Ser
65				70					75					80	
Ser	Ser	Pro	Glu	Ala	Lys	Arg	Cys	Lys	Leu	Ala	Ser	Glu	Ser	Ser	Pro
			85						90				95		
Gly	Asp	Ser	Cys	Ser	Asn	Ile	Asp	Phe	Val	Gln	Val	Lys	Ala	Pro	Thr
		100					105						110		
Ala	Leu	Glu	Val	Ser	Val	Ala	Ser	Ala	Glu	Ser	Asp	Leu	Cys	Leu	Lys
		115				120						125			
Leu	Gly	Lys	Arg	Thr	Tyr	Ser	Glu	Glu	Tyr	Trp	Gly	Arg	Asn	Asn	Asn
	130				135						140				
Glu	Ile	Ser	Ala	Val	Ser	Met	Lys	Leu	Leu	Thr	Pro	Ser	Val	Val	Ala
145				150						155					160
Gly	Lys	Ser	Lys	Leu	Cys	Gly	Gln	Ser	Met	Pro	Val	Pro	Arg	Cys	Gln
			165						170					175	
Ile	Asp	Gly	Cys	Glu	Leu	Asp	Leu	Ser	Ser	Ala	Lys	Gly	Tyr	His	Arg
		180					185						190		
Lys	His	Lys	Val	Cys	Glu	Lys	His	Ser	Lys	Cys	Pro	Lys	Val	Ser	Val
		195				200						205			
Ser	Gly	Leu	Glu	Arg	Arg	Phe	Cys	Gln	Gln	Cys	Ser	Arg	Phe	His	Ala
	210				215						220				
Val	Ser	Glu	Phe	Asp	Glu	Lys	Lys	Arg	Ser	Cys	Arg	Lys	Arg	Leu	Ser
225				230						235				240	
His	His	Asn	Ala	Arg	Arg	Arg	Lys	Pro	Gln	Gly	Val	Phe	Ser	Met	Asn
			245						250					255	
Pro	Glu	Arg	Val	Tyr	Asp	Arg	Arg	Gln	His	Thr	Asn	Met	Leu	Trp	Asn
		260					265						270		
Gly	Val	Ser	Leu	Asn	Ala	Arg	Ser	Glu	Arg	Asn	Val				
		275				280									

(2) INFORMATION FOR SEQ ID NO:793:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 280 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..280
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498995

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:793:

Met Val Ser Ser Ser Gln Trp Asp Trp Glu His Leu Ile Met Ser Asn

1	5	10	15
Pro Ser Arg Thr	Glu Asp Asp Ser	Lys Gln Leu Pro	Thr Glu Trp Glu
	20	25	30
Ile Glu Lys Gly	Glu Gly Ile Glu	Ser Ile Val Pro	His Phe Ser Gly
	35	40	45
Leu Glu Arg Val	Ser Ser Gly Ser	Ala Thr Ser Phe	Trp His Thr Ala
	50	55	60
Val Ser Lys Ser	Ser Gln Ser Thr	Ser Ile Asn Ser	Ser Ser Pro Glu
	65	70	75
Ala Lys Arg Cys	Lys Leu Ala Ser	Glu Ser Ser Pro	Gly Asp Ser Cys
	85	90	95
Ser Asn Ile Asp	Phe Val Gln Val	Lys Ala Pro Thr	Ala Leu Glu Val
	100	105	110
Ser Val Ala Ser	Ala Glu Ser Asp	Leu Cys Leu Lys	Leu Gly Lys Arg
	115	120	125
Thr Tyr Ser Glu	Glu Tyr Trp Gly	Arg Asn Asn Asn	Glu Ile Ser Ala
	130	135	140
Val Ser Met Lys	Leu Leu Thr Pro	Ser Val Val Ala	Gly Lys Ser Lys
	145	150	155
Leu Cys Gly Gln	Ser Met Pro Val	Pro Arg Cys Gln	Ile Asp Gly Cys
	165	170	175
Glu Leu Asp Leu	Ser Ser Ala Lys	Gly Tyr His Arg	Lys His Lys Val
	180	185	190
Cys Glu Lys His	Ser Lys Cys Pro	Lys Val Ser Val	Ser Gly Leu Glu
	195	200	205
Arg Arg Phe Cys	Gln Gln Cys Ser	Arg Phe His Ala	Val Ser Glu Phe
	210	215	220
Asp Glu Lys Lys	Arg Ser Cys Arg	Lys Arg Leu Ser	His His Asn Ala
	225	230	235
Arg Arg Arg Lys	Pro Gln Gly Val	Phe Ser Met Asn	Pro Glu Arg Val
	245	250	255
Tyr Asp Arg Arg	Gln His Thr Asn	Met Leu Trp Asn	Gly Val Ser Leu
	260	265	270
Asn Ala Arg Ser	Glu Arg Asn Val		
	275	280	

(2) INFORMATION FOR SEQ ID NO:794:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 267 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..267

(D) OTHER INFORMATION: / Ceres Seq. ID 1498996

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:794:

Met Ser Asn Pro	Ser Arg Thr Glu	Asp Ser Lys Gln	Leu Pro Thr
1	5	10	15
Glu Trp Glu Ile	Glu Lys Gly Glu	Gly Ile Glu Ser	Ile Val Pro His
	20	25	30
Phe Ser Gly Leu	Glu Arg Val Ser	Ser Gly Ser Ala	Thr Ser Phe Trp
	35	40	45
His Thr Ala Val	Ser Lys Ser Ser	Gln Ser Thr Ser	Ile Asn Ser Ser
	50	55	60
Ser Pro Glu Ala	Lys Arg Cys Lys	Leu Ala Ser Glu	Ser Ser Pro Gly
	65	70	75
Asp Ser Cys Ser	Asn Ile Asp Phe	Val Gln Val Lys	Ala Pro Thr Ala
	85	90	95
Leu Glu Val Ser	Val Ala Ser Ala	Glu Ser Asp Leu	Cys Leu Lys Leu
	100	105	110

Gly Lys Arg Thr Tyr Ser Glu Glu Tyr Trp Gly Arg Asn Asn Asn Glu
115 120 125
Ile Ser Ala Val Ser Met Lys Leu Leu Thr Pro Ser Val Val Ala Gly
130 135 140
Lys Ser Lys Leu Cys Gly Gln Ser Met Pro Val Pro Arg Cys Gln Ile
145 150 155 160
Asp Gly Cys Glu Leu Asp Leu Ser Ser Ala Lys Gly Tyr His Arg Lys
165 170 175
His Lys Val Cys Glu Lys His Ser Lys Cys Pro Lys Val Ser Val Ser
180 185 190
Gly Leu Glu Arg Arg Phe Cys Gln Cys Ser Arg Phe His Ala Val
195 200 205
Ser Glu Phe Asp Glu Lys Lys Arg Ser Cys Arg Lys Arg Leu Ser His
210 215 220
His Asn Ala Arg Arg Arg Lys Pro Gln Gly Val Phe Ser Met Asn Pro
225 230 235 240
Glu Arg Val Tyr Asp Arg Arg Gln His Thr Asn Met Leu Trp Asn Gly
245 250 255
Val Ser Leu Asn Ala Arg Ser Glu Arg Asn Val
260 265

(2) INFORMATION FOR SEQ ID NO:795:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1631 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1631
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499001

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:795:

aagcgacgac	tgactcttct	tcctcctcct	cctccacctc	ttgttttaggt	tcttagcaact	60
gaaatttgat	cagaaggtgt	tgacggtgta	gagcttcacg	aaacataaac	tttcatttct	120
tctagcttct	tgatttgctc	ttaaaggtgc	atggtgaagt	gattgaaagc	gatttacatg	180
tgacttgcag	ctcggtcaga	cattatacat	tacactcaac	acgagattgg	aaaggatgct	240
tgagaatcca	aagttcgatt	tgacgctgt	tggcaatcac	aacaacgaca	acaattacta	300
tgccttcacc	caagactttt	atcaaaaagct	cggggaagaa	ggtacaaaaca	tgtctgttga	360
cagtatgcag	acaagtaatg	ctggagggtc	tgtgtcaatg	tctgtcgata	acagtagcgt	420
tggttcgagt	gatgctctta	ttggccatcc	tggtttgaag	cctatgcgcc	atccctactc	480
tctctcggat	ggccaaagcg	tatttcggcc	aggaaaagtt	actcatgcac	ttaacgatga	540
tgccttagca	caagcgttga	tggatagtta	gtatccaacc	gagggaactgg	tgaactatga	600
agagtggaca	atagatctga	ggaaactaca	tatgggtcct	gcttttgctc	aaggggcttt	660
tggaaagtta	tacagagggg	cttacaacgg	agaagatgta	gccattaagc	tactcgagag	720
gtcagatagc	aaccctgaaa	aggcacaagc	cctcgaacag	cagtttcagc	aggaagtttc	780
tatgcttgca	tttttgaaagc	atcctaacat	cgttaggttt	attggtgcgt	gcattaaacc	840
gatggtgtgg	tgcatcgtga	ctgaatatgc	aaaaggaggg	tctgtcagac	agttttctgac	900
taagagacaa	aaccgagctg	tgccctttgaa	gttagctgtt	atgcaggcgt	tggatgttgc	960
caggggtatg	gcttacgtcc	atgagcgcaa	ctttatacac	cgggatctaa	agtcagataa	1020
cctcctcata	tcagctgata	gggccatcaa	gattgctgat	tttgggtgtg	caagaattga	1080
agttcaaacc	gaagggatga	caccagagac	tggaacttac	agatggatgg	caccagagat	1140
gatccagcac	agaccctaca	ctcaaaaagt	ggacgtgtat	agttttggaa	tcgtgctgtg	1200
ggagttgatt	acaggtctgt	taccgttcca	gaacatgacg	gcggttcagg	ctgcatttgc	1260
agtggatgaac	agaggagtcc	gtccaacagt	cccagcagat	tgtcttctctg	tgcttggaga	1320
gatcatgaca	cgttgctggg	atgcggagcc	tgaagtcagt	ccttgttttg	cagagattgt	1380
caatcttctg	gaggcgccg	aaactgagat	aatgacgaat	gtgagaaaag	cccgtttcag	1440
atgttgcattg	acgcaaccaa	tgacagtcga	ctaattctgtt	gtgaagaaaag	agagaggaga	1500
agaagaggaa	tgaacaaaga	agagaacata	aaagaaaaaa	acagagagag	agagagagaa	1560
agcaagaagg	gcttttagata	tatgtaagtt	tgtgtgtgta	tctatctatc	tatatatata	1620
tatccgattg	c					

(2) INFORMATION FOR SEQ ID NO:796:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 412 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..412
 (D) OTHER INFORMATION: / Ceres Seq. ID 1499002
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:796:

Met	Leu	Glu	Asn	Pro	Lys	Phe	Asp	Leu	His	Ala	Val	Gly	Asn	His	Asn
1				5					10					15	
Asn	Asp	Asn	Asn	Tyr	Tyr	Ala	Phe	Thr	Gln	Asp	Phe	Tyr	Gln	Lys	Leu
			20					25					30		
Gly	Glu	Glu	Gly	Thr	Asn	Met	Ser	Val	Asp	Ser	Met	Gln	Thr	Ser	Asn
		35				40						45			
Ala	Gly	Gly	Ser	Val	Ser	Met	Ser	Val	Asp	Asn	Ser	Ser	Val	Gly	Ser
	50					55					60				
Ser	Asp	Ala	Leu	Ile	Gly	His	Pro	Gly	Leu	Lys	Pro	Met	Arg	His	Pro
65				70					75					80	
Tyr	Ser	Leu	Ser	Asp	Gly	Gln	Ser	Val	Phe	Arg	Pro	Gly	Lys	Val	Thr
			85					90					95		
His	Ala	Leu	Asn	Asp	Asp	Ala	Leu	Ala	Gln	Ala	Leu	Met	Asp	Ser	Lys
		100					105					110			
Tyr	Pro	Thr	Glu	Gly	Leu	Val	Asn	Tyr	Glu	Glu	Trp	Thr	Ile	Asp	Leu
		115				120					125				
Arg	Lys	Leu	His	Met	Gly	Pro	Ala	Phe	Ala	Gln	Gly	Ala	Phe	Gly	Lys
	130				135					140					
Leu	Tyr	Arg	Gly	Thr	Tyr	Asn	Gly	Glu	Asp	Val	Ala	Ile	Lys	Leu	Leu
145				150				155					160		
Glu	Arg	Ser	Asp	Ser	Asn	Pro	Glu	Lys	Ala	Gln	Ala	Leu	Glu	Gln	Gln
			165					170					175		
Phe	Gln	Gln	Glu	Val	Ser	Met	Leu	Ala	Phe	Leu	Lys	His	Pro	Asn	Ile
		180					185					190			
Val	Arg	Phe	Ile	Gly	Ala	Cys	Ile	Lys	Pro	Met	Val	Trp	Cys	Ile	Val
	195					200					205				
Thr	Glu	Tyr	Ala	Lys	Gly	Gly	Ser	Val	Arg	Gln	Phe	Leu	Thr	Lys	Arg
	210				215					220					
Gln	Asn	Arg	Ala	Val	Pro	Leu	Lys	Leu	Ala	Val	Met	Gln	Ala	Leu	Asp
225				230					235					240	
Val	Ala	Arg	Gly	Met	Ala	Tyr	Val	His	Glu	Arg	Asn	Phe	Ile	His	Arg
			245					250					255		
Asp	Leu	Lys	Ser	Asp	Asn	Leu	Leu	Ile	Ser	Ala	Asp	Arg	Ser	Ile	Lys
		260				265						270			
Ile	Ala	Asp	Phe	Gly	Val	Ala	Arg	Ile	Glu	Val	Gln	Thr	Glu	Gly	Met
	275					280					285				
Thr	Pro	Glu	Thr	Gly	Thr	Tyr	Arg	Trp	Met	Ala	Pro	Glu	Met	Ile	Gln
	290				295					300					
His	Arg	Pro	Tyr	Thr	Gln	Lys	Val	Asp	Val	Tyr	Ser	Phe	Gly	Ile	Val
305				310					315					320	
Leu	Trp	Glu	Leu	Ile	Thr	Gly	Leu	Leu	Pro	Phe	Gln	Asn	Met	Thr	Ala
			325					330					335		
Val	Gln	Ala	Ala	Phe	Ala	Val	Val	Asn	Arg	Gly	Val	Arg	Pro	Thr	Val
		340					345					350			
Pro	Ala	Asp	Cys	Leu	Pro	Val	Leu	Gly	Glu	Ile	Met	Thr	Arg	Cys	Trp
		355				360					365				
Asp	Ala	Asp	Pro	Glu	Val	Arg	Pro	Cys	Phe	Ala	Glu	Ile	Val	Asn	Leu
	370				375					380					
Leu	Glu	Ala	Ala	Glu	Thr	Glu	Ile	Met	Thr	Asn	Val	Arg	Lys	Ala	Arg
385				390					395					400	

(2) INFORMATION FOR SEQ ID NO:797:

(A) LENGTH: 374 amino acids

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ix) FEATURE:

(B) LOCATION: 1..374

(D) OTHER INFORMATION: / Ceres Seq. ID 1499003

Met Ser Val Asp Ser Met Gln Thr Ser Asn Ala Gly Gly Ser Val Ser
1 5 10 15

Met Ser Val Asp Asn Ser Ser Val Gly Ser Ser Asp Ala Leu Ile Gly
20 25 30

His Pro Gly Leu Lys Pro Met Arg His Pro Tyr Ser Leu Ser Asp Gly
35 40 45

Gln Ser Val Phe Arg Pro Gly Lys Val Thr His Ala Leu Asn Asp Asp
50 55 60

Ala Leu Ala Gln Ala Leu Met Asp Ser Lys Tyr Pro Thr Glu Gly Leu
65 70 75 80

Val Asn Tyr Glu Glu Trp Thr Ile Asp Leu Arg Lys Leu His Met Gly
85 90 95

Pro Ala Phe Ala Gln Gly Ala Phe Gly Lys Leu Tyr Arg Gly Thr Tyr
100 105 110

Asn Gly Glu Asp Val Ala Ile Lys Leu Leu Glu Arg Ser Asp Ser Asn

Pro Glu Lys Ala Gln Ala Leu Glu Gln Gln Phe Gln Gln Glu Val Ser
130 135 140

Met Leu Ala Phe Leu Lys His Pro Asn Ile Val Arg Phe Ile Gly Ala

Cys Ile Lys Pro Met Val Trp Cys Ile Val Thr Glu Tyr Ala Lys Gly

Gly Ser Val Arg Gln Phe Leu Thr Lys Arg Gln Asn Arg Ala Val Pro

Leu Lys Leu Ala Val Met Gln Ala Leu Asp Val Ala Arg Gly Met Ala

Tyr Val His Glu Arg Asn Phe Ile His Arg Asp Leu Lys Ser Asp Asn

Leu Leu Ile Ser Ala Asp Arg Ser Ile Lys Ile Ala Asp Phe Gly Val

Ala Arg Ile Glu Val Gln Thr Glu Gly Met Thr Pro Glu Thr Gly Thr

Tyr Arg Trp Met Ala Pro Glu Met Ile Gln His Arg Pro Tyr Thr Gln

Lys Val Asp Val Tyr Ser Phe Gly Ile Val Leu Trp Glu Leu Ile Thr

Gly 275 Leu 280 Pro 285 Phe 290 Gln 295 Asn 300 Met Thr Ala Val Gln Ala Ala Phe Ala

Val	Val	Asn	Arg	Gly	Val	Arg	Pro	Thr	Val	Pro	Ala	Asp	Cys	Leu	Pro
305					310					315					320

Val Leu Gly Glu Ile Met Thr Arg Cys Trp Asp Ala Asp Pro Glu Val

Arg Pro Cys Phe Ala Glu Ile Val Asn Leu Leu Glu Ala Ala Glu Thr

Glu Ile Met Thr Asn Val Arg Lys Ala Arg Phe Arg Cys Cys Met Thr

Gln Pro Met Thr Val Asp

370

(2) INFORMATION FOR SEQ ID NO:798:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 369 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..369

(D) OTHER INFORMATION: / Ceres Seq. ID 1499004

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:798:

Met	Gln	Thr	Ser	Asn	Ala	Gly	Gly	Ser	Val	Ser	Met	Ser	Val	Asp	Asn	
1				5				10						15		
Ser	Ser	Val	Gly	Ser	Ser	Asp	Ala	Leu	Ile	Gly	His	Pro	Gly	Leu	Lys	
		20						25					30			
Pro	Met	Arg	His	Pro	Tyr	Ser	Leu	Ser	Asp	Gly	Gln	Ser	Val	Phe	Arg	
		35					40					45				
Pro	Gly	Lys	Val	Thr	His	Ala	Leu	Asn	Asp	Asp	Ala	Leu	Ala	Gln	Ala	
	50					55					60					
Leu	Met	Asp	Ser	Lys	Tyr	Pro	Thr	Glu	Gly	Leu	Val	Asn	Tyr	Glu	Glu	
65					70					75				80		
Trp	Thr	Ile	Asp	Leu	Arg	Lys	Leu	His	Met	Gly	Pro	Ala	Phe	Ala	Gln	
			85					90						95		
Gly	Ala	Phe	Gly	Lys	Leu	Tyr	Arg	Gly	Thr	Tyr	Asn	Gly	Glu	Asp	Val	
		100						105					110			
Ala	Ile	Lys	Leu	Leu	Glu	Arg	Ser	Asp	Ser	Asn	Pro	Glu	Lys	Ala	Gln	
	115					120						125				
Ala	Leu	Glu	Gln	Gln	Phe	Gln	Gln	Glu	Val	Ser	Met	Leu	Ala	Phe	Leu	
	130					135					140					
Lys	His	Pro	Asn	Ile	Val	Arg	Phe	Ile	Gly	Ala	Cys	Ile	Lys	Pro	Met	
145					150					155					160	
Val	Trp	Cys	Ile	Val	Thr	Glu	Tyr	Ala	Lys	Gly	Gly	Ser	Val	Arg	Gln	
			165						170					175		
Phe	Leu	Thr	Lys	Arg	Gln	Asn	Arg	Ala	Val	Pro	Leu	Lys	Leu	Ala	Val	
		180						185					190			
Met	Gln	Ala	Leu	Asp	Val	Ala	Arg	Gly	Met	Ala	Tyr	Val	His	Glu	Arg	
	195					200						205				
Asn	Phe	Ile	His	Arg	Asp	Leu	Lys	Ser	Asp	Asn	Leu	Leu	Ile	Ser	Ala	
	210					215					220					
Asp	Arg	Ser	Ile	Lys	Ile	Ala	Asp	Phe	Gly	Val	Ala	Arg	Ile	Glu	Val	
225				230						235				240		
Gln	Thr	Glu	Gly	Met	Thr	Pro	Glu	Thr	Gly	Thr	Tyr	Arg	Trp	Met	Ala	
			245						250					255		
Pro	Glu	Met	Ile	Gln	His	Arg	Pro	Tyr	Thr	Gln	Lys	Val	Asp	Val	Tyr	
		260						265					270			
Ser	Phe	Gly	Ile	Val	Leu	Trp	Glu	Leu	Ile	Thr	Gly	Leu	Leu	Pro	Phe	
	275						280					285				
Gln	Asn	Met	Thr	Ala	Val	Gln	Ala	Ala	Phe	Ala	Val	Val	Asn	Arg	Gly	
	290					295					300					
Val	Arg	Pro	Thr	Val	Pro	Ala	Asp	Cys	Leu	Pro	Val	Leu	Gly	Glu	Ile	
305				310						315				320		
Met	Thr	Arg	Cys	Trp	Asp	Ala	Asp	Pro	Glu	Val	Arg	Pro	Cys	Phe	Ala	
			325						330					335		
Glu	Ile	Val	Asn	Leu	Leu	Glu	Ala	Ala	Glu	Thr	Glu	Ile	Met	Thr	Asn	
		340						345				350				
Val	Arg	Lys	Ala	Arg	Phe	Arg	Cys	Cys	Met	Thr	Gln	Pro	Met	Thr	Val	
		355					360					365				

Asp

(2) INFORMATION FOR SEQ ID NO:799:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1182 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1182
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499009

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:799:

```
agattaagtc ttcttcgtca tcttcgagtg tgagtggatc cagagagaga attagatatatt      60
tccgacacga ggcaaattcc tagtggctca tggcgctcatc atctgatcac acggcggaaga      120
taatcgacgg caaggcgatt gctcatacca tcagatcaga gatcgccgag gaagttcgcg      180
gtctatctga gaaacacggc aaggtcccag gactagctgt agttattggt gggagccgaa      240
aggattcaca gacctatgtg aatacgaaga ggaaagcgtg cgctgaggtt gggattaagt      300
catttgacgt gggcctacca gaggaagttt ctgaagctga tcttattagc aaagttcatg      360
aactaaattc aaatccggat gtccatggca tattagttca actcccattg ccgaaacata      420
ttaatgagga gaatatattg ggtgcaatca gcattgataa agatgtcgat ggcttccatc      480
ctttgaatat tggtaagcta gccatgaaag gcagagaacc cctcttcctt ccttgacacc      540
caaaggggatg tttggaactc ctagctagaa gcggcgtaaa gataaagggg caacgagcag      600
ttgttgtagg tcggagtaac attgttggtt tgcccgtttc acttcttttg ctcaaggctg      660
atgctactgt cacaactgta cattctcaca ccaaggatcc tgaggctatc atacgggaag      720
ctgacattgt tattgctgca tgcggacaag cccacatgat taagggaac tggataaagc      780
caggggctgc agtaattgat gttggaacta atgcagtcag cgacccgagc aagaaatcag      840
gataccggtt ggttgagatg gttgatttcg cagaagcttc aaaagttgca ggtttcataa      900
ctccggtccc tgggtggtga ggccaatga cagtggcaat gcttctcagg aacaccgtag      960
acggtgccaa gcgtgtcttt ggcgagtaaa acaatctact gtatgtaata aagaaaccaa     1020
gagtttctcc attctgtaat tgtgtacttg gcttgacgat atttttccac tcaaataaat     1080
tgaaattggc gttccctttg gattacctta cattgttctg caactagcta gaacgattat     1140
ttccgcaatt cagttaaata caagggtgtc atcatgtgac cc
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(2) INFORMATION FOR SEQ ID NO:800:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 299 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..299
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499010

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:800:

```
Met Ala Ser Ser Ser Asp His Thr Ala Lys Ile Ile Asp Gly Lys Ala
1           5           10          15
Ile Ala His Thr Ile Arg Ser Glu Ile Ala Glu Glu Val Arg Gly Leu
          20          25          30
Ser Glu Lys His Gly Lys Val Pro Gly Leu Ala Val Val Ile Val Gly
          35          40          45
Ser Arg Lys Asp Ser Gln Thr Tyr Val Asn Thr Lys Arg Lys Ala Cys
          50          55          60
Ala Glu Val Gly Ile Lys Ser Phe Asp Val Gly Leu Pro Glu Glu Val
65          70          75          80
Ser Glu Ala Asp Leu Ile Ser Lys Val His Glu Leu Asn Ser Asn Pro
          85          90          95
Asp Val His Gly Ile Leu Val Gln Leu Pro Leu Pro Lys His Ile Asn
          100         105         110
Glu Glu Asn Ile Leu Gly Ala Ile Ser Ile Asp Lys Asp Val Asp Gly
          115         120         125
Phe His Pro Leu Asn Ile Gly Lys Leu Ala Met Lys Gly Arg Glu Pro
```

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1542

(D) OTHER INFORMATION: / Ceres Seq. ID 1499012

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:802:

```
cttgcgtttt cgtcccacaa tctttgtcgt ggttttctgc tgtcttcttc tccgtcgaac      60
ttctccgacc acttcgtata gagagagaga gtgacgaaga gtttacggaa tcgaatccaa      120
taatgagtag tgcgtcggtt ttttagttcaa tccaaggatg ctggttcaag ggcgaaagga      180
aaattcgtgt agcggataag cgagccaaga ggcttacttt gggatcccat gtggcttcgc      240
catcttcaat gagcttcaga gtttcagcta gtagttctgt taaacctgaa aaggatatta      300
ggattgggtct tcttggtgca agtggtctaca ctgggtgctga gatcgttagg cttcttgcaa      360
atcatccgca ttccaggtc actttgatga ctgctgatag aaaagctggc cagtcaatgg      420
aaagcgtttt cccacacctg agagctcaaa aactacctac tttggtctcs gtaaaggatg      480
cagatttttc tactgtggat gctgtattct gctgtttacc tcacggaaca actcaggaaa      540
tcatcaagga actgcctact gcattgaaaa tcgttgatct ttcagcggac ttccggttgc      600
gtaatatgtg agaatatgaa gaatggtagt gtcagcctca caaggcagta gagttacaga      660
aagaagttgt gtatggtcta acagagatac taagggagga cataaaaaag gcacgacttg      720
tggttaaccc aggtgtttac ccgactacga ttcaacttcc tcttgttcct ttactaaagg      780
caaattctcat caaacatgaa aacatcatta tcgatgcaaa atctggtgtt agtggagcag      840
gacgtggtgc taaggaggca aatctttact ctgagatagc tgaaggcatt tcttcttatg      900
gtgtcaccgg tcatcgccat gttcctgaaa ttgaacaggg attatctgat gttgcacagt      960
caaaagtaac agtcagtttt acgccacatc tcatgccaat gatccgtgga atgcaatcga     1020
ctatatatgt ggaaatggct cccgggggta gaaccgaaga tttacaccag caattgaaga     1080
cgtcttatga ggatgaagaa ttgtgcaaag tgttggatga aggagttgtt cctcggacac     1140
acaacgttag aggatccaac tattgtcata tgagtgtctt tccatgatga attcctggaa     1200
gagctatcat aatctcagtg attgataatc ttgtgaaagg agcttcggga caagcgttgc     1260
agaatcttaa cataatgttg ggatatcccg aaacaacggg gctcctacac cagccgcttt     1320
tcccttaaaa atcccacctt taaatcgatg accaatctga agctgttgag acggcaatgt     1380
taagcataaa gatggttggt tatatgattc atatttatag acaataaagc ctcttctttt     1440
accattacaa ataaatggtt ttgttggttg tttattaagg ttttgatgaa cctttattct     1500
tgttatctct attttctgaa ttgcaatttt cgtttgagtc gc
```

(2) INFORMATION FOR SEQ ID NO:803:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 441 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..441

(D) OTHER INFORMATION: / Ceres Seq. ID 1499013

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:803:

```
Cys Val Phe Val Pro Gln Ser Leu Ser Trp Phe Ser Ala Val Phe Phe
1          5          10          15
Ser Val Glu Leu Arg Pro Leu Arg Ile Glu Arg Glu Ser Asp Glu
          20          25          30
Glu Phe Thr Glu Ser Asn Pro Ile Met Ser Thr Ala Ser Ala Phe Ser
          35          40          45
Ser Ile Gln Gly Cys Trp Phe Lys Gly Glu Arg Lys Ile Arg Val Ala
          50          55          60
Asp Lys Arg Ala Lys Arg Leu Thr Leu Gly Ser His Val Ala Ser Pro
65          70          75          80
Ser Ser Met Ser Phe Arg Val Ser Ala Ser Ser Ser Val Lys Pro Glu
          85          90          95
Lys Asp Ile Arg Ile Gly Leu Leu Gly Ala Ser Gly Tyr Thr Gly Ala
          100         105         110
Glu Ile Val Arg Leu Leu Ala Asn His Pro His Phe Gln Val Thr Leu
          115         120         125
Met Thr Ala Asp Arg Lys Ala Gly Gln Ser Met Glu Ser Val Phe Pro
```

130	135	140
His Leu Arg Ala Gln Lys	Leu Pro Thr Leu Val	Xaa Val Lys Asp Ala
145	150	155
Asp Phe Ser Thr Val Asp	Ala Val Phe Cys Cys	Leu Pro His Gly Thr
165	170	175
Thr Gln Glu Ile Ile Lys	Glu Leu Pro Thr Ala	Leu Lys Ile Val Asp
180	185	190
Leu Ser Ala Asp Phe Arg	Leu Arg Asn Ile Ala	Glu Tyr Glu Glu Trp
195	200	205
Tyr Gly Gln Pro His Lys	Ala Val Glu Leu Gln	Lys Glu Val Val Tyr
210	215	220
Gly Leu Thr Glu Ile Leu	Arg Glu Asp Ile Lys	Lys Ala Arg Leu Val
225	230	235
Ala Asn Pro Gly Cys Tyr	Pro Thr Thr Ile Gln	Leu Pro Leu Val Pro
245	250	255
Leu Leu Lys Ala Asn Leu	Ile Lys His Glu Asn	Ile Ile Ile Asp Ala
260	265	270
Lys Ser Gly Val Ser Gly	Ala Gly Arg Gly Ala	Lys Glu Ala Asn Leu
275	280	285
Tyr Ser Glu Ile Ala Glu	Gly Ile Ser Ser Tyr	Gly Val Thr Arg His
290	295	300
Arg His Val Pro Glu Ile	Glu Gln Gly Leu Ser	Asp Val Ala Gln Ser
305	310	315
Lys Val Thr Val Ser Phe	Thr Pro His Leu Met	Pro Met Ile Arg Gly
325	330	335
Met Gln Ser Thr Ile Tyr	Val Glu Met Ala Pro	Gly Val Arg Thr Glu
340	345	350
Asp Leu His Gln Gln Leu	Lys Thr Ser Tyr Glu	Asp Glu Glu Phe Val
355	360	365
Lys Val Leu Asp Glu Gly	Val Val Pro Arg Thr	His Asn Val Arg Gly
370	375	380
Ser Asn Tyr Cys His Met	Ser Val Phe Pro Asp	Arg Ile Pro Gly Arg
385	390	395
Ala Ile Ile Ile Ser Val	Ile Asp Asn Leu Val	Lys Gly Ala Ser Gly
405	410	415
Gln Ala Leu Gln Asn Leu	Asn Ile Met Leu Gly	Tyr Pro Glu Thr Thr
420	425	430
Gly Leu Leu His Gln Pro	Leu Phe Pro	
435	440	

(2) INFORMATION FOR SEQ ID NO:804:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 401 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..401

(D) OTHER INFORMATION: / Ceres Seq. ID 1499014

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:804:

Met	Ser	Thr	Ala	Ser	Ala	Phe	Ser	Ser	Ile	Gln	Gly	Cys	Trp	Phe	Lys
1				5					10					15	
Gly	Glu	Arg	Lys	Ile	Arg	Val	Ala	Asp	Lys	Arg	Ala	Lys	Arg	Leu	Thr
			20					25					30		
Leu	Gly	Ser	His	Val	Ala	Ser	Pro	Ser	Ser	Met	Ser	Phe	Arg	Val	Ser
		35				40					45				
Ala	Ser	Ser	Ser	Val	Lys	Pro	Glu	Lys	Asp	Ile	Arg	Ile	Gly	Leu	Leu
	50				55				60						
Gly	Ala	Ser	Gly	Tyr	Thr	Gly	Ala	Glu	Ile	Val	Arg	Leu	Leu	Ala	Asn
65				70				75						80	


```

His Pro His Phe Gln Val Thr Leu Met Thr Ala Asp Arg Lys Ala Gly
      85      90      95
Gln Ser Met Glu Ser Val Phe Pro His Leu Arg Ala Gln Lys Leu Pro
      100      105      110
Thr Leu Val Xaa Val Lys Asp Ala Asp Phe Ser Thr Val Asp Ala Val
      115      120      125
Phe Cys Cys Leu Pro His Gly Thr Thr Gln Glu Ile Ile Lys Glu Leu
      130      135      140
Pro Thr Ala Leu Lys Ile Val Asp Leu Ser Ala Asp Phe Arg Leu Arg
      145      150      155      160
Asn Ile Ala Glu Tyr Glu Glu Trp Tyr Gly Gln Pro His Lys Ala Val
      165      170      175
Glu Leu Gln Lys Glu Val Val Tyr Gly Leu Thr Glu Ile Leu Arg Glu
      180      185      190
Asp Ile Lys Lys Ala Arg Leu Val Ala Asn Pro Gly Cys Tyr Pro Thr
      195      200      205
Thr Ile Gln Leu Pro Leu Val Pro Leu Leu Lys Ala Asn Leu Ile Lys
      210      215      220
His Glu Asn Ile Ile Ile Asp Ala Lys Ser Gly Val Ser Gly Ala Gly
      225      230      235      240
Arg Gly Ala Lys Glu Ala Asn Leu Tyr Ser Glu Ile Ala Glu Gly Ile
      245      250      255
Ser Ser Tyr Gly Val Thr Arg His Arg His Val Pro Glu Ile Glu Gln
      260      265      270
Gly Leu Ser Asp Val Ala Gln Ser Lys Val Thr Val Ser Phe Thr Pro
      275      280      285
His Leu Met Pro Met Ile Arg Gly Met Gln Ser Thr Ile Tyr Val Glu
      290      295      300
Met Ala Pro Gly Val Arg Thr Glu Asp Leu His Gln Gln Leu Lys Thr
      305      310      315      320
Ser Tyr Glu Asp Glu Glu Phe Val Lys Val Leu Asp Glu Gly Val Val
      325      330      335
Pro Arg Thr His Asn Val Arg Gly Ser Asn Tyr Cys His Met Ser Val
      340      345      350
Phe Pro Asp Arg Ile Pro Gly Arg Ala Ile Ile Ile Ser Val Ile Asp
      355      360      365
Asn Leu Val Lys Gly Ala Ser Gly Gln Ala Leu Gln Asn Leu Asn Ile
      370      375      380
Met Leu Gly Tyr Pro Glu Thr Thr Gly Leu Leu His Gln Pro Leu Phe
      385      390      395      400
Pro

```

(2) INFORMATION FOR SEQ ID NO:805:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 359 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..359
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499015

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:805:

```

Met Ser Phe Arg Val Ser Ala Ser Ser Val Lys Pro Glu Lys Asp
1      5      10      15
Ile Arg Ile Gly Leu Leu Gly Ala Ser Gly Tyr Thr Gly Ala Glu Ile
      20      25      30
Val Arg Leu Leu Ala Asn His Pro His Phe Gln Val Thr Leu Met Thr
      35      40      45
Ala Asp Arg Lys Ala Gly Gln Ser Met Glu Ser Val Phe Pro His Leu

```

50 55 60
Arg Ala Gln Lys Leu Pro Thr Leu Val Xaa Val Lys Asp Ala Asp Phe
65 70 75 80
Ser Thr Val Asp Ala Val Phe Cys Cys Leu Pro His Gly Thr Thr Gln
85 90 95
Glu Ile Ile Lys Glu Leu Pro Thr Ala Leu Lys Ile Val Asp Leu Ser
100 105 110
Ala Asp Phe Arg Leu Arg Asn Ile Ala Glu Tyr Glu Glu Trp Tyr Gly
115 120 125
Gln Pro His Lys Ala Val Glu Leu Gln Lys Glu Val Val Tyr Gly Leu
130 135 140
Thr Glu Ile Leu Arg Glu Asp Ile Lys Lys Ala Arg Leu Val Ala Asn
145 150 155 160
Pro Gly Cys Tyr Pro Thr Thr Ile Gln Leu Pro Leu Val Pro Leu Leu
165 170 175
Lys Ala Asn Leu Ile Lys His Glu Asn Ile Ile Ile Asp Ala Lys Ser
180 185 190
Gly Val Ser Gly Ala Gly Arg Gly Ala Lys Glu Ala Asn Leu Tyr Ser
195 200 205
Glu Ile Ala Glu Gly Ile Ser Ser Tyr Gly Val Thr Arg His Arg His
210 215 220
Val Pro Glu Ile Glu Gln Gly Leu Ser Asp Val Ala Gln Ser Lys Val
225 230 235 240
Thr Val Ser Phe Thr Pro His Leu Met Pro Met Ile Arg Gly Met Gln
245 250 255
Ser Thr Ile Tyr Val Glu Met Ala Pro Gly Val Arg Thr Glu Asp Leu
260 265 270
His Gln Gln Leu Lys Thr Ser Tyr Glu Asp Glu Glu Phe Val Lys Val
275 280 285
Leu Asp Glu Gly Val Val Pro Arg Thr His Asn Val Arg Gly Ser Asn
290 295 300
Tyr Cys His Met Ser Val Phe Pro Asp Arg Ile Pro Gly Arg Ala Ile
305 310 315 320
Ile Ile Ser Val Ile Asp Asn Leu Val Lys Gly Ala Ser Gly Gln Ala
325 330 335
Leu Gln Asn Leu Asn Ile Met Leu Gly Tyr Pro Glu Thr Thr Gly Leu
340 345 350
Leu His Gln Pro Leu Phe Pro
355

(2) INFORMATION FOR SEQ ID NO:806:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1481 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1481

(D) OTHER INFORMATION: / Ceres Seq. ID 1499016

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:806:

gcgttacact acaactctct atctctctct cttcttttct gctcattttt gggtaattct 60
tctggtttta tggtcttggt cctattactg actcacaatc agccaacgca aatcttttctt 120
tgaccatttt taatagattc tcttagtcac ttgttggtt tcaaagtcga agttgacctc 180
atcttcttct tcttcgaggt tttatacaag ttactccata aaccttcgag cttccagcaa 240
ctttggcttc tctgttggtga attattgctt attatatcct caacacgaaa tcaaatgcc 300
aagaccaaga gtttcagagt tgtctcagag gcaagctcca aggctgaggt catcgtcatc 360
tacttctgat tccaatcatt ccaaccgtct gatcactacg gatcaaagtt ttaagcccgg 420
tggtgaccgt aaatctcctc gaagcgggtg acctaacagt gatccgcttg gtcagaagaa 480
acttggggga cgaatatcgg atctagagtc gcagtttaga caagcgcaag aggaactgag 540
attgctcaag gagcagttgg ctaatgctga agctgtgaag aaacaagctc aagatgagct 600

tcataagaag	tccaagaaac	caaaccgct	ggctcgagt	gaggaatctg	caactgaggc	660
tgagaggatt	gatagagacg	aaatccctgg	tgatgtgcag	aaagagactg	atgtgtttga	720
ggttcccgtt	gaaaagattg	cagtagaaga	agaagaactg	agaagcggca	atgacgaagc	780
tgagaaattg	gttgcaaagg	aagatgagat	aaagatgctg	aaagctagac	tctatgacat	840
ggagaaagag	catgaatcac	taggcaaaga	aaacgagagc	ttgaagaatc	agttgagcga	900
ttcagcttca	gagattttcta	atgtgaaaagc	taatgaagat	gagatggttt	caaaggtgag	960
taggattggg	gaagagtttag	aagaaagcag	agcaaagacg	gctcacctga	aggagaagct	1020
tgagtccatg	gaagaagcaa	aagatgcttt	agaggctgag	atgaagaagc	tcagggttca	1080
aaccgagcag	tggaggaagg	cagcggatgc	tgcagcagca	gttctttctg	gagagtttga	1140
gatgaatggg	cgggatcgat	ctgggtcaac	tgagaagtat	tatgcagggtg	ggttctttga	1200
cccgtcagct	gggttcatgg	atccaccggg	aatggctgat	gattatgatg	atggactggg	1260
aagtggcaag	aggaagagtt	ctgggatgaa	gatgtttggg	gagttgtgga	ggaagaaaagg	1320
gcaaaagtga	gttacagatt	gtgtggagtg	tcattcaaga	aatgggtgtgc	tcaccgtttc	1380
tctcttttat	tttctgtgat	ttacctgsaa	gtttttgtaa	gtgggtccgc	ttcatcagaa	1440
gctaactatc	aatccaaatc	aattgcaaaa	acaatttcat	g		

(2) INFORMATION FOR SEQ ID NO:807:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 344 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..344

(D) OTHER INFORMATION: / Ceres Seq. ID 1499017

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:807:

Met	Pro	Arg	Pro	Arg	Val	Ser	Glu	Leu	Ser	Gln	Arg	Gln	Ala	Pro	Arg
1			5					10					15		
Leu	Arg	Ser	Ser	Ser	Ser	Thr	Ser	Asp	Ser	Asn	His	Ser	Asn	Arg	Leu
			20					25					30		
Ile	Thr	Thr	Asp	Gln	Ser	Phe	Lys	Pro	Gly	Val	Asp	Arg	Lys	Ser	Pro
			35				40					45			
Arg	Ser	Gly	Gly	Pro	Asn	Ser	Asp	Pro	Leu	Gly	Gln	Lys	Lys	Leu	Gly
			50			55					60				
Gly	Arg	Ile	Ser	Asp	Leu	Glu	Ser	Gln	Leu	Gly	Gln	Ala	Gln	Glu	Glu
65					70					75				80	
Leu	Arg	Leu	Leu	Lys	Glu	Gln	Leu	Ala	Asn	Ala	Glu	Ala	Val	Lys	Lys
				85				90						95	
Gln	Ala	Gln	Asp	Glu	Leu	His	Lys	Lys	Ser	Lys	Lys	Pro	Asn	Pro	Leu
			100					105					110		
Ala	Arg	Val	Glu	Glu	Ser	Ala	Thr	Glu	Ala	Glu	Arg	Ile	Asp	Arg	Asp
			115				120					125			
Glu	Ile	Pro	Gly	Asp	Val	Gln	Lys	Glu	Thr	Asp	Val	Phe	Glu	Val	Pro
			130			135					140				
Val	Glu	Lys	Ile	Ala	Val	Glu	Glu	Glu	Glu	Leu	Arg	Ser	Gly	Asn	Asp
145					150					155					160
Glu	Ala	Glu	Lys	Leu	Val	Ala	Lys	Glu	Asp	Glu	Ile	Lys	Met	Leu	Lys
				165				170						175	
Ala	Arg	Leu	Tyr	Asp	Met	Glu	Lys	Glu	His	Glu	Ser	Leu	Gly	Lys	Glu
				180				185					190		
Asn	Glu	Ser	Leu	Lys	Asn	Gln	Leu	Ser	Asp	Ser	Ala	Ser	Glu	Ile	Ser
			195				200					205			
Asn	Val	Lys	Ala	Asn	Glu	Asp	Glu	Met	Val	Ser	Lys	Val	Ser	Arg	Ile
			210			215						220			
Gly	Glu	Glu	Leu	Glu	Glu	Ser	Arg	Ala	Lys	Thr	Ala	His	Leu	Lys	Glu
225					230					235				240	
Lys	Leu	Glu	Ser	Met	Glu	Glu	Ala	Lys	Asp	Ala	Leu	Glu	Ala	Glu	Met
				245					250					255	
Lys	Lys	Leu	Arg	Val	Gln	Thr	Glu	Gln	Trp	Arg	Lys	Ala	Ala	Asp	Ala
			260				265						270		

Ala Ala Ala Val Leu Ser Gly Glu Phe Glu Met Asn Gly Arg Asp Arg
275 280 285
Ser Gly Ser Thr Glu Lys Tyr Tyr Ala Gly Gly Phe Phe Asp Pro Ser
290 295 300
Ala Gly Phe Met Asp Pro Pro Gly Met Ala Asp Asp Tyr Asp Asp Gly
305 310 315 320
Leu Gly Ser Gly Lys Arg Lys Ser Ser Gly Met Lys Met Phe Gly Glu
325 330 335
Leu Trp Arg Lys Lys Gly Gln Lys
340

(2) INFORMATION FOR SEQ ID NO:808:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 559 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..559
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499021

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:808:

ggcttctttc	aaccactctt	ggctctcttc	tccactcacc	gaaactccca	ctttcttttt	60
tcctccatct	ccacacccaa	aatccttgaa	actctcactt	ttccgaactc	ggagcaactc	120
gtcctcaccg	gaccgctcgt	cagagggttg	gctcgatgtg	gatccggtga	agctcgcatt	180
gaagaaagcc	gaagcttata	agaaatcgaa	atcagagcaa	aaagaaccag	agaaaaacgc	240
cggcgacgag	gaattgccgc	tctctgtaa	ggctgctatg	caaaaagcca	atgcttataa	300
gaaaaggaaa	ggacttgaaa	ctgatgcagt	gcgaaaagct	aaaccagta	atacagagca	360
aagttttggt	agattaacaa	ataaggttgt	tgaagataat	gatgttaaga	agaaagaatt	420
gaaagtctcc	agcattgatt	tcatggggct	tggctttgct	gataagaaga	gcacaagggg	480
gcttccagcg	ggacttgttc	ctgttggtga	ctatcttcct	gaaggagact	tacctgaggt	540
ggagttttatt	gttggtgat					

(2) INFORMATION FOR SEQ ID NO:809:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 186 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..186
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499022

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:809:

Ala	Ser	Phe	Asn	His	Ser	Trp	Leu	Ser	Ser	Pro	Leu	Thr	Glu	Thr	Pro
1			5					10					15		
Thr	Phe	Phe	Phe	Pro	Pro	Ser	Pro	His	Pro	Lys	Ser	Leu	Lys	Leu	Ser
			20					25					30		
Leu	Phe	Arg	Thr	Arg	Ser	Asn	Ser	Ser	Pro	Asp	Arg	Ser	Ser	Glu	
			35				40					45			
Val	Glu	Leu	Asp	Val	Asp	Pro	Val	Lys	Leu	Ala	Leu	Lys	Lys	Ala	Glu
			50				55				60				
Ala	Tyr	Lys	Lys	Ser	Lys	Ser	Glu	Gln	Lys	Glu	Pro	Glu	Lys	Asn	Ala
							70				75			80	
Gly	Asp	Glu	Glu	Leu	Pro	Leu	Ser	Val	Lys	Ala	Ala	Met	Gln	Lys	Ala
							85				90			95	
Asn	Ala	Tyr	Lys	Lys	Arg	Lys	Gly	Leu	Gly	Thr	Asp	Ala	Val	Ala	Lys
			100				105						110		
Ala	Lys	Pro	Ser	Asn	Thr	Glu	Gln	Ser	Phe	Val	Arg	Leu	Thr	Asn	Lys
							115						125		
Val	Val	Glu	Asp	Asn	Asp	Val	Lys	Lys	Lys	Glu	Leu	Lys	Val	Ser	Ser

130 135 140
Ile Asp Phe Met Gly Leu Gly Phe Ala Asp Lys Lys Ser Thr Arg Gly
145 150 155 160
Leu Pro Ala Gly Leu Val Pro Val Val Asp Tyr Leu Pro Glu Gly Asp
165 170 175
Leu Pro Glu Val Glu Phe Ile Val Gly Asp
180 185

(2) INFORMATION FOR SEQ ID NO:810:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 94 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..94

(D) OTHER INFORMATION: / Ceres Seq. ID 1499023

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:810:

Met Gln Lys Ala Asn Ala Tyr Lys Lys Arg Lys Gly Leu Gly Thr Asp
1 5 10 15
Ala Val Ala Lys Ala Lys Pro Ser Asn Thr Glu Gln Ser Phe Val Arg
20 25 30
Leu Thr Asn Lys Val Val Glu Asp Asn Asp Val Lys Lys Lys Glu Leu
35 40 45
Lys Val Ser Ser Ile Asp Phe Met Gly Leu Gly Phe Ala Asp Lys Lys
50 55 60
Ser Thr Arg Gly Leu Pro Ala Gly Leu Val Pro Val Val Asp Tyr Leu
65 70 75 80
Pro Glu Gly Asp Leu Pro Glu Val Glu Phe Ile Val Gly Asp
85 90

(2) INFORMATION FOR SEQ ID NO:811:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1527 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1527

(D) OTHER INFORMATION: / Ceres Seq. ID 1499024

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:811:

aacgcattat tgacacgtgt cttttcattt ctcttcttcc ggcgttttct ctccgccggt 60
tcgccaccgt acgtgacaat gtctgtttct ctctccgccg cctctcactt actctgttcc 120
tccaccagag tctctctttc ccccgccgtc acctcttctg cctcgctccc tgctgttgct 180
ctttcttccct ctacatcgcc acattctctt ggaagcgtcg catcttcttc tctgtttcct 240
cactcctcck tcgtgcttca gaaaaaacat ccgatcaatg ggacgagcac gaggatgatt 300
tcaccaaagt gtgccgcttc tgatgcagct caattgataa gcgctaaaga agatatcaaa 360
gttcttctcc ggactaagtt ttgccatccc atcttggtta gattggggtg gcacgatgct 420
ggtacttata acaagaatat tgaggagtgg ccaactgagag gtggagctaa tggaagtctt 480
aggtttgagg ctgagcttaa gcatgctgca aatgctgggtc tgcttaatgc tttaaagctc 540
attcagcctc tcaaagacaa gtatcctaac atctcttatg cggacttatt ccagttagct 600
agtgccacag caatagagga ggctgggtgg cctgatatcc cgatgaaata tgggagagtt 660
gatgtttagt cacctgaaca gtgtccagaa gaaggaagac tccctgatgc tggacctcct 720
tcaccagctg atcatttgag agatgttttc tacagaatgg gacttgatga caaggaaata 780
gttgccctgt ctggtgcaca taccttaggg agagccagac cagaccgtag tgggtgggga 840
aaacctgaga caaagtacac gaaaactgga cctggagaag caggaggaca gtcattggaca 900
gtgaaatggc tcaagttcga caactcttat ttcaaggata tcaaagaaaa gagggacgac 960
gatcttctgg tgttacccac tgatgcggcg ctatttgaag atccttcatt caagaactat 1020
gcagagaagt atgctgaaga tgtggctgca tttttcaagg actacgctga agcccatgcc 1080

aagcttagca atctcgggtgc aaaatttgat cctcccgagg gcatagtcac tgaaaacggt	1140
ccagagaagt tcgtagctgc aaagtattct acgggaaaga aggagctttc ggattcgaag	1200
aaaaagaaga taagagcaga gtatgaagca attggaggaa gccagataa gccattaccc	1260
acaaattact tcctcaacat cataattgcc attggcggtt tggtcctctt gtccactctc	1320
tttggtggtg ataacaactc cgatttctct ggtttctaat tgacaaaatta tatattttga	1380
tttctcttac ctacatacat aattacgtgg tgatcatata ttccttgcaa acaaaaacat	1440
cattgtaaag ttgcttgaa taaaatcacc ttataaataa cattgtttat ttggttttta	1500
gaattttgag attagtgtga gtttctt	

(2) INFORMATION FOR SEQ ID NO:812:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 452 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..452

(D) OTHER INFORMATION: / Ceres Seq. ID 1499025

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:812:

Asn	Ala	Leu	Leu	Thr	Arg	Val	Phe	Ser	Phe	Leu	Phe	Phe	Arg	Arg	Phe
1				5				10					15		
Leu	Ser	Ala	Val	Ser	Pro	Pro	Tyr	Val	Thr	Met	Ser	Val	Ser	Leu	Ser
			20					25					30		
Ala	Ala	Ser	His	Leu	Leu	Cys	Ser	Thr	Arg	Val	Ser	Leu	Ser	Pro	
			35				40					45			
Ala	Val	Thr	Ser	Ser	Ser	Ser	Ser	Pro	Val	Val	Ala	Leu	Ser	Ser	Ser
			50				55				60				
Thr	Ser	Pro	His	Ser	Leu	Gly	Ser	Val	Ala	Ser	Ser	Ser	Leu	Phe	Pro
65					70					75				80	
His	Ser	Ser	Xaa	Val	Leu	Gln	Lys	Lys	His	Pro	Ile	Asn	Gly	Thr	Ser
			85						90					95	
Thr	Arg	Met	Ile	Ser	Pro	Lys	Cys	Ala	Ala	Ser	Asp	Ala	Ala	Gln	Leu
			100					105					110		
Ile	Ser	Ala	Lys	Glu	Asp	Ile	Lys	Val	Leu	Leu	Arg	Thr	Lys	Phe	Cys
			115				120					125			
His	Pro	Ile	Leu	Val	Arg	Leu	Gly	Trp	His	Asp	Ala	Gly	Thr	Tyr	Asn
			130				135				140				
Lys	Asn	Ile	Glu	Glu	Trp	Pro	Leu	Arg	Gly	Gly	Ala	Asn	Gly	Ser	Leu
145					150					155				160	
Arg	Phe	Glu	Ala	Glu	Leu	Lys	His	Ala	Ala	Asn	Ala	Gly	Leu	Leu	Asn
			165					170						175	
Ala	Leu	Lys	Leu	Ile	Gln	Pro	Leu	Lys	Asp	Lys	Tyr	Pro	Asn	Ile	Ser
			180					185					190		
Tyr	Ala	Asp	Leu	Phe	Gln	Leu	Ala	Ser	Ala	Thr	Ala	Ile	Glu	Glu	Ala
			195				200					205			
Gly	Gly	Pro	Asp	Ile	Pro	Met	Lys	Tyr	Gly	Arg	Val	Asp	Val	Val	Ala
			210				215					220			
Pro	Glu	Gln	Cys	Pro	Glu	Gly	Arg	Leu	Pro	Asp	Ala	Gly	Pro	Pro	
225					230					235				240	
Ser	Pro	Ala	Asp	His	Leu	Arg	Asp	Val	Phe	Tyr	Arg	Met	Gly	Leu	Asp
			245						250					255	
Asp	Lys	Glu	Ile	Val	Ala	Leu	Ser	Gly	Ala	His	Thr	Leu	Gly	Arg	Ala
			260					265						270	
Arg	Pro	Asp	Arg	Ser	Gly	Trp	Gly	Lys	Pro	Glu	Thr	Lys	Tyr	Thr	Lys
			275				280						285		
Thr	Gly	Pro	Gly	Glu	Ala	Gly	Gly	Gln	Ser	Trp	Thr	Val	Lys	Trp	Leu
			290				295					300			
Lys	Phe	Asp	Asn	Ser	Tyr	Phe	Lys	Asp	Ile	Lys	Glu	Lys	Arg	Asp	Asp
305					310					315				320	
Asp	Leu	Leu	Val	Leu	Pro	Thr	Asp	Ala	Ala	Leu	Phe	Glu	Asp	Pro	Ser

				325						330						335			
Phe	Lys	Asn	Tyr	Ala	Glu	Lys	Tyr	Ala	Glu	Asp	Val	Ala	Ala	Phe	Phe				
				340					345					350					
Lys	Asp	Tyr	Ala	Glu	Ala	His	Ala	Lys	Leu	Ser	Asn	Leu	Gly	Ala	Lys				
				355				360						365					
Phe	Asp	Pro	Pro	Glu	Gly	Ile	Val	Ile	Glu	Asn	Val	Pro	Glu	Lys	Phe				
				370				375						380					
Val	Ala	Ala	Lys	Tyr	Ser	Thr	Gly	Lys	Lys	Glu	Leu	Ser	Asp	Ser	Met				
															400				
Lys	Lys	Lys	Ile	Arg	Ala	Glu	Tyr	Glu	Ala	Ile	Gly	Gly	Ser	Pro	Asp				
				405						410					415				
Lys	Pro	Leu	Pro	Thr	Asn	Tyr	Phe	Leu	Asn	Ile	Ile	Ile	Ala	Ile	Gly				
				420				425						430					
Val	Leu	Val	Leu	Leu	Ser	Thr	Leu	Phe	Gly	Gly	Asn	Asn	Asn	Ser	Asp				
				435				440						445					
Phe	Ser	Gly	Phe																
				450															

(2) INFORMATION FOR SEQ ID NO:813:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 426 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..426

(D) OTHER INFORMATION: / Ceres Seq. ID 1499026

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:813:

Met	Ser	Val	Ser	Leu	Ser	Ala	Ala	Ser	His	Leu	Leu	Cys	Ser	Ser	Thr				
1				5				10						15					
Arg	Val	Ser	Leu	Ser	Pro	Ala	Val	Thr	Ser	Ser	Ser	Ser	Ser	Pro	Val				
				20				25						30					
Val	Ala	Leu	Ser	Ser	Ser	Thr	Ser	Pro	His	Ser	Leu	Gly	Ser	Val	Ala				
				35				40					45						
Ser	Ser	Ser	Leu	Phe	Pro	His	Ser	Ser	Xaa	Val	Leu	Gln	Lys	Lys	His				
				50				55				60							
Pro	Ile	Asn	Gly	Thr	Ser	Thr	Arg	Met	Ile	Ser	Pro	Lys	Cys	Ala	Ala				
				65				70				75			80				
Ser	Asp	Ala	Ala	Gln	Leu	Ile	Ser	Ala	Lys	Glu	Asp	Ile	Lys	Val	Leu				
				85				90						95					
Leu	Arg	Thr	Lys	Phe	Cys	His	Pro	Ile	Leu	Val	Arg	Leu	Gly	Trp	His				
				100				105						110					
Asp	Ala	Gly	Thr	Tyr	Asn	Lys	Asn	Ile	Glu	Glu	Trp	Pro	Leu	Arg	Gly				
				115				120						125					
Gly	Ala	Asn	Gly	Ser	Leu	Arg	Phe	Glu	Ala	Glu	Leu	Lys	His	Ala	Ala				
				130				135						140					
Asn	Ala	Gly	Leu	Leu	Asn	Ala	Leu	Lys	Leu	Ile	Gln	Pro	Leu	Lys	Asp				
				145				150						155					
Lys	Tyr	Pro	Asn	Ile	Ser	Tyr	Ala	Asp	Leu	Phe	Gln	Leu	Ala	Ser	Ala				
				165				170						175					
Thr	Ala	Ile	Glu	Glu	Ala	Gly	Gly	Pro	Asp	Ile	Pro	Met	Lys	Tyr	Gly				
				180				185						190					
Arg	Val	Asp	Val	Val	Ala	Pro	Glu	Gln	Cys	Pro	Glu	Gly	Arg	Leu					
				195				200						205					
Pro	Asp	Ala	Gly	Pro	Pro	Ser	Pro	Ala	Asp	His	Leu	Arg	Asp	Val	Phe				
				210				215						220					
Tyr	Arg	Met	Gly	Leu	Asp	Asp	Lys	Glu	Ile	Val	Ala	Leu	Ser	Gly	Ala				
				225				230						235					
His	Thr	Leu	Gly	Arg	Ala	Arg	Pro	Asp	Arg	Ser	Gly	Trp	Gly	Lys	Pro				
				245				250						255					

Glu Thr Lys Tyr Thr Lys Thr Gly Pro Gly Glu Ala Gly Gly Gln Ser
260 265 270
Trp Thr Val Lys Trp Leu Lys Phe Asn Ser Tyr Phe Lys Asp Ile
275 280 285
Lys Glu Lys Arg Asp Asp Asp Leu Leu Val Leu Pro Thr Asp Ala Ala
290 295 300
Leu Phe Glu Asp Pro Ser Phe Lys Asn Tyr Ala Glu Lys Tyr Ala Glu
305 310 315 320
Asp Val Ala Ala Phe Phe Lys Asp Tyr Ala Glu Ala His Ala Lys Leu
325 330 335
Ser Asn Leu Gly Ala Lys Phe Asp Pro Glu Gly Ile Val Ile Glu
340 345 350
Asn Val Pro Glu Lys Phe Val Ala Ala Lys Tyr Ser Thr Gly Lys Lys
355 360 365
Glu Leu Ser Asp Ser Met Lys Lys Lys Ile Arg Ala Glu Tyr Glu Ala
370 375 380
Ile Gly Gly Ser Pro Asp Lys Pro Leu Pro Thr Asn Tyr Phe Leu Asn
385 390 395 400
Ile Ile Ile Ala Ile Gly Val Leu Val Leu Ser Thr Leu Phe Gly
405 410 415
Gly Asn Asn Asn Ser Asp Phe Ser Gly Phe
420 425

(2) INFORMATION FOR SEQ ID NO:814:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 354 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..354

(D) OTHER INFORMATION: / Ceres Seq. ID 1499027

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:814:

Met Ile Ser Pro Lys Cys Ala Ala Ser Asp Ala Ala Gln Leu Ile Ser
1 5 10 15
Ala Lys Glu Asp Ile Lys Val Leu Leu Arg Thr Lys Phe Cys His Pro
20 25 30
Ile Leu Val Arg Leu Gly Trp His Asp Ala Gly Thr Tyr Asn Lys Asn
35 40 45
Ile Glu Glu Trp Pro Leu Arg Gly Gly Ala Asn Gly Ser Leu Arg Phe
50 55 60
Glu Ala Glu Leu Lys His Ala Ala Asn Ala Gly Leu Leu Asn Ala Leu
65 70 75 80
Lys Leu Ile Gln Pro Leu Lys Asp Lys Tyr Pro Asn Ile Ser Tyr Ala
85 90 95
Asp Leu Phe Gln Leu Ala Ser Ala Thr Ala Ile Glu Glu Ala Gly Gly
100 105 110
Pro Asp Ile Pro Met Lys Tyr Gly Arg Val Asp Val Val Ala Pro Glu
115 120 125
Gln Cys Pro Glu Glu Gly Arg Leu Pro Asp Ala Gly Pro Pro Ser Pro
130 135 140
Ala Asp His Leu Arg Asp Val Phe Tyr Arg Met Gly Leu Asp Asp Lys
145 150 155 160
Glu Ile Val Ala Leu Ser Gly Ala His Thr Leu Gly Arg Ala Arg Pro
165 170 175
Asp Arg Ser Gly Trp Gly Lys Pro Glu Thr Lys Tyr Thr Lys Thr Gly
180 185 190
Pro Gly Glu Ala Gly Gly Gln Ser Trp Thr Val Lys Trp Leu Lys Phe
195 200 205
Asp Asn Ser Tyr Phe Lys Asp Ile Lys Glu Lys Arg Asp Asp Asp Leu

210 215 220
Leu Val Leu Pro Thr Asp Ala Ala Leu Phe Glu Asp Pro Ser Phe Lys
225 230 235 240
Asn Tyr Ala Glu Lys Tyr Ala Glu Asp Val Ala Ala Phe Phe Lys Asp
245 250 255
Tyr Ala Glu Ala His Ala Lys Leu Ser Asn Leu Gly Ala Lys Phe Asp
260 265 270
Pro Pro Glu Gly Ile Val Ile Glu Asn Val Pro Glu Lys Phe Val Ala
275 280 285
Ala Lys Tyr Ser Thr Gly Lys Lys Glu Leu Ser Asp Ser Met Lys Lys
290 295 300
Lys Ile Arg Ala Glu Tyr Glu Ala Ile Gly Gly Ser Pro Asp Lys Pro
305 310 315 320
Leu Pro Thr Asn Tyr Phe Leu Asn Ile Ile Ile Ala Ile Gly Val Leu
325 330 335
Val Leu Leu Ser Thr Leu Phe Gly Gly Asn Asn Asn Ser Asp Phe Ser
340 345 350
Gly Phe

(2) INFORMATION FOR SEQ ID NO:815:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 631 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..631
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499028

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:815:

aanttcgcgg gatagactcy tcaaggaggat ggatcatgcg aattttctcaa tttatatataca	60
ttcagttacct ggtttcgtgt tcaatgaaga aactacacga tcacagtatt tctataatcg	120
ccaattgaac aatagcatta aggtagtatg gggagaatca agcatgattg aagcagaaag	180
attgttgctt gcatctgctt tataggatca ctccaatcaa agatttggtc ttctctctga	240
cagatgtgct ccattatatg actttggcta tatatacaaa tatcttatct cttcaccgag	300
gagttttgtg gatagttttc ttcatactaa agagacacgg tacagtgtga aaatgtctcc	360
tgtcatacct gaagagaaat ggcgaaaagg atcccagtg atagctttga tcagaagtca	420
tgcagaggtc attgtaaatg atggtatcgt attcccagtt ttttaaggaat tctgcaagag	480
atgtccacct ttaggtacca atgaggcatg gttgtttctt aaacagaagc gacgcaactg	540
catcccgat gaacactatg tgcaaacatt gcttacgatg caaggactag agagtgaat	600
ggaacgaaga acagtgcacat acactgtatg g	

(2) INFORMATION FOR SEQ ID NO:816:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 67 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..67
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499029

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:816:

Xaa Ser Arg Asp Arg Leu Xaa Lys Gly Val Asp His Ala Asn Phe Ser
1 5 10 15
Ile Tyr Ile His Ser Val Pro Gly Phe Val Phe Asn Glu Glu Thr Thr
20 25 30
Arg Ser Gln Tyr Phe Tyr Asn Arg Gln Leu Asn Asn Ser Ile Lys Val
35 40 45
Val Trp Gly Glu Ser Ser Met Ile Glu Ala Glu Arg Leu Leu Leu Ala

50
Ser Ala Leu
65

55

60

(2) INFORMATION FOR SEQ ID NO:817:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 93 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..93
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499030

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:817:

Met	Ser	Pro	Val	Ile	Pro	Glu	Glu	Lys	Trp	Arg	Lys	Gly	Ser	Gln	Trp
1				5					10					15	
Ile	Ala	Leu	Ile	Arg	Ser	His	Ala	Glu	Val	Ile	Val	Asn	Asp	Gly	Ile
				20					25				30		
Val	Phe	Pro	Val	Phe	Lys	Glu	Phe	Cys	Lys	Arg	Cys	Pro	Pro	Leu	Gly
				35					40				45		
Thr	Asn	Glu	Ala	Trp	Leu	Phe	Leu	Lys	Gln	Lys	Arg	Arg	Asn	Cys	Ile
				50					55				60		
Pro	Asp	Glu	His	Tyr	Val	Gln	Thr	Leu	Leu	Thr	Met	Gln	Gly	Leu	Glu
65					70					75				80	
Ser	Glu	Met	Glu	Arg	Thr	Val	Thr	Tyr	Thr	Val	Trp				
				85					90						

(2) INFORMATION FOR SEQ ID NO:818:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 674 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..674
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499031

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:818:

mcccctgctc	grgcgcaggg	attgttgcat	tatgtgccac	cagtactact	tatgatgaca	60
ctgaaatagc	tactaggatt	cttccaaata	tcgttgtgct	aaccattgac	caagacagtg	120
atgttcggtc	aaaggcattt	caggccgtag	aacagtttct	tcagatattg	aaacagaact	180
atgagaagac	aaatgctgga	gaaataggag	ccagcggagg	agcctcagct	atacctgaaa	240
ctgctgggtc	gatcggtatg	gctatgagtt	ctttgacctt	caagggtatg	ccattagaac	300
aagcgcctct	tgcttcttct	tcttcagcac	catccctagc	agctgctgct	tcaaagtcta	360
caagcacagc	aacggaggca	ccgagtgtca	aagccagtca	tcatacacgt	tccaactcgg	420
atttcacaga	tcaacctgca	ccaccatccc	caacatcaac	agatgggttg	ggagatgctg	480
agaatggcat	tagcgaaggt	catgagagtg	acaaagacgg	ttgggatctc	gaaccgctgg	540
atgaacaaaa	accttctcca	gctcttgcta	acattcaagc	agctcaaaaa	cgacctgtgt	600
ctcagtcctc	tagaccttca	gctgcgacaa	gctcaagacc	aaagattagc	acagtgaag	660
cagctgcgaa	aacg					

(2) INFORMATION FOR SEQ ID NO:819:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 224 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..224

(D) OTHER INFORMATION: / Ceres Seq. ID 1499032

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:819:

Pro	Cys	Ser	Xaa	Ala	Gly	Ile	Val	Ala	Leu	Cys	Ala	Thr	Ser	Thr	Thr
1				5					10					15	
Tyr	Asp	Asp	Thr	Glu	Ile	Ala	Thr	Arg	Ile	Leu	Pro	Asn	Ile	Val	Val
			20					25					30		
Leu	Thr	Ile	Asp	Gln	Asp	Ser	Asp	Val	Arg	Ser	Lys	Ala	Phe	Gln	Ala
			35				40					45			
Val	Glu	Gln	Phe	Leu	Gln	Ile	Leu	Lys	Gln	Asn	Tyr	Glu	Lys	Thr	Asn
	50					55				60					
Ala	Gly	Glu	Ile	Gly	Ala	Ser	Gly	Gly	Ala	Ser	Ala	Ile	Pro	Glu	Thr
65					70					75				80	
Ala	Gly	Leu	Ile	Gly	Trp	Ala	Met	Ser	Ser	Leu	Thr	Leu	Lys	Gly	Lys
			85					90						95	
Pro	Leu	Glu	Gln	Ala	Pro	Leu	Ala	Ser	Ser	Ser	Ser	Ala	Pro	Ser	Leu
			100					105					110		
Ala	Ala	Ala	Ala	Ser	Asn	Ala	Thr	Ser	Thr	Ala	Thr	Glu	Ala	Pro	Ser
			115				120					125			
Val	Lys	Ala	Ser	His	His	Thr	Arg	Ser	Asn	Ser	Asp	Phe	Thr	Asp	Gln
	130					135					140				
Pro	Ala	Pro	Pro	Ser	Pro	Thr	Ser	Thr	Asp	Gly	Trp	Gly	Asp	Ala	Glu
145					150					155				160	
Asn	Gly	Ile	Ser	Glu	Gly	His	Glu	Ser	Asp	Lys	Asp	Gly	Trp	Asp	Leu
			165					170						175	
Glu	Pro	Leu	Asp	Glu	Pro	Lys	Pro	Ser	Pro	Ala	Leu	Ala	Asn	Ile	Gln
			180				185						190		
Ala	Ala	Gln	Lys	Arg	Pro	Val	Ser	Gln	Ser	Ser	Arg	Pro	Ser	Ala	Ala
		195				200						205			
Thr	Ser	Ser	Arg	Pro	Lys	Ile	Ser	Thr	Val	Lys	Ala	Ala	Ala	Lys	Thr
	210					215					220				

(2) INFORMATION FOR SEQ ID NO:820:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 137 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..137

(D) OTHER INFORMATION: / Ceres Seq. ID 1499033

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:820:

Met	Ser	Ser	Leu	Thr	Leu	Lys	Gly	Lys	Pro	Leu	Glu	Gln	Ala	Pro	Leu
1			5					10						15	
Ala	Ser	Ser	Ser	Ser	Ala	Pro	Ser	Leu	Ala	Ala	Ala	Ala	Ser	Asn	Ala
			20					25					30		
Thr	Ser	Thr	Ala	Thr	Glu	Ala	Pro	Ser	Val	Lys	Ala	Ser	His	His	Thr
		35				40						45			
Arg	Ser	Asn	Ser	Asp	Phe	Thr	Asp	Gln	Pro	Ala	Pro	Pro	Ser	Pro	Thr
	50				55					60					
Ser	Thr	Asp	Gly	Trp	Gly	Asp	Ala	Glu	Asn	Gly	Ile	Ser	Glu	Gly	His
65					70					75				80	
Glu	Ser	Asp	Lys	Asp	Gly	Trp	Asp	Leu	Glu	Pro	Leu	Asp	Glu	Pro	Lys
			85					90					95		
Pro	Ser	Pro	Ala	Leu	Ala	Asn	Ile	Gln	Ala	Ala	Gln	Lys	Arg	Pro	Val
			100					105					110		
Ser	Gln	Ser	Ser	Arg	Pro	Ser	Ala	Ala	Thr	Ser	Ser	Arg	Pro	Lys	Ile
		115				120						125			
Ser	Thr	Val	Lys	Ala	Ala	Ala	Lys	Thr							

130 135
(2) INFORMATION FOR SEQ ID NO:821:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1639 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: DNA (genomic)
 (ix) FEATURE:
 (A) NAME/KEY: -
 (B) LOCATION: 1..1639
 (D) OTHER INFORMATION: / Ceres Seq. ID 1499042
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:821:
accggttttg atctggttgt ttgtcgtcga tatggcgagg atctcgtgtg acttgagatt 60
tcttctcatc ccggcagctt tcatgttcat ctacatccag atgaggcttt tccagacgca 120
atcacagtat gcagatcgcc tcagttccgc tatcgaatct gagaaccatt gcactagtca 180
aatgcgaggc ctcatagatg aagtttagcat caaacagtcg cggattgttg ccctcgaaga 240
tatgaagaac cgccaggacg aagaacttgt gcagcttaag gatctaattc agacgtttga 300
aaaaaaagga atagcaaaac tcactcaagg tggacagatg cctgtggctg ctgtagtggg 360
tatggcctgc agtcgtgcag actatcttga aaggactgtt aaatcagttt taacatatca 420
aactcccgtt gcttcaaaat atcctctatt tatatctcag gatggatctg atcaagctgt 480
caagagcaag tcattgagct ataatcaatt aacacatatg cagcacttgg attttgaacc 540
agtggctact gaaaggcctg gtgaactgac tgcgtactac aagattgcac gtcactacaa 600
gtgggcactg gaccagttgt tttaaaaca caaatttagt cgagtgatta tactagaaga 660
tgatatggaa attgctccag acttctttga ttactttgag gctgcagcta gtctcatgga 720
tagggataaa accattatgg ctgcttcacg atggaatgat aatggacaga agcagtttgt 780
gcatgatccc tatcgctcat accgatcaga ttttttccct ggccttgggt ggatgctcaa 840
gagatcgact tgggatgagt tatcacaaa gtggccaaag gcttactggg atgattggct 900
gagactaaag gaaaaccata aaggccgcca attcattcga ccggaagtct gtagaacata 960
caatttttgt gaacatgggt ctagtttggg acagtttttc agtcagtatc tggaaacctat 1020
aaagctaaac gatgtgacgg ttgactggaa agcaaaggac ctgggatacc tgacagaggg 1080
aaactatacc aagtactttt ctggcttagt gagacaagca cgaccaattc aaggttctga 1140
ccttgcttta aaggctcaaa acataaaagga tgatgttcgt atccgggtata aagaccaagt 1200
agagtttgaa cgcattgcag gggaaatttg tatatttgaa gaattggaag atggtgtgcc 1260
tcgaacagca tataaaggag tagtgggtgt tcgaatccag acaacaagac gtgtattcct 1320
ggttgggcca gattctgtaa tgcagcttgg aattcgaaat tcctgatgca aaacatatga 1380
aaggaaaaga agattttgga ccgcatgcag cctccttcta gcagctgtta agttgtattg 1440
ttatttatgg atgagtttgt agagcgggtg ggtaacttt aacagcaagg aagctctggg 1500
gacctggctg attggcttag aagttatggg aacccttga aagggtcagg gttaaataata 1560
tttcagttgt tttattagt attatcttgt gggttaacta tacgaatgca aatcattcta 1620
tgcagttttt ctgcgtccc
(2) INFORMATION FOR SEQ ID NO:822:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 454 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: peptide
 (ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..454
 (D) OTHER INFORMATION: / Ceres Seq. ID 1499043
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:822:
Pro Val Leu Ile Trp Leu Phe Val Val Asp Met Ala Arg Ile Ser Cys
1 5 10 15
Asp Leu Arg Phe Leu Leu Ile Pro Ala Ala Phe Met Phe Ile Tyr Ile
20 25 30
Gln Met Arg Leu Phe Gln Thr Gln Ser Gln Tyr Ala Asp Arg Leu Ser
35 40 45
Ser Ala Ile Glu Ser Glu Asn His Cys Thr Ser Gln Met Arg Gly Leu
50 55 60

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Ile Asp Glu Val Ser Ile Lys Gln Ser Arg Ile Val Ala Leu Glu Asp
65      70      75      80
Met Lys Asn Arg Gln Asp Glu Glu Leu Val Gln Leu Lys Asp Leu Ile
      85      90      95
Gln Thr Phe Glu Lys Lys Gly Ile Ala Lys Leu Thr Gln Gly Gly Gln
      100      105      110
Met Pro Val Ala Ala Val Val Val Met Ala Cys Ser Arg Ala Asp Tyr
      115      120      125
Leu Glu Arg Thr Val Lys Ser Val Leu Thr Tyr Gln Thr Pro Val Ala
      130      135      140
Ser Lys Tyr Pro Leu Phe Ile Ser Gln Asp Gly Ser Asp Gln Ala Val
145      150      155      160
Lys Ser Lys Ser Leu Ser Tyr Asn Gln Leu Thr His Met Gln His Leu
      165      170      175
Asp Phe Glu Pro Val Val Thr Glu Arg Pro Gly Glu Leu Thr Ala Tyr
      180      185      190
Tyr Lys Ile Ala Arg His Tyr Lys Trp Ala Leu Asp Gln Leu Phe Tyr
      195      200      205
Lys His Lys Phe Ser Arg Val Ile Ile Leu Glu Asp Asp Met Glu Ile
210      215      220
Ala Pro Asp Phe Phe Asp Tyr Phe Glu Ala Ala Ala Ser Leu Met Asp
225      230      235      240
Arg Asp Lys Thr Ile Met Ala Ala Ser Ser Trp Asn Asp Asn Gly Gln
      245      250      255
Lys Gln Phe Val His Asp Pro Tyr Ala Leu Tyr Arg Ser Asp Phe Phe
      260      265      270
Pro Gly Leu Gly Trp Met Leu Lys Arg Ser Thr Trp Asp Glu Leu Ser
      275      280      285
Pro Lys Trp Pro Lys Ala Tyr Trp Asp Asp Trp Leu Arg Leu Lys Glu
290      295      300
Asn His Lys Gly Arg Gln Phe Ile Arg Pro Glu Val Cys Arg Thr Tyr
305      310      315      320
Asn Phe Gly Glu His Gly Ser Ser Leu Gly Gln Phe Phe Ser Gln Tyr
      325      330      335
Leu Glu Pro Ile Lys Leu Asn Asp Val Thr Val Asp Trp Lys Ala Lys
      340      345      350
Asp Leu Gly Tyr Leu Thr Glu Gly Asn Tyr Thr Lys Tyr Phe Ser Gly
      355      360      365
Leu Val Arg Gln Ala Arg Pro Ile Gln Gly Ser Asp Leu Val Leu Lys
      370      375      380
Ala Gln Asn Ile Lys Asp Asp Val Arg Ile Arg Tyr Lys Asp Gln Val
385      390      395      400
Glu Phe Glu Arg Ile Ala Gly Glu Phe Gly Ile Phe Glu Glu Trp Lys
      405      410      415
Asp Gly Val Pro Arg Thr Ala Tyr Lys Gly Val Val Val Phe Arg Ile
      420      425      430
Gln Thr Thr Arg Arg Val Phe Leu Val Gly Pro Asp Ser Val Met Gln
      435      440      445
Leu Gly Ile Arg Asn Ser
450

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(2) INFORMATION FOR SEQ ID NO:823:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 444 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..444
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499044

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:823:

Met	Ala	Arg	Ile	Ser	Cys	Asp	Leu	Arg	Phe	Leu	Leu	Ile	Pro	Ala	Ala
1				5					10					15	
Phe	Met	Phe	Ile	Tyr	Ile	Gln	Met	Arg	Leu	Phe	Gln	Thr	Gln	Ser	Gln
			20				25						30		
Tyr	Ala	Asp	Arg	Leu	Ser	Ser	Ala	Ile	Glu	Ser	Glu	Asn	His	Cys	Thr
		35					40					45			
Ser	Gln	Met	Arg	Gly	Leu	Ile	Asp	Glu	Val	Ser	Ile	Lys	Gln	Ser	Arg
	50					55					60				
Ile	Val	Ala	Leu	Glu	Asp	Met	Lys	Asn	Arg	Gln	Asp	Glu	Glu	Leu	Val
65					70					75					80
Gln	Leu	Lys	Asp	Leu	Ile	Gln	Thr	Phe	Glu	Lys	Lys	Gly	Ile	Ala	Lys
			85					90						95	
Leu	Thr	Gln	Gly	Gly	Gln	Met	Pro	Val	Ala	Ala	Val	Val	Val	Met	Ala
			100					105						110	
Cys	Ser	Arg	Ala	Asp	Tyr	Leu	Glu	Arg	Thr	Val	Lys	Ser	Val	Leu	Thr
		115					120					125			
Tyr	Gln	Thr	Pro	Val	Ala	Ser	Lys	Tyr	Pro	Leu	Phe	Ile	Ser	Gln	Asp
	130						135				140				
Gly	Ser	Asp	Gln	Ala	Val	Lys	Ser	Lys	Ser	Leu	Ser	Tyr	Asn	Gln	Leu
145					150					155					160
Thr	His	Met	Gln	His	Leu	Asp	Phe	Glu	Pro	Val	Val	Thr	Glu	Arg	Pro
			165					170						175	
Gly	Glu	Leu	Thr	Ala	Tyr	Tyr	Lys	Ile	Ala	Arg	His	Tyr	Lys	Trp	Ala
			180					185					190		
Leu	Asp	Gln	Leu	Phe	Tyr	Lys	His	Lys	Phe	Ser	Arg	Val	Ile	Ile	Leu
		195					200					205			
Glu	Asp	Asp	Met	Glu	Ile	Ala	Pro	Asp	Phe	Phe	Asp	Tyr	Phe	Glu	Ala
	210					215					220				
Ala	Ala	Ser	Leu	Met	Asp	Arg	Asp	Lys	Thr	Ile	Met	Ala	Ala	Ser	Ser
225					230					235					240
Trp	Asn	Asp	Asn	Gly	Gln	Lys	Gln	Phe	Val	His	Asp	Pro	Tyr	Ala	Leu
			245					250						255	
Tyr	Arg	Ser	Asp	Phe	Phe	Pro	Gly	Leu	Gly	Trp	Met	Leu	Lys	Arg	Ser
		260						265					270		
Thr	Trp	Asp	Glu	Leu	Ser	Pro	Lys	Trp	Pro	Lys	Ala	Tyr	Trp	Asp	Asp
		275					280					285			
Trp	Leu	Arg	Leu	Lys	Glu	Asn	His	Lys	Gly	Arg	Gln	Phe	Ile	Arg	Pro
	290					295					300				
Glu	Val	Cys	Arg	Thr	Tyr	Asn	Phe	Gly	Glu	His	Gly	Ser	Ser	Leu	Gly
305					310					315					320
Gln	Phe	Phe	Ser	Gln	Tyr	Leu	Glu	Pro	Ile	Lys	Leu	Asn	Asp	Val	Thr
			325						330					335	
Val	Asp	Trp	Lys	Ala	Lys	Asp	Leu	Gly	Tyr	Leu	Thr	Glu	Gly	Asn	Tyr
		340						345					350		
Thr	Lys	Tyr	Phe	Ser	Gly	Leu	Val	Arg	Gln	Ala	Arg	Pro	Ile	Gln	Gly
		355					360					365			
Ser	Asp	Leu	Val	Leu	Lys	Ala	Gln	Asn	Ile	Lys	Asp	Asp	Val	Arg	Ile
	370					375					380				
Arg	Tyr	Lys	Asp	Gln	Val	Glu	Phe	Glu	Arg	Ile	Ala	Gly	Glu	Phe	Gly
385					390					395					400
Ile	Phe	Glu	Glu	Trp	Lys	Asp	Gly	Val	Pro	Arg	Thr	Ala	Tyr	Lys	Gly
			405						410					415	
Val	Val	Val	Phe	Arg	Ile	Gln	Thr	Thr	Arg	Arg	Val	Phe	Leu	Val	Gly
			420					425					430		
Pro	Asp	Ser	Val	Met	Gln	Leu	Gly	Ile	Arg	Asn	Ser				
		435					440								

(2) INFORMATION FOR SEQ ID NO:824:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 427 amino acids

(B) TYPE: amino acid

- (C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..427
(D) OTHER INFORMATION: / Ceres Seq. ID 1499045
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:824:

Met	Phe	Ile	Tyr	Ile	Gln	Met	Arg	Leu	Phe	Gln	Thr	Gln	Ser	Gln	Tyr
1				5				10						15	
Ala	Asp	Arg	Leu	Ser	Ser	Ala	Ile	Glu	Ser	Glu	Asn	His	Cys	Thr	Ser
			20					25					30		
Gln	Met	Arg	Gly	Leu	Ile	Asp	Glu	Val	Ser	Ile	Lys	Gln	Ser	Arg	Ile
			35				40					45			
Val	Ala	Leu	Glu	Asp	Met	Lys	Asn	Arg	Gln	Asp	Glu	Glu	Leu	Val	Gln
			50			55				60					
Leu	Lys	Asp	Leu	Ile	Gln	Thr	Phe	Glu	Lys	Lys	Gly	Ile	Ala	Lys	Leu
65					70					75					80
Thr	Gln	Gly	Gly	Gln	Met	Pro	Val	Ala	Ala	Val	Val	Val	Met	Ala	Cys
				85				90						95	
Ser	Arg	Ala	Asp	Tyr	Leu	Glu	Arg	Thr	Val	Lys	Ser	Val	Leu	Thr	Tyr
			100					105					110		
Gln	Thr	Pro	Val	Ala	Ser	Lys	Tyr	Pro	Leu	Phe	Ile	Ser	Gln	Asp	Gly
			115				120					125			
Ser	Asp	Gln	Ala	Val	Lys	Ser	Lys	Ser	Leu	Ser	Tyr	Asn	Gln	Leu	Thr
			130				135				140				
His	Met	Gln	His	Leu	Asp	Phe	Glu	Pro	Val	Val	Thr	Glu	Arg	Pro	Gly
145					150					155					160
Glu	Leu	Thr	Ala	Tyr	Tyr	Lys	Ile	Ala	Arg	His	Tyr	Lys	Trp	Ala	Leu
				165				170						175	
Asp	Gln	Leu	Phe	Tyr	Lys	His	Lys	Phe	Ser	Arg	Val	Ile	Ile	Leu	Glu
			180					185					190		
Asp	Asp	Met	Glu	Ile	Ala	Pro	Asp	Phe	Phe	Asp	Tyr	Phe	Glu	Ala	Ala
			195				200					205			
Ala	Ser	Leu	Met	Asp	Arg	Asp	Lys	Thr	Ile	Met	Ala	Ala	Ser	Ser	Trp
			210				215				220				
Asn	Asp	Asn	Gly	Gln	Lys	Gln	Phe	Val	His	Asp	Pro	Tyr	Ala	Leu	Tyr
225					230					235					240
Arg	Ser	Asp	Phe	Phe	Pro	Gly	Leu	Gly	Trp	Met	Leu	Lys	Arg	Ser	Thr
			245					250						255	
Trp	Asp	Glu	Leu	Ser	Pro	Lys	Trp	Pro	Lys	Ala	Tyr	Trp	Asp	Asp	Trp
			260				265						270		
Leu	Arg	Leu	Lys	Glu	Asn	His	Lys	Gly	Arg	Gln	Phe	Ile	Arg	Pro	Glu
			275				280					285			
Val	Cys	Arg	Thr	Tyr	Asn	Phe	Gly	Glu	His	Gly	Ser	Ser	Leu	Gly	Gln
			290				295				300				
Phe	Phe	Ser	Gln	Tyr	Leu	Glu	Pro	Ile	Lys	Leu	Asn	Asp	Val	Thr	Val
305					310					315					320
Asp	Trp	Lys	Ala	Lys	Asp	Leu	Gly	Tyr	Leu	Thr	Glu	Gly	Asn	Tyr	Thr
			325					330						335	
Lys	Tyr	Phe	Ser	Gly	Leu	Val	Arg	Gln	Ala	Arg	Pro	Ile	Gln	Gly	Ser
			340					345					350		
Asp	Leu	Val	Leu	Lys	Ala	Gln	Asn	Ile	Lys	Asp	Asp	Val	Arg	Ile	Arg
			355				360					365			
Tyr	Lys	Asp	Gln	Val	Glu	Phe	Glu	Arg	Ile	Ala	Gly	Glu	Phe	Gly	Ile
			370			375					380				
Phe	Glu	Glu	Trp	Lys	Asp	Gly	Val	Pro	Arg	Thr	Ala	Tyr	Lys	Gly	Val
385					390					395					400
Val	Val	Phe	Arg	Ile	Gln	Thr	Thr	Arg	Arg	Val	Phe	Leu	Val	Gly	Pro
			405					410						415	
Asp	Ser	Val	Met	Gln	Leu	Gly	Ile	Arg	Asn	Ser					

420

425

(2) INFORMATION FOR SEQ ID NO:825:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1220 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1220
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499046

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:825:

agcgattgtc	cttttttgac	tcacttggtc	ttcttctaaa	gaaagcgaag	tttctttctct	60
ccagaataat	gttgattctc	tgtgttgatg	tcctccatag	gataaatccc	tagacaatcc	120
tcttgatcgc	gcttttcggt	tcgaaaaatt	taaacttttt	aactccggtg	atcgagatgg	180
tacagtcagc	ggtggaagtt	ctattaccgt	cggcgtggga	gattgaggtc	gcgggtggcg	240
cttctgtggt	tttaatcgct	tcctattggc	tattcgctta	cagaggaggc	ggagatgacg	300
atgtcgtcgg	tggtggattt	gatcgggtct	gtctcatgca	gaatctcgat	tccgggtgacg	360
cctttgacaa	agacaagata	ggacacttga	gaggagacac	tcaaactaat	gctgcttata	420
tagtcaaggt	ggaactcttg	gctgctaaga	atctaattgg	tgctaactta	aatggaacat	480
cagatcctta	tgctattggt	aattgtggat	cagaaaagcg	attcagttct	atggtccctg	540
gctcgagaaa	tccaatgtgg	ggtgaagagt	tcaattttcc	cacagatgaa	cttcctgcta	600
agattaatgt	aacaattcat	gattgggata	tcatttgga	aagtactggt	cttggtctcag	660
taactattaa	tgttgaacgt	gaaggccaaa	cgggtccagt	gtggcactca	ttagacagcc	720
cgtctgggca	ggtttgccct	aacattaatg	caatcaaact	acccgtgaat	gctcctaggg	780
ctgtaactgg	atatgctgga	gccggtagaa	gaagggtcac	attggatcag	caaggcccaa	840
caattgtaca	tcaaaagcca	gggcctctgc	agacgatatt	tgatctcctc	ccggatgagg	900
ttgtcgagca	cagttattca	tgtgccctgg	agaggtcatt	cctgtatcat	ggccgaatgt	960
atgtttccgc	gtggcacata	tgtttccact	ccaatgtttt	ctctaagcaa	atgaagggtg	1020
ttgtccctct	cggagatata	gatgagattc	gtagaagtca	acacgcattg	ataaaccag	1080
ctataacaat	catactacgg	atgggtgctg	gtggacatgg	tgttccccct	cttgggactc	1140
ctgatggtag	agtgaggtat	aaatttgcat	cgttttggaa	caggaacct	acactaaaag	1200
cattgcaacg	tgcggtgaat					

(2) INFORMATION FOR SEQ ID NO:826:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 348 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..348
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499047

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:826:

Met	Val	Gln	Ser	Ala	Val	Glu	Val	Leu	Leu	Pro	Ser	Ala	Trp	Glu	Ile	
1				5				10						15		
Glu	Val	Ala	Val	Val	Ala	Ser	Val	Phe	Leu	Ile	Ala	Ser	Tyr	Trp	Leu	
				20				25					30			
Phe	Ala	Tyr	Arg	Gly	Gly	Gly	Asp	Asp	Asp	Val	Val	Gly	Val	Gly	Phe	
				35			40					45				
Asp	Arg	Ser	Arg	Leu	Met	Gln	Asn	Leu	Asp	Ser	Gly	Asp	Ala	Phe	Asp	
				50			55				60					
Lys	Asp	Lys	Ile	Gly	His	Leu	Arg	Gly	Asp	Thr	Gln	Thr	Asn	Ala	Ala	
65					70				75					80		
Tyr	Ile	Val	Lys	Val	Glu	Leu	Leu	Ala	Ala	Lys	Asn	Leu	Ile	Gly	Ala	
				85				90						95		
Asn	Leu	Asn	Gly	Thr	Ser	Asp	Pro	Tyr	Ala	Ile	Val	Asn	Cys	Gly	Ser	
				100				105					110			
Glu	Lys	Arg	Phe	Ser	Ser	Met	Val	Pro	Gly	Ser	Arg	Asn	Pro	Met	Trp	

	115		120		125										
Gly	Glu	Phe	Asn	Phe	Pro	Thr	Asp	Glu	Leu	Pro	Ala	Lys	Ile	Asn	
	130				135					140					
Val	Thr	Ile	His	Asp	Trp	Asp	Ile	Ile	Trp	Lys	Ser	Thr	Val	Leu	Gly
145					150					155					160
Ser	Val	Thr	Ile	Asn	Val	Glu	Arg	Glu	Gly	Gln	Thr	Gly	Pro	Val	Trp
				165						170					175
His	Ser	Leu	Asp	Ser	Pro	Ser	Gly	Gln	Val	Cys	Leu	Asn	Ile	Asn	Ala
			180							185					190
Ile	Lys	Leu	Pro	Val	Asn	Ala	Pro	Arg	Ala	Val	Thr	Gly	Tyr	Ala	Gly
			195							200					205
Ala	Gly	Arg	Arg	Arg	Val	Thr	Leu	Asp	Gln	Gln	Gly	Pro	Thr	Ile	Val
	210									215					220
His	Gln	Lys	Pro	Gly	Pro	Leu	Gln	Thr	Ile	Phe	Asp	Leu	Leu	Pro	Asp
225					230					235					240
Glu	Val	Val	Glu	His	Ser	Tyr	Ser	Cys	Ala	Leu	Glu	Arg	Ser	Phe	Leu
				245						250					255
Tyr	His	Gly	Arg	Met	Tyr	Val	Ser	Ala	Trp	His	Ile	Cys	Phe	His	Ser
			260							265					270
Asn	Val	Phe	Ser	Lys	Gln	Met	Lys	Val	Val	Val	Pro	Leu	Gly	Asp	Ile
			275							280					285
Asp	Glu	Ile	Arg	Arg	Ser	Gln	His	Ala	Leu	Ile	Asn	Pro	Ala	Ile	Thr
	290					295					300				
Ile	Ile	Leu	Arg	Met	Gly	Ala	Gly	Gly	His	Gly	Val	Pro	Pro	Leu	Gly
305					310					315					320
Thr	Pro	Asp	Gly	Arg	Val	Arg	Tyr	Lys	Phe	Ala	Ser	Phe	Trp	Asn	Arg
				325						330					335
Asn	His	Thr	Leu	Lys	Ala	Leu	Gln	Arg	Ala	Val	Asn				
			340							345					

(2) INFORMATION FOR SEQ ID NO:827:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 295 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..295

(D) OTHER INFORMATION: / Ceres Seq. ID 1499048

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:827:

Met	Gln	Asn	Leu	Asp	Ser	Gly	Asp	Ala	Phe	Asp	Lys	Asp	Lys	Ile	Gly
1			5				10							15	
His	Leu	Arg	Gly	Asp	Thr	Gln	Thr	Asn	Ala	Ala	Tyr	Ile	Val	Lys	Val
			20				25						30		
Glu	Leu	Leu	Ala	Ala	Lys	Asn	Leu	Ile	Gly	Ala	Asn	Leu	Asn	Gly	Thr
		35				40					45				
Ser	Asp	Pro	Tyr	Ala	Ile	Val	Asn	Cys	Gly	Ser	Glu	Lys	Arg	Phe	Ser
	50					55				60					
Ser	Met	Val	Pro	Gly	Ser	Arg	Asn	Pro	Met	Trp	Gly	Glu	Glu	Phe	Asn
65					70					75					80
Phe	Pro	Thr	Asp	Glu	Leu	Pro	Ala	Lys	Ile	Asn	Val	Thr	Ile	His	Asp
			85						90					95	
Trp	Asp	Ile	Ile	Trp	Lys	Ser	Thr	Val	Leu	Gly	Ser	Val	Thr	Ile	Asn
			100					105						110	
Val	Glu	Arg	Gly	Gln	Thr	Gly	Pro	Val	Trp	His	Ser	Leu	Asp	Ser	
		115				120					125				
Pro	Ser	Gly	Gln	Val	Cys	Leu	Asn	Ile	Asn	Ala	Ile	Lys	Leu	Pro	Val
	130					135					140				
Asn	Ala	Pro	Arg	Ala	Val	Thr	Gly	Tyr	Ala	Gly	Ala	Gly	Arg	Arg	Arg
145					150					155					160

Val Thr Leu Asp Gln Gln Gly Pro Thr Ile Val His Gln Lys Pro Gly
165 170 175
Pro Leu Gln Thr Ile Phe Asp Leu Leu Pro Asp Glu Val Val Glu His
180 185 190
Ser Tyr Ser Cys Ala Leu Glu Arg Ser Phe Leu Tyr His Gly Arg Met
195 200 205
Tyr Val Ser Ala Trp His Ile Cys Phe His Ser Asn Val Phe Ser Lys
210 215 220
Gln Met Lys Val Val Val Pro Leu Gly Asp Ile Asp Glu Ile Arg Arg
225 230 235 240
Ser Gln His Ala Leu Ile Asn Pro Ala Ile Thr Ile Ile Leu Arg Met
245 250 255
Gly Ala Gly Gly His Gly Val Pro Pro Leu Gly Thr Pro Asp Gly Arg
260 265 270
Val Arg Tyr Lys Phe Ala Ser Phe Trp Asn Arg Asn His Thr Leu Lys
275 280 285
Ala Leu Gln Arg Ala Val Asn
290 295

(2) INFORMATION FOR SEQ ID NO:828:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 230 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..230

(D) OTHER INFORMATION: / Ceres Seq. ID 1499049

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:828:

Met Val Pro Gly Ser Arg Asn Pro Met Trp Gly Glu Glu Phe Asn Phe
1 5 10 15
Pro Thr Asp Glu Leu Pro Ala Lys Ile Asn Val Thr Ile His Asp Trp
20 25 30
Asp Ile Ile Trp Lys Ser Thr Val Leu Gly Ser Val Thr Ile Asn Val
35 40 45
Glu Arg Glu Gly Gln Thr Gly Pro Val Trp His Ser Leu Asp Ser Pro
50 55 60
Ser Gly Gln Val Cys Leu Asn Ile Asn Ala Ile Lys Leu Pro Val Asn
65 70 75 80
Ala Pro Arg Ala Val Thr Gly Tyr Ala Gly Ala Gly Arg Arg Arg Val
85 90 95
Thr Leu Asp Gln Gln Gly Pro Thr Ile Val His Gln Lys Pro Gly Pro
100 105 110
Leu Gln Thr Ile Phe Asp Leu Leu Pro Asp Glu Val Val Glu His Ser
115 120 125
Tyr Ser Cys Ala Leu Glu Arg Ser Phe Leu Tyr His Gly Arg Met Tyr
130 135 140
Val Ser Ala Trp His Ile Cys Phe His Ser Asn Val Phe Ser Lys Gln
145 150 155 160
Met Lys Val Val Val Pro Leu Gly Asp Ile Asp Glu Ile Arg Arg Ser
165 170 175
Gln His Ala Leu Ile Asn Pro Ala Ile Thr Ile Ile Leu Arg Met Gly
180 185 190
Ala Gly Gly His Gly Val Pro Pro Leu Gly Thr Pro Asp Gly Arg Val
195 200 205
Arg Tyr Lys Phe Ala Ser Phe Trp Asn Arg Asn His Thr Leu Lys Ala
210 215 220
Leu Gln Arg Ala Val Asn
225 230

(2) INFORMATION FOR SEQ ID NO:829:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1226 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1226
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499050

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:829:

gacgagacaa aagatagaga agcaaaagta agctgataag gtttgataca gtagaaaata	60
cactctctta acttcttctt cttcttcttc ttcttctcct atctttgaaa atggcgatga	120
ctccggtcgc gtcacatctt ccagtttcaa cctgcagact ctttcgctgc aatctcctcc	180
ctgatctctt acctaaagcct ctgtttctct cctccccaac acgaaacaga attgcctcgt	240
gccgcttcac tgtacgtgcc tccgcgaatg ctaccgtcga atcccctaac ggtgtccctg	300
cctccacatc agatacggat acggagacgg ataccacctc ctatggccga cagtttttcc	360
ctttggccgc agttgttggc caggaaggca taaaaactgc tcttttactt ggcgcggttg	420
atcgtgaaat cggagggaat gccatttcag gtcgtagagg cactgcaaaa acagtcatgg	480
cgcgagggtc tcatgaaatc ctccctccta ttgaagtgtg tgtaggctca atatcaaatg	540
ctgaccacgc ttgtccagat gagtgggaag atgacttaga tgagcgcata gagtacaatg	600
ctgacaatac cattaagact gagattgtca aatctccttt cattcagatt ccactaggag	660
ttacagaaga cagactcatt gggctctgtt atgttgagga gtctgtgaaa agggggacaa	720
ctgttttcca acctggtctt ttggctgaag cccatagagg agtggtgtat gttgatgaaa	780
taaatctctt agatgaggga attagtaatt tgcttctcaa tgtattgacg gatggtgtta	840
atatagttga aagagaagga atcagcttta ggcacccgtg caaaccactt ttaattgcaa	900
cctataaccc tgaagaaggt gctgttcgag agcatttgct agaccgtgtt gcggttgctt	960
ctgctacatc tggaggtgga ggaggtggtg gtgctcctgc tgcgtagtcg aagaaagaag	1020
agaagaagga agaaaaggaa gaatccgatg atgacatggg tttcagtcta ttcgagtaag	1080
ctggtagtag catgaaaagt ccggttttgt tgtcctcttt taatattgkg accttttgaa	1140
atctatatgt tgttggtgtt tagtttgtat tcatcatct ttttagaca ttgctgaaat	1200
tctcaagagt ttttgacccg aatgcc	

(2) INFORMATION FOR SEQ ID NO:830:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 322 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..322
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499051

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:830:

Met	Ala	Met	Thr	Pro	Val	Ala	Ser	Ser	Ser	Pro	Val	Ser	Thr	Cys	Arg
1				5					10					15	
Leu	Phe	Arg	Cys	Asn	Leu	Leu	Pro	Asp	Leu	Leu	Pro	Lys	Pro	Leu	Phe
			20					25					30		
Leu	Ser	Leu	Pro	Lys	Arg	Asn	Arg	Ile	Ala	Ser	Cys	Arg	Phe	Thr	Val
			35				40					45			
Arg	Ala	Ser	Ala	Asn	Ala	Thr	Val	Glu	Ser	Pro	Asn	Gly	Val	Pro	Ala
			50				55					60			
Ser	Thr	Ser	Asp	Thr	Asp	Thr	Glu	Thr	Asp	Thr	Thr	Ser	Tyr	Gly	Arg
65					70				75					80	
Gln	Phe	Phe	Pro	Leu	Ala	Ala	Val	Val	Gly	Gln	Glu	Gly	Ile	Lys	Thr
			85					90						95	
Ala	Leu	Leu	Leu	Gly	Ala	Val	Asp	Arg	Glu	Ile	Gly	Gly	Ile	Ala	Ile
			100					105					110		
Ser	Gly	Arg	Arg	Gly	Thr	Ala	Lys	Thr	Val	Met	Ala	Arg	Gly	Leu	His
			115				120					125			
Glu	Ile	Leu	Pro	Pro	Ile	Glu	Val	Val	Val	Gly	Ser	Ile	Ser	Asn	Ala

130	135	140
Asp Pro Ala Cys Pro	Asp Glu Trp Glu Asp	Asp Leu Asp Glu Arg Ile
145	150	155
Glu Tyr Asn Ala Asp	Asn Thr Ile Lys Thr	Glu Ile Val Lys Ser Pro
165	170	175
Phe Ile Gln Ile Pro	Leu Gly Val Thr Glu	Asp Arg Leu Ile Gly Ser
180	185	190
Val Asp Val Glu Glu	Ser Val Lys Arg Gly	Thr Thr Val Phe Gln Pro
195	200	205
Gly Leu Leu Ala Glu	Ala His Arg Gly Val	Leu Tyr Val Asp Glu Ile
210	215	220
Asn Leu Leu Asp Glu	Gly Ile Ser Asn Leu	Leu Leu Asn Val Leu Thr
225	230	235
Asp Gly Val Asn Ile	Val Glu Arg Glu Gly	Ile Ser Phe Arg His Pro
245	250	255
Cys Lys Pro Leu Leu	Ile Ala Thr Tyr Asn	Pro Glu Glu Gly Ala Val
260	265	270
Arg Glu His Leu Leu	Asp Arg Val Ala Val	Ala Ser Ala Thr Ser Gly
275	280	285
Gly Gly Gly Gly Gly	Ala Pro Ala Ala Glu	Ser Lys Lys Glu Glu
290	295	300
Lys Lys Glu Glu Lys	Glu Glu Ser Asp Asp	Asp Met Gly Phe Ser Leu
305	310	315
Phe Glu		

(2) INFORMATION FOR SEQ ID NO:831:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 320 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..320

(D) OTHER INFORMATION: / Ceres Seq. ID 1499052

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:831:

Met Thr Pro Val Ala Ser Ser Ser Pro Val Ser Thr Cys Arg Leu Phe	
1 5 10 15	
Arg Cys Asn Leu Leu Pro Asp Leu Leu Pro Lys Pro Leu Phe Leu Ser	
20 25 30	
Leu Pro Lys Arg Asn Arg Ile Ala Ser Cys Arg Phe Thr Val Arg Ala	
35 40 45	
Ser Ala Asn Ala Thr Val Glu Ser Pro Asn Gly Val Pro Ala Ser Thr	
50 55 60	
Ser Asp Thr Asp Thr Glu Thr Asp Thr Thr Ser Tyr Gly Arg Gln Phe	
65 70 75 80	
Phe Pro Leu Ala Ala Val Val Gly Gln Glu Gly Ile Lys Thr Ala Leu	
85 90 95	
Leu Leu Gly Ala Val Asp Arg Glu Ile Gly Gly Ile Ala Ile Ser Gly	
100 105 110	
Arg Arg Gly Thr Ala Lys Thr Val Met Ala Arg Gly Leu His Glu Ile	
115 120 125	
Leu Pro Pro Ile Glu Val Val Val Gly Ser Ile Ser Asn Ala Asp Pro	
130 135 140	
Ala Cys Pro Asp Glu Trp Glu Asp Asp Leu Asp Glu Arg Ile Glu Tyr	
145 150 155 160	
Asn Ala Asp Asn Thr Ile Lys Thr Glu Ile Val Lys Ser Pro Phe Ile	
165 170 175	
Gln Ile Pro Leu Gly Val Thr Glu Asp Arg Leu Ile Gly Ser Val Asp	
180 185 190	

Val	Glu	Glu	Ser	Val	Lys	Arg	Gly	Thr	Thr	Val	Phe	Gln	Pro	Gly	Leu
	195						200					205			
Leu	Ala	Glu	Ala	His	Arg	Gly	Val	Leu	Tyr	Val	Asp	Glu	Ile	Asn	Leu
	210					215					220				
Leu	Asp	Glu	Gly	Ile	Ser	Asn	Leu	Leu	Leu	Asn	Val	Leu	Thr	Asp	Gly
225					230					235					240
Val	Asn	Ile	Val	Glu	Arg	Glu	Gly	Ile	Ser	Phe	Arg	His	Pro	Cys	Lys
				245					250					255	
Pro	Leu	Leu	Ile	Ala	Thr	Tyr	Asn	Pro	Glu	Glu	Gly	Ala	Val	Arg	Glu
			260					265						270	
His	Leu	Leu	Asp	Arg	Val	Ala	Val	Ala	Ser	Ala	Thr	Ser	Gly	Gly	Gly
	275						280					285			
Gly	Gly	Gly	Gly	Ala	Pro	Ala	Ala	Glu	Ser	Lys	Lys	Glu	Glu	Lys	Lys
	290					295					300				
Glu	Glu	Lys	Glu	Glu	Ser	Asp	Asp	Asp	Met	Gly	Phe	Ser	Leu	Phe	Glu
305					310					315					320

(2) INFORMATION FOR SEQ ID NO:832:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 200 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..200

(D) OTHER INFORMATION: / Ceres Seq. ID 1499053

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:832:

Met	Ala	Arg	Gly	Leu	His	Glu	Ile	Leu	Pro	Pro	Ile	Glu	Val	Val	Val
1				5					10					15	
Gly	Ser	Ile	Ser	Asn	Ala	Asp	Pro	Ala	Cys	Pro	Asp	Glu	Trp	Glu	Asp
			20					25					30		
Asp	Leu	Asp	Glu	Arg	Ile	Glu	Tyr	Asn	Ala	Asp	Asn	Thr	Ile	Lys	Thr
		35					40					45			
Glu	Ile	Val	Lys	Ser	Pro	Phe	Ile	Gln	Ile	Pro	Leu	Gly	Val	Thr	Glu
	50					55				60					
Asp	Arg	Leu	Ile	Gly	Ser	Val	Asp	Val	Glu	Glu	Ser	Val	Lys	Arg	Gly
65				70					75					80	
Thr	Thr	Val	Phe	Gln	Pro	Gly	Leu	Leu	Ala	Glu	Ala	His	Arg	Gly	Val
			85					90					95		
Leu	Tyr	Val	Asp	Glu	Ile	Asn	Leu	Leu	Asp	Glu	Gly	Ile	Ser	Asn	Leu
			100				105						110		
Leu	Leu	Asn	Val	Leu	Thr	Asp	Gly	Val	Asn	Ile	Val	Glu	Arg	Glu	Gly
		115					120					125			
Ile	Ser	Phe	Arg	His	Pro	Cys	Lys	Pro	Leu	Leu	Ile	Ala	Thr	Tyr	Asn
130						135					140				
Pro	Glu	Glu	Gly	Ala	Val	Arg	Glu	His	Leu	Leu	Asp	Arg	Val	Ala	Val
145				150						155					160
Ala	Ser	Ala	Thr	Ser	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Ala	Pro	Ala	Ala
				165					170					175	
Glu	Ser	Lys	Lys	Glu	Glu	Lys	Lys	Glu	Lys	Glu	Glu	Ser	Asp	Asp	
		180					185						190		
Asp	Met	Gly	Phe	Ser	Leu	Phe	Glu								
	195						200								

(2) INFORMATION FOR SEQ ID NO:833:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 540 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

- (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
 (A) NAME/KEY: -
 (B) LOCATION: 1..540
(D) OTHER INFORMATION: / Ceres Seq. ID 1499054

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:833:

acatctgtcg ccgcccgtga gaccgccact taaggccgctc tcctccgctc tatccatatc	60
caaaacagct ataaagataa acttccagag cttggtgaag gagcagcaac cctagttttc	120
aatccctaaa gatattagtt ctccagcgag ttgacacaaa acccgattac gtttcatccg	180
gcgactcgct ttgatattcc atggattctc agttgaatcc ttccaagaga cgcaagataa	240
gtgtcaggca cagatgcgtt gcgtgctata agatgttcaa tagacgagaa cacctcgttg	300
agcacatgaa gatttcctac cactcacttc accagcctcg ctgtgggggtt tgcctcaagc	360
actgtaaadc cttcgaatcc gtgagggaac accttaacgt tccagaccat ctttccaaag	420
gaaactgcaa agccattttc actaaacgag gctgtactct ctgtcttcaa atctttgagg	480
aggcctttgc tctcgccgag cataaaaaca agtgtcacct ctccccamct cgtcctcttg	540

(2) INFORMATION FOR SEQ ID NO:834:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..113

(D) OTHER INFORMATION: / Ceres Seq. ID 1499055

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:834:

Met Asp Ser Gln Leu Asn Pro Ser Lys Arg Arg Lys Ile Ser Val Arg	
1 5 10 15	
His Arg Cys Val Ala Cys Tyr Lys Met Phe Asn Arg Arg Glu His Leu	
20 25 30	
Val Glu His Met Lys Ile Ser Tyr His Ser Leu His Gln Pro Arg Cys	
35 40 45	
Gly Val Cys Leu Lys His Cys Lys Ser Phe Glu Ser Val Arg Glu His	
50 55 60	
Leu Asn Val Pro Asp His Leu Ser Lys Gly Asn Cys Lys Ala Ile Phe	
65 70 75 80	
Thr Lys Arg Gly Cys Thr Leu Cys Leu Gln Ile Phe Glu Glu Ala Phe	
85 90 95	
Ala Leu Ala Glu His Lys Asn Lys Cys His Leu Ser Pro Xaa Arg Pro	
100 105 110	
Leu	

(2) INFORMATION FOR SEQ ID NO:835:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 89 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..89

(D) OTHER INFORMATION: / Ceres Seq. ID 1499056

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:835:

Met Phe Asn Arg Arg Glu His Leu Val Glu His Met Lys Ile Ser Tyr	
1 5 10 15	
His Ser Leu His Gln Pro Arg Cys Gly Val Cys Leu Lys His Cys Lys	
20 25 30	

Ser Phe Glu Ser Val Arg Glu His Leu Asn Val Pro Asp His Leu Ser
35 40 45
Lys Gly Asn Cys Lys Ala Ile Phe Thr Lys Arg Gly Cys Thr Leu Cys
50 55 60
Leu Gln Ile Phe Glu Glu Ala Phe Ala Leu Ala Glu His Lys Asn Lys
65 70 75 80
Cys His Leu Ser Pro Xaa Arg Pro Leu
85

(2) INFORMATION FOR SEQ ID NO:836:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 78 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..78
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499057

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:836:

Met Lys Ile Ser Tyr His Ser Leu His Gln Pro Arg Cys Gly Val Cys
1 5 10 15
Leu Lys His Cys Lys Ser Phe Glu Ser Val Arg Glu His Leu Asn Val
20 25 30
Pro Asp His Leu Ser Lys Gly Asn Cys Lys Ala Ile Phe Thr Lys Arg
35 40 45
Gly Cys Thr Leu Cys Leu Gln Ile Phe Glu Glu Ala Phe Ala Leu Ala
50 55 60
Glu His Lys Asn Lys Cys His Leu Ser Pro Xaa Arg Pro Leu
65 70 75

(2) INFORMATION FOR SEQ ID NO:837:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1347 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1347
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499066

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:837:

acaaacccta	agaagcttct	catcttctct	acaaacccta	agaagcttct	catcttctct	60
ttctctcgaa	gattccgatt	tgctcttttg	aaacttccga	tgacgaagaa	actcgatcca	120
ccaacggcac	cttcaagcga	cgaagatgac	gtcagagactt	ccgaagatga	ttcctcttca	180
tctgaagaag	acgaaccaat	caaattccctt	cccgccacaa	ccgcccgtgc	tccgtgctaaa	240
tccaccgccc	tctccgccc	tactccagct	aaatccaccg	ccgtctccgc	cgctgctcct	300
tctaaatcca	ccgcccgtct	cgcccgtgct	gattcagatt	ctgggttcgga	gagtgaacaa	360
gattcggatt	ctgaatcgac	ggatcctccg	aaatctggat	ccggtaaaac	aatcgcttca	420
aagaagaaag	aggatccgtc	gtcgtcgtct	gctacttttag	ctttaccggc	ggtgaaatct	480
ggagcaaaga	gggcagcgag	tgaagctgcg	acgacttcaa	cgaaacgagt	caagaaagat	540
gaagagagtg	taaagaagcc	agcacttttt	caaagactat	ggagtgcga	tgacgaaatc	600
tctatgttac	aaggaatgat	agattatcat	gctgatacag	ggaagtctcc	ttccgcagat	660
actaatgcgt	tttacgagtt	ccagaagaaa	tctatcagct	ttgaggttag	taagagtcaa	720
ttctcggata	aggttaggag	tttaaggaag	aagtaccgtg	ctaaagaagg	aaaggacgaa	780
cctagggttg	tgaaagctca	tgataagaaa	gcttttgtat	tgtcaaagtt	tatttgggga	840
cctaaaggaa	tagctcttga	ttctaattgct	aagtccaacg	gtgtgtcgaa	aaagaatgcg	900
agtaagacga	aggagaagct	tgattctgta	aagcaagact	tggcgtttgt	tgggtgtttct	960
tcaactaatg	gagatgattg	gtttgagaag	tcgtctcttg	ctaggatgat	tgctgggttcg	1020
ggtattgatg	agtattatgt	gaggcagaaa	tggagttcgt	ttactcttga	gactaagaag	1080
attgttgaag	agaagtttca	gttgatgcaa	gctaaagagc	ttgaggctaa	gttgagagaag	1140

aatgtgcggtt tgactgacct tacgtcttac ttcgttgatg cttcgaagaa ctagagctat 1200
tagttactta gatttgcgg ttttttgtat cggaatgcta tgcataatgc tttcttttgt 1260
ttttcggatt taggatttga ttctttctgg tttgtttttt tgggggtgaa agattctcta 1320
ccttataata tttatttttt tattcgt

(2) INFORMATION FOR SEQ ID NO:838:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 397 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..397

(D) OTHER INFORMATION: / Ceres Seq. ID 1499067

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:838:

Thr	Asn	Pro	Lys	Lys	Leu	Leu	Ile	Phe	Leu	Thr	Asn	Pro	Lys	Lys	Leu
1			5						10					15	
Leu	Ile	Phe	Ser	Phe	Ser	Arg	Arg	Phe	Arg	Phe	Ala	Leu	Leu	Lys	Leu
			20					25					30		
Pro	Met	Thr	Lys	Lys	Leu	Asp	Pro	Pro	Thr	Ala	Pro	Ser	Ser	Asp	Glu
			35				40					45			
Asp	Asp	Val	Glu	Thr	Ser	Glu	Asp	Asp	Ser	Ser	Ser	Ser	Glu	Glu	Asp
	50					55				60					
Glu	Pro	Ile	Lys	Ser	Leu	Pro	Ala	Thr	Thr	Ala	Ala	Pro	Ala	Lys	
65					70				75					80	
Ser	Thr	Ala	Val	Ser	Ala	Ala	Thr	Pro	Ala	Lys	Ser	Thr	Ala	Val	Ser
			85					90					95		
Ala	Ala	Ala	Pro	Ser	Lys	Ser	Thr	Ala	Val	Ser	Ala	Ala	Ala	Asp	Ser
			100					105					110		
Asp	Ser	Gly	Ser	Glu	Ser	Glu	Thr	Asp	Ser	Asp	Ser	Glu	Ser	Thr	Asp
	115						120					125			
Pro	Pro	Lys	Ser	Gly	Ser	Gly	Lys	Thr	Ile	Ala	Ser	Lys	Lys	Lys	Glu
	130					135					140				
Asp	Pro	Ser	Ser	Ser	Ser	Ala	Thr	Leu	Ala	Leu	Pro	Ala	Val	Lys	Ser
145					150				155					160	
Gly	Ala	Lys	Arg	Ala	Ala	Ser	Glu	Ala	Ala	Thr	Thr	Ser	Thr	Lys	Arg
			165					170						175	
Val	Lys	Lys	Asp	Glu	Glu	Ser	Val	Lys	Lys	Pro	Ala	Leu	Phe	Gln	Arg
			180					185					190		
Leu	Trp	Ser	Asp	Asp	Asp	Glu	Ile	Ser	Met	Leu	Gln	Gly	Met	Ile	Asp
	195					200					205				
Tyr	His	Ala	Asp	Thr	Gly	Lys	Ser	Pro	Ser	Ala	Asp	Thr	Asn	Ala	Phe
	210				215					220					
Tyr	Glu	Phe	Gln	Lys	Lys	Ser	Ile	Ser	Phe	Glu	Val	Ser	Lys	Ser	Gln
225				230					235					240	
Phe	Ser	Asp	Lys	Val	Arg	Ser	Leu	Arg	Lys	Lys	Tyr	Arg	Ala	Lys	Glu
			245						250					255	
Gly	Lys	Asp	Glu	Pro	Arg	Phe	Val	Lys	Ala	His	Asp	Lys	Lys	Ala	Phe
			260				265						270		
Val	Leu	Ser	Lys	Phe	Ile	Trp	Gly	Pro	Lys	Gly	Ile	Ala	Leu	Asp	Ser
			275				280					285			
Asn	Ala	Lys	Ser	Asn	Gly	Val	Ser	Lys	Lys	Asn	Ala	Ser	Lys	Thr	Lys
	290				295					300					
Glu	Lys	Leu	Asp	Ser	Val	Lys	Gln	Asp	Leu	Ala	Phe	Val	Gly	Val	Ser
305				310					315					320	
Ser	Thr	Asn	Gly	Asp	Asp	Trp	Phe	Glu	Lys	Ser	Ser	Leu	Ala	Arg	Met
			325					330						335	
Ile	Ala	Gly	Ser	Gly	Ile	Asp	Glu	Tyr	Tyr	Val	Arg	Gln	Lys	Trp	Ser
			340				345					350			
Ser	Phe	Thr	Leu	Glu	Thr	Lys	Lys	Ile	Val	Glu	Glu	Lys	Phe	Gln	Leu

355	360	365
Met Gln Ala Lys Glu Leu Glu Ala Lys Leu Glu Lys Asn Val Arg Leu		
370	375	380
Thr Asp Leu Thr Ser Tyr Phe Val Asp Ala Ser Lys Asn		
385	390	395

(2) INFORMATION FOR SEQ ID NO:839:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 364 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..364

(D) OTHER INFORMATION: / Ceres Seq. ID 1499068

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:839:

Met Thr Lys Lys Leu Asp Pro Pro Thr Ala Pro Ser Ser Asp Glu Asp		
1	5	10
Asp Val Glu Thr Ser Glu Asp Asp Ser Ser Ser Ser Glu Glu Asp Glu		
	20	30
Pro Ile Lys Ser Leu Pro Ala Thr Thr Ala Ala Ala Pro Ala Lys Ser		
	35	45
Thr Ala Val Ser Ala Ala Thr Pro Ala Lys Ser Thr Ala Val Ser Ala		
	50	60
Ala Ala Pro Ser Lys Ser Thr Ala Val Ser Ala Ala Asp Ser Asp		
65	70	80
Ser Gly Ser Glu Ser Glu Thr Asp Ser Asp Ser Glu Ser Thr Asp Pro		
	85	95
Pro Lys Ser Gly Ser Gly Lys Thr Ile Ala Ser Lys Lys Lys Glu Asp		
	100	110
Pro Ser Ser Ser Ala Thr Leu Ala Leu Pro Ala Val Lys Ser Gly		
	115	125
Ala Lys Arg Ala Ala Ser Glu Ala Ala Thr Thr Ser Thr Lys Arg Val		
	130	140
Lys Lys Asp Glu Glu Ser Val Lys Lys Pro Ala Leu Phe Gln Arg Leu		
145	150	160
Trp Ser Asp Asp Asp Glu Ile Ser Met Leu Gln Gly Met Ile Asp Tyr		
	165	175
His Ala Asp Thr Gly Lys Ser Pro Ser Ala Asp Thr Asn Ala Phe Tyr		
	180	190
Glu Phe Gln Lys Lys Ser Ile Ser Phe Glu Val Ser Lys Ser Gln Phe		
	195	205
Ser Asp Lys Val Arg Ser Leu Arg Lys Lys Tyr Arg Ala Lys Glu Gly		
	210	220
Lys Asp Glu Pro Arg Phe Val Lys Ala His Asp Lys Lys Ala Phe Val		
225	230	240
Leu Ser Lys Phe Ile Trp Gly Pro Lys Gly Ile Ala Leu Asp Ser Asn		
	245	255
Ala Lys Ser Asn Gly Val Ser Lys Lys Asn Ala Ser Lys Thr Lys Glu		
	260	270
Lys Leu Asp Ser Val Lys Gln Asp Leu Ala Phe Val Gly Val Ser Ser		
	275	285
Thr Asn Gly Asp Asp Trp Phe Glu Lys Ser Ser Leu Ala Arg Met Ile		
	290	300
Ala Gly Ser Gly Ile Asp Glu Tyr Tyr Val Arg Gln Lys Trp Ser Ser		
305	310	320
Phe Thr Leu Glu Thr Lys Lys Ile Val Glu Glu Lys Phe Gln Leu Met		
	325	335
Gln Ala Lys Glu Leu Glu Ala Lys Leu Glu Lys Asn Val Arg Leu Thr		
	340	350

Asp Leu Thr Ser Tyr Phe Val Asp Ala Ser Lys Asn
355 360

(2) INFORMATION FOR SEQ ID NO:840:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1565 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1565
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499073

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:840:

```
atggttccag tcgtctttgt tcccttattg atagaataat caaaaatccg agtcggagac      60
gacgaagacc cgagttccag ctattaacta tgcagatacc atcaagagag catagtttca      120
ttctatttct cttcatatct gcttttgtaa ttggtgctgc gtctgtacct gtacctgatt      180
ctaattgcta cgctctcgac aattcaagtc gtcttgctga ttttagcagc tggatcggtc      240
atccatttga atatgatggc aaggaatttg atttggtggg tagattttgc aaggatgttg      300
aaacaagagg gcaggcggga tatgttgatt ttggacgatt tgacccggtta agctactttg      360
tttctagttc tgaaaatttc gatttcgtgc aagggtttta ccatggcgac ctgtcaaatt      420
gtgaacagag ttatgacaaa cttggacgta cagcacaggt taatattatt tgtgggaact      480
gtagtgatgg acggtgtaaa ggtggacttg gatgcatatg tagtgtcacc caagattcaa      540
ctttagagat tactgtcgac ttggctattc catgtgagaa acctgggtccg cgggtgttta      600
agggatttac agtcggtttg catcctcgct catgggaaat tatctataat gggatgacac      660
agtttgatt  tgataagccc cgtcgtgagt ttagcttcaa gaccgagcag actcatctca      720
ctctctatat gactgcaatt gcttctcttt caacattggg agggaagcct atcatcaagg      780
tttccccaga gaatggtctt gatgttaaga tagctggttc ttccttgact gggaatcatc      840
caacaacttt atcaccgtca acttttagtac tggattggaa ttgtgagaaa tctcggcgaa      900
ctccatatga agtcaatgtc accatcccag tggatgggta tgatcctgtt cagtttttcc      960
ttacaaaact ctgcgaatac aatcaaggta acgaaggagg atcagcgaaa ggatgggcta     1020
tatttgagat tttttcctgc gtattcctcg ttgcatctgc acttttctgc tgtgggggct     1080
ttatttataa aacaagagta gagcgtgtgc gtggaactga tgcattgccg gggatgtcac     1140
ttctatcggt cttactagaa actgtgagt  gaagtggaca aagctactca agaactgaag     1200
acatcaacaa tgcttttgcc aatgaagtct catgggaccg ctcttcgcga tcttctactc     1260
aagcgacaac aacacagaga ccaagtgaag gaacatatgg tgcgatctaa ttttgtcaag     1320
tgcctcacia gaggtacttt ttcaagccat ggtatggcac gcttgatgat tgcgatttct     1380
ggattttgct ttgtatgttt attttctacc ttctagaaag aggtcaaaaa gttaatagct     1440
tcaccgtgag aatgttgttt tcaccagatt catgtgctat gatagaaaaa gacaaagcaa     1500
acaagagttc tttctttgct taggttacaa gaacaagagt atcgttataa agtcaacaaa     1560
gattg
```

(2) INFORMATION FOR SEQ ID NO:841:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 435 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..435
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499074

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:841:

```
Gly Ser Ser Arg Leu Cys Ser Leu Ile Asp Arg Ile Ile Lys Asn Pro
1           5           10           15
Ser Arg Arg Arg Arg Arg Pro Glu Phe Gln Leu Leu Thr Met Gln Ile
20           25           30
Pro Ser Arg Glu His Ser Phe Ile Leu Phe Leu Phe Ile Ser Ala Phe
35           40           45
Val Ile Gly Ala Ala Ser Val Pro Val Pro Asp Ser Asn Cys Tyr Ala
50           55           60
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Leu Asp Asn Ser Ser Arg Leu Val Asp Phe Ser Ser Trp Ile Gly His
65          70          75          80
Pro Phe Glu Tyr Asp Gly Lys Glu Phe Asp Leu Val Val Arg Phe Cys
          85          90          95
Lys Asp Val Glu Thr Arg Gly Gln Ala Gly Tyr Val Asp Phe Gly Arg
          100          105          110
Phe Asp Pro Leu Ser Tyr Phe Val Ser Ser Ser Glu Asn Phe Asp Phe
          115          120          125
Val Gln Gly Phe Tyr His Gly Asp Leu Ser Asn Cys Glu Gln Ser Tyr
          130          135          140
Asp Lys Leu Gly Arg Thr Ala Gln Val Asn Ile Ile Cys Gly Asn Cys
145          150          155          160
Ser Asp Gly Arg Cys Lys Gly Gly Leu Gly Cys Ile Cys Ser Val Thr
          165          170          175
Gln Asp Ser Thr Cys Arg Val Thr Val Asp Leu Ala Ile Pro Cys Glu
          180          185          190
Lys Pro Gly Pro Arg Val Phe Lys Gly Phe Thr Val Gly Leu His Pro
          195          200          205
Arg Ser Trp Glu Ile Ile Tyr Asn Gly Met Thr Gln Phe Gly Phe Asp
          210          215          220
Lys Pro Arg Arg Glu Phe Ser Phe Lys Thr Glu Gln Thr His Leu Thr
225          230          235          240
Leu Tyr Met Thr Ala Ile Ala Ser Leu Ser Thr Leu Val Gly Lys Pro
          245          250          255
Ile Ile Lys Val Ser Pro Glu Asn Gly Leu Asp Val Lys Ile Ala Gly
          260          265          270
Ser Ser Leu Thr Gly Asn His Pro Thr Thr Leu Ser Pro Ser Thr Leu
          275          280          285
Val Leu Asp Trp Asn Cys Glu Lys Ser Arg Arg Thr Pro Tyr Glu Val
          290          295          300
Asn Val Thr Ile Pro Val Asp Gly Tyr Asp Pro Val Gln Phe Phe Leu
305          310          315          320
Thr Lys Leu Cys Glu Tyr Asn Gln Gly Asn Glu Gly Gly Ser Ala Lys
          325          330          335
Gly Trp Ala Ile Phe Gly Val Phe Ser Cys Val Phe Leu Val Ala Ser
          340          345          350
Ala Leu Phe Cys Cys Gly Gly Phe Ile Tyr Lys Thr Arg Val Glu Arg
          355          360          365
Val Arg Gly Thr Asp Ala Leu Pro Gly Met Ser Leu Leu Ser Gly Leu
          370          375          380
Leu Glu Thr Val Ser Gly Ser Gly Gln Ser Tyr Ser Arg Thr Glu Asp
385          390          395          400
Ile Asn Asn Ala Phe Ala Asn Glu Val Ser Trp Asp Arg Ser Ser Ala
          405          410          415
Ser Ser Thr Gln Ala Thr Thr Thr Gln Arg Pro Ser Glu Arg Thr Tyr
          420          425          430
Gly Ala Ile
          435

```

(2) INFORMATION FOR SEQ ID NO:842:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 406 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..406
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499075

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:842:

Met Gln Ile Pro Ser Arg Glu His Ser Phe Ile Leu Phe Leu Phe Ile

1	5	10	15
Ser Ala Phe Val Ile Gly Ala Ala Ser Val Pro Val Pro Asp Ser Asn			
20	25	30	
Cys Tyr Ala Leu Asp Asn Ser Ser Arg Leu Val Asp Phe Ser Ser Trp			
35	40	45	
Ile Gly His Pro Phe Glu Tyr Asp Gly Lys Glu Phe Asp Leu Val Val			
50	55	60	
Arg Phe Cys Lys Asp Val Glu Thr Arg Gly Gln Ala Gly Tyr Val Asp			
65	70	75	80
Phe Gly Arg Phe Asp Pro Leu Ser Tyr Phe Val Ser Ser Ser Glu Asn			
85	90	95	
Phe Asp Phe Val Gln Gly Phe Tyr His Gly Asp Leu Ser Asn Cys Glu			
100	105	110	
Gln Ser Tyr Asp Lys Leu Gly Arg Thr Ala Gln Val Asn Ile Ile Cys			
115	120	125	
Gly Asn Cys Ser Asp Gly Arg Cys Lys Gly Gly Leu Gly Cys Ile Cys			
130	135	140	
Ser Val Thr Gln Asp Ser Thr Cys Arg Val Thr Val Asp Leu Ala Ile			
145	150	155	160
Pro Cys Glu Lys Pro Gly Pro Arg Val Phe Lys Gly Phe Thr Val Gly			
165	170	175	
Leu His Pro Arg Ser Trp Glu Ile Ile Tyr Asn Gly Met Thr Gln Phe			
180	185	190	
Gly Phe Asp Lys Pro Arg Arg Glu Phe Ser Phe Lys Thr Glu Gln Thr			
195	200	205	
His Leu Thr Leu Tyr Met Thr Ala Ile Ala Ser Leu Ser Thr Leu Val			
210	215	220	
Gly Lys Pro Ile Ile Lys Val Ser Pro Glu Asn Gly Leu Asp Val Lys			
225	230	235	240
Ile Ala Gly Ser Ser Leu Thr Gly Asn His Pro Thr Thr Leu Ser Pro			
245	250	255	
Ser Thr Leu Val Leu Asp Trp Asn Cys Glu Lys Ser Arg Arg Thr Pro			
260	265	270	
Tyr Glu Val Asn Val Thr Ile Pro Val Asp Gly Tyr Asp Pro Val Gln			
275	280	285	
Phe Phe Leu Thr Lys Leu Cys Glu Tyr Asn Gln Gly Asn Glu Gly Gly			
290	295	300	
Ser Ala Lys Gly Trp Ala Ile Phe Gly Val Phe Ser Cys Val Phe Leu			
305	310	315	320
Val Ala Ser Ala Leu Phe Cys Cys Gly Gly Phe Ile Tyr Lys Thr Arg			
325	330	335	
Val Glu Arg Val Arg Gly Thr Asp Ala Leu Pro Gly Met Ser Leu Leu			
340	345	350	
Ser Gly Leu Leu Glu Thr Val Ser Gly Ser Gly Gln Ser Tyr Ser Arg			
355	360	365	
Thr Glu Asp Ile Asn Asn Ala Phe Ala Asn Glu Val Ser Trp Asp Arg			
370	375	380	
Ser Ser Ala Ser Ser Thr Gln Ala Thr Thr Thr Gln Arg Pro Ser Glu			
385	390	395	400
Arg Thr Tyr Gly Ala Ile			
405			

(2) INFORMATION FOR SEQ ID NO:843:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 218 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..218

(D) OTHER INFORMATION: / Ceres Seq. ID 1499076

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:843:

Met Thr Gln Phe Gly Phe Asp Lys Pro Arg Arg Glu Phe Ser Phe Lys
1 5 10 15
Thr Glu Gln Thr His Leu Thr Leu Tyr Met Thr Ala Ile Ala Ser Leu
20 25 30
Ser Thr Leu Val Gly Lys Pro Ile Ile Lys Val Ser Pro Glu Asn Gly
35 40 45
Leu Asp Val Lys Ile Ala Gly Ser Ser Leu Thr Gly Asn His Pro Thr
50 55 60
Thr Leu Ser Pro Ser Thr Leu Val Leu Asp Trp Asn Cys Glu Lys Ser
65 70 75 80
Arg Arg Thr Pro Tyr Glu Val Asn Val Thr Ile Pro Val Asp Gly Tyr
85 90 95
Asp Pro Val Gln Phe Phe Leu Thr Lys Leu Cys Glu Tyr Asn Gln Gly
100 105 110
Asn Glu Gly Gly Ser Ala Lys Gly Trp Ala Ile Phe Gly Val Phe Ser
115 120 125
Cys Val Phe Leu Val Ala Ser Ala Leu Phe Cys Cys Gly Gly Phe Ile
130 135 140
Tyr Lys Thr Arg Val Glu Arg Val Arg Gly Thr Asp Ala Leu Pro Gly
145 150 155 160
Met Ser Leu Leu Ser Gly Leu Leu Glu Thr Val Ser Gly Ser Gly Gln
165 170 175
Ser Tyr Ser Arg Thr Glu Asp Ile Asn Asn Ala Phe Ala Asn Glu Val
180 185 190
Ser Trp Asp Arg Ser Ser Ala Ser Ser Thr Gln Ala Thr Thr Thr Gln
195 200 205
Arg Pro Ser Glu Arg Thr Tyr Gly Ala Ile
210 215

(2) INFORMATION FOR SEQ ID NO:844:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1358 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1358

(D) OTHER INFORMATION: / Ceres Seq. ID 1499077

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:844:

agcacaataa tactgtctaa atgcttctct acttttctcat cacttgtctc tcttttctttt 60
tcttttacc aa atctcttttct ctctctccat gggcatctga aaccaaacc ttgtctcct 120
tctacttcat caagaatccc tttatgaaca ccctacatca gaccaaacc gatccagcct 180
ctccggtgat cgaccaaagt tcggttcttg acctccctga gctggctctt gactgcattc 240
ttgaccttct tccacctctt ggactctgca gcatggctag ggttttagtc tccctgaggg 300
agagatgtgt tagtgatcat ctatgggaga aacatttgaa gaccaaagt ggcaaatcc 360
ttggccctgc tgctcacaga gagggaat gctatatctc ctcttccaca tatcatcttg 420
attctcctca tcatcaaaact gggaatcttg gttttgcaa aatcatctct ctgacccgat 480
ctcttttcac cgttttccga gaggataaac aaaggagggg atatgcatct tctctgccac 540
ttgattccag catgagctgc tacctctccc ttgaaacagg tcgttttttg ttcccagctc 600
aagttttaca ccgtgagaat ggacatgtag ggttcatgtt gtcattgctat gatgcggagc 660
tcagctatga tactcacacg gatacgttcc aagccaggta tccaccacat ggtagacgag 720
catctgcgat tgaaggagg gtgacatggg atagaataag agcagctccc attgatgcat 780
cacctcatct tctccatgta tcagattctt taaaagagtt gaaacctgga gatcacatcg 840
aaatccagtg gagaaggaac aaagagttcc catatggatg gtggtatggt cttgttcgcc 900
acttggaaac ctgtgatgga gatcataacc attgccattg ccatcttagt gagacggtag 960
tggttgaatt caaccagtac acagtcggat caaggtggag aagaacgatg atcatgagag 1020
atcataaaga ggaaggtaac gaagaagacg ggttctatgg aggaatccga aagctaaatt 1080
gtaaagaaga gattgcaatg tggaaacgct actggccttg ctccatcttg gaatagcatt 1140

aaagaagctt tgcttaaaca catgggggaaa gatattacac atcactatac tgagagtagg 1200
ttgttaaatt tagacgtcta ttctctttta tccaatgtat ggttgatcgt gaattatttg 1260
ttgggaataa agtctatacg tgaaattatt gtgtcacttc gatttgagaa atattgtgtt 1320
gtatagggaa aacttaatac aattgatttg aatactcc

(2) INFORMATION FOR SEQ ID NO:845:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 371 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..371

(D) OTHER INFORMATION: / Ceres Seq. ID 1499078

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:845:

Met	Leu	Leu	Tyr	Phe	Leu	Ile	Thr	Cys	Leu	Ser	Phe	Phe	Phe	Thr
1			5					10					15	
Lys	Ser	Leu	Ser	Leu	Pro	Pro	Trp	Ala	Ser	Glu	Thr	Lys	Thr	Leu
			20					25				30		
Ser	Phe	Tyr	Phe	Ile	Lys	Asn	Pro	Phe	Met	Asn	Thr	Leu	His	Gln
			35				40					45		
Lys	His	Asp	Pro	Ala	Ser	Pro	Val	Ile	Asp	Gln	Met	Ser	Val	Leu
			50				55				60			
Leu	Pro	Glu	Leu	Ala	Leu	Asp	Cys	Ile	Leu	Asp	Leu	Leu	Pro	Ser
65						70				75				80
Gly	Leu	Cys	Ser	Met	Ala	Arg	Val	Cys	Ser	Ser	Leu	Arg	Glu	Arg
						85				90			95	
Val	Ser	Asp	His	Leu	Trp	Glu	Lys	His	Leu	Lys	Thr	Lys	Trp	Gly
			100					105					110	
Ile	Leu	Gly	Pro	Ala	Ala	His	Arg	Glu	Trp	Gln	Cys	Tyr	Ile	Ser
			115				120					125		
Ser	Thr	Tyr	His	Leu	Asp	Ser	Pro	His	His	Gln	Thr	Gly	Asn	Leu
			130				135				140			
Phe	Ala	Lys	Ile	Ile	Ser	Leu	Ile	Arg	Ser	Leu	Ser	Ser	Val	Phe
145						150				155				160
Glu	Asp	Lys	Gln	Arg	Arg	Gly	Tyr	Ala	Ser	Ser	Leu	Pro	Leu	Asp
						165				170				175
Ser	Met	Ser	Cys	Tyr	Leu	Ser	Leu	Glu	Thr	Gly	Arg	Phe	Trp	Phe
			180					185				190		
Ala	Gln	Val	Tyr	Asn	Arg	Glu	Asn	Gly	His	Val	Gly	Phe	Met	Leu
			195				200					205		
Cys	Tyr	Asp	Ala	Glu	Leu	Ser	Tyr	Asp	Thr	His	Thr	Asp	Thr	Phe
			210				215				220			
Ala	Arg	Tyr	Pro	Pro	His	Gly	Arg	Arg	Ala	Ser	Ala	Ile	Glu	Lys
225						230				235				240
Val	Thr	Trp	Asp	Arg	Ile	Arg	Ala	Ala	Pro	Ile	Asp	Ala	Ser	Pro
						245				250				255
Leu	Leu	His	Val	Ser	Asp	Ser	Leu	Lys	Glu	Leu	Lys	Pro	Gly	Asp
			260					265					270	
Ile	Glu	Ile	Gln	Trp	Arg	Arg	Asn	Lys	Glu	Phe	Pro	Tyr	Gly	Trp
			275				280					285		
Tyr	Gly	Leu	Val	Arg	His	Leu	Glu	Ser	Cys	Asp	Gly	Asp	His	Asn
			290				295				300			
Cys	His	Cys	His	Leu	Ser	Glu	Thr	Val	Val	Leu	Glu	Phe	Asn	Gln
305						310				315				320
Thr	Val	Gly	Ser	Arg	Trp	Arg	Arg	Thr	Met	Ile	Met	Arg	Asp	His
						325				330				335
Glu	Glu	Gly	Asn	Glu	Glu	Asp	Gly	Phe	Tyr	Gly	Gly	Ile	Arg	Lys
			340					345					350	
Asn	Cys	Lys	Glu	Glu	Ile	Ala	Met	Trp	Lys	Arg	His	Trp	Pro	Cys

355 360 365
Ile Leu Glu
370
(2) INFORMATION FOR SEQ ID NO:846:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 330 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: peptide
 (ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..330
 (D) OTHER INFORMATION: / Ceres Seq. ID 1499079
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:846:
Met Asn Thr Leu His Gln Thr Lys His Asp Pro Ala Ser Pro Val Ile
1 5 10 15
Asp Gln Met Ser Val Leu Asp Leu Pro Glu Leu Ala Leu Asp Cys Ile
20 25 30
Leu Asp Leu Leu Pro Pro Ser Gly Leu Cys Ser Met Ala Arg Val Cys
35 40 45
Ser Ser Leu Arg Glu Arg Cys Val Ser Asp His Leu Trp Glu Lys His
50 55 60
Leu Lys Thr Lys Trp Gly Lys Ile Leu Gly Pro Ala Ala His Arg Glu
65 70 75 80
Trp Gln Cys Tyr Ile Ser Ser Ser Thr Tyr His Leu Asp Ser Pro His
85 90 95
His Gln Thr Gly Asn Leu Gly Phe Ala Lys Ile Ile Ser Leu Ile Arg
100 105 110
Ser Leu Ser Ser Val Phe Arg Glu Asp Lys Gln Arg Arg Gly Tyr Ala
115 120 125
Ser Ser Leu Pro Leu Asp Ser Ser Met Ser Cys Tyr Leu Ser Leu Glu
130 135 140
Thr Gly Arg Phe Trp Phe Pro Ala Gln Val Tyr Asn Arg Glu Asn Gly
145 150 155 160
His Val Gly Phe Met Leu Ser Cys Tyr Asp Ala Glu Leu Ser Tyr Asp
165 170 175
Thr His Thr Asp Thr Phe Gln Ala Arg Tyr Pro Pro His Gly Arg Arg
180 185 190
Ala Ser Ala Ile Glu Lys Gly Val Thr Trp Asp Arg Ile Arg Ala Ala
195 200 205
Pro Ile Asp Ala Ser Pro His Leu Leu His Val Ser Asp Ser Leu Lys
210 215 220
Glu Leu Lys Pro Gly Asp His Ile Glu Ile Gln Trp Arg Arg Asn Lys
225 230 235 240
Glu Phe Pro Tyr Gly Trp Trp Tyr Gly Leu Val Arg His Leu Glu Ser
245 250 255
Cys Asp Gly Asp His Asn His Cys His Cys His Leu Ser Glu Thr Val
260 265 270
Val Leu Glu Phe Asn Gln Tyr Thr Val Gly Ser Arg Trp Arg Arg Thr
275 280 285
Met Ile Met Arg Asp His Lys Glu Glu Gly Asn Glu Glu Asp Gly Phe
290 295 300
Tyr Gly Gly Ile Arg Lys Leu Asn Cys Lys Glu Glu Ile Ala Met Trp
305 310 315 320
Lys Arg His Trp Pro Cys Ser Ile Leu Glu
325 330

(2) INFORMATION FOR SEQ ID NO:847:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 312 amino acids
 (B) TYPE: amino acid

(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..312
(D) OTHER INFORMATION: / Ceres Seq. ID 1499080
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:847:

Met	Ser	Val	Leu	Asp	Leu	Pro	Glu	Leu	Ala	Leu	Asp	Cys	Ile	Leu	Asp
1			5					10						15	
Leu	Leu	Pro	Pro	Ser	Gly	Leu	Cys	Ser	Met	Ala	Arg	Val	Cys	Ser	Ser
			20					25					30		
Leu	Arg	Glu	Arg	Cys	Val	Ser	Asp	His	Leu	Trp	Glu	Lys	His	Leu	Lys
			35					40					45		
Thr	Lys	Trp	Gly	Lys	Ile	Leu	Gly	Pro	Ala	Ala	His	Arg	Glu	Trp	Gln
			50					55				60			
Cys	Tyr	Ile	Ser	Ser	Ser	Thr	Tyr	His	Leu	Asp	Ser	Pro	His	His	Gln
65					70					75					80
Thr	Gly	Asn	Leu	Gly	Phe	Ala	Lys	Ile	Ile	Ser	Leu	Ile	Arg	Ser	Leu
				85					90					95	
Ser	Ser	Val	Phe	Arg	Glu	Asp	Lys	Gln	Arg	Arg	Gly	Tyr	Ala	Ser	Ser
			100					105					110		
Leu	Pro	Leu	Asp	Ser	Ser	Met	Ser	Cys	Tyr	Leu	Ser	Leu	Glu	Thr	Gly
			115					120					125		
Arg	Phe	Trp	Phe	Pro	Ala	Gln	Val	Tyr	Asn	Arg	Glu	Asn	Gly	His	Val
			130					135				140			
Gly	Phe	Met	Leu	Ser	Cys	Tyr	Asp	Ala	Glu	Leu	Ser	Tyr	Asp	Thr	His
145					150					155					160
Thr	Asp	Thr	Phe	Gln	Ala	Arg	Tyr	Pro	Pro	His	Gly	Arg	Arg	Ala	Ser
				165						170				175	
Ala	Ile	Glu	Lys	Gly	Val	Thr	Trp	Asp	Arg	Ile	Arg	Ala	Ala	Pro	Ile
			180					185					190		
Asp	Ala	Ser	Pro	His	Leu	Leu	His	Val	Ser	Asp	Ser	Leu	Lys	Glu	Leu
			195					200				205			
Lys	Pro	Gly	Asp	His	Ile	Glu	Ile	Gln	Trp	Arg	Arg	Asn	Lys	Glu	Phe
			210					215				220			
Pro	Tyr	Gly	Trp	Trp	Tyr	Gly	Leu	Val	Arg	His	Leu	Glu	Ser	Cys	Asp
225					230					235					240
Gly	Asp	His	Asn	His	Cys	His	Cys	His	Leu	Ser	Glu	Thr	Val	Val	Leu
				245						250				255	
Glu	Phe	Asn	Gln	Tyr	Thr	Val	Gly	Ser	Arg	Trp	Arg	Arg	Thr	Met	Ile
			260					265					270		
Met	Arg	Asp	His	Lys	Glu	Glu	Gly	Asn	Glu	Glu	Asp	Gly	Phe	Tyr	Gly
			275					280				285			
Gly	Ile	Arg	Lys	Leu	Asn	Cys	Lys	Glu	Glu	Ile	Ala	Met	Trp	Lys	Arg
			290			295					300				
His	Trp	Pro	Cys	Ser	Ile	Leu	Glu								
305					310										

(2) INFORMATION FOR SEQ ID NO:848:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 470 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
(A) NAME/KEY: -
(B) LOCATION: 1..470
(D) OTHER INFORMATION: / Ceres Seq. ID 1499085
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:848:

aaaacattac tcattcacaa aaccatctta aagcaactac acaaatcttg aaattttctc

atatttttcta ttactatat aaacttttta tcaaatacaag attaactatg gctgaggagt 120
acaagaacaa cgttccccgag cagcagacac caacggtcgc aacagaggaa tcaccagcga 180
cgacaacaga ggttacggat cgtggattgt ttgatttctt ggggaagaag gaagaggaag 240
tgaaacctca agagacaacg acgctcgagt ctgagtgtcg atcataaggc tcagatctct 300
gaaccggagt tagctgcgga sacgaggaag taaaggagaa caagattact ctgctagagg 360
agcttcaaga aaagaccgag gaagatgagg agaacaagcc tagtgctcgc gaaaagcttc 420
accgatccaa cagctcttct tccctcttcg agcgatgaag aagagctgtt

(2) INFORMATION FOR SEQ ID NO:849:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 94 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..94
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499086

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:849:

Asn Ile Thr His Ser Gln Asn His Leu Lys Ala Thr Thr Gln Ile Leu
1 5 10 15
Lys Phe Ser His Ile Phe Tyr Leu Leu Tyr Lys Leu Leu Ile Lys Ser
20 25 30
Arg Leu Thr Met Ala Glu Glu Tyr Lys Asn Asn Val Pro Glu His Glu
35 40 45
Thr Pro Thr Val Ala Thr Glu Glu Ser Pro Ala Thr Thr Thr Glu Val
50 55 60
Thr Asp Arg Gly Leu Phe Asp Phe Leu Gly Lys Lys Glu Glu Glu Val
65 70 75 80
Lys Pro Gln Glu Thr Thr Thr Leu Glu Ser Glu Cys Arg Ser
85 90

(2) INFORMATION FOR SEQ ID NO:850:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 59 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..59
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499087

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:850:

Met Ala Glu Glu Tyr Lys Asn Asn Val Pro Glu His Glu Thr Pro Thr
1 5 10 15
Val Ala Thr Glu Glu Ser Pro Ala Thr Thr Thr Glu Val Thr Asp Arg
20 25 30
Gly Leu Phe Asp Phe Leu Gly Lys Lys Glu Glu Glu Val Lys Pro Gln
35 40 45
Glu Thr Thr Thr Leu Glu Ser Glu Cys Arg Ser
50 55

(2) INFORMATION FOR SEQ ID NO:851:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 678 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..678

(D) OTHER INFORMATION: / Ceres Seq. ID 1499088

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:851:

cggkgtgataa aggaaatatt aastccatgc caaacagaag catgccagct tctccttatac	60
ctactccagg ggctctgtta atgggagatg catttaacat gcgtcatcct ttgacgggtg	120
gaggaatgac gggtgcatta gctgacattg ttgtcctgcg taatctcctt agaccgctgc	180
gtgatcttag tgacggcgct agtctctgca aatatcttga atcattttac actctgcgaa	240
agccagtggc agcaacaatc aacacccttg cgaatgctct ttaccaagtt ttctgttcat	300
cagaaaatga agcaagaaac gagatgaggg aagcttgctt cgattatctg ggactcgggg	360
gtatgtgcac aagtggacca gtatctttgc ttctcgggtt gaaccctcga ccattaacac	420
ttgtctgccca ttctcttgcg gttgcgggtt atggagtcac acggttggtta atccattcc	480
cttccccaaa acgaatctgg cttggagcta aattgatctc gggagcatcg gggataatat	540
ttccaataat aaaagcggaa ggagttaggg agatgttttt cccagcaact gtacctgcat	600
actactacaa agctcctaca gttggagaaa ccaaatgttc atagttccaa ataaattctg	660
tcacgagaaa tgccatac	

(2) INFORMATION FOR SEQ ID NO:852:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 213 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..213

(D) OTHER INFORMATION: / Ceres Seq. ID 1499089

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:852:

Xaa	Asp	Lys	Gly	Asn	Ile	Xaa	Ser	Met	Pro	Asn	Arg	Ser	Met	Pro	Ala	
1				5					10					15		
Ser	Pro	Tyr	Pro	Thr	Pro	Gly	Ala	Leu	Leu	Met	Gly	Asp	Ala	Phe	Asn	
			20					25					30			
Met	Arg	His	Pro	Leu	Thr	Gly	Gly	Met	Thr	Val	Ala	Leu	Ala	Asp		
		35				40					45					
Ile	Val	Val	Leu	Arg	Asn	Leu	Leu	Arg	Pro	Leu	Arg	Asp	Leu	Ser	Asp	
		50				55					60					
Gly	Ala	Ser	Leu	Cys	Lys	Tyr	Leu	Glu	Ser	Phe	Tyr	Thr	Leu	Arg	Lys	
65					70					75				80		
Pro	Val	Ala	Ala	Thr	Ile	Asn	Thr	Leu	Ala	Asn	Ala	Leu	Tyr	Gln	Val	
				85				90					95			
Phe	Cys	Ser	Ser	Glu	Asn	Glu	Ala	Arg	Asn	Glu	Met	Arg	Glu	Ala	Cys	
			100					105					110			
Phe	Asp	Tyr	Leu	Gly	Leu	Gly	Gly	Met	Cys	Thr	Ser	Gly	Pro	Val	Ser	
		115				120						125				
Leu	Leu	Ser	Gly	Leu	Asn	Pro	Arg	Pro	Leu	Thr	Leu	Val	Cys	His	Phe	
		130				135					140					
Phe	Ala	Val	Ala	Val	Tyr	Gly	Val	Ile	Arg	Leu	Leu	Ile	Pro	Phe	Pro	
145					150					155					160	
Ser	Pro	Lys	Arg	Ile	Trp	Leu	Gly	Ala	Lys	Leu	Ile	Ser	Gly	Ala	Ser	
			165						170					175		
Gly	Ile	Ile	Phe	Pro	Ile	Ile	Lys	Ala	Glu	Gly	Val	Arg	Gln	Met	Phe	
		180					185						190			
Phe	Pro	Ala	Thr	Val	Pro	Ala	Tyr	Tyr	Tyr	Lys	Ala	Pro	Thr	Val	Gly	
		195					200						205			
Glu	Thr	Lys	Cys	Ser												
																210

(2) INFORMATION FOR SEQ ID NO:853:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 205 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..205

(D) OTHER INFORMATION: / Ceres Seq. ID 1499090

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:853:

Met	Pro	Asn	Arg	Ser	Met	Pro	Ala	Ser	Pro	Tyr	Pro	Thr	Pro	Gly	Ala
1				5					10					15	
Leu	Leu	Met	Gly	Asp	Ala	Phe	Asn	Met	Arg	His	Pro	Leu	Thr	Gly	Gly
			20					25					30		
Gly	Met	Thr	Val	Ala	Leu	Ala	Asp	Ile	Val	Val	Leu	Arg	Asn	Leu	Leu
		35					40					45			
Arg	Pro	Leu	Arg	Asp	Leu	Ser	Asp	Gly	Ala	Ser	Leu	Cys	Lys	Tyr	Leu
		50				55					60				
Glu	Ser	Phe	Tyr	Thr	Leu	Arg	Lys	Pro	Val	Ala	Ala	Thr	Ile	Asn	Thr
65					70					75					80
Leu	Ala	Asn	Ala	Leu	Tyr	Gln	Val	Phe	Cys	Ser	Ser	Glu	Asn	Glu	Ala
				85					90					95	
Arg	Asn	Glu	Met	Arg	Glu	Ala	Cys	Phe	Asp	Tyr	Leu	Gly	Leu	Gly	Gly
		100						105					110		
Met	Cys	Thr	Ser	Gly	Pro	Val	Ser	Leu	Leu	Ser	Gly	Leu	Asn	Pro	Arg
		115					120					125			
Pro	Leu	Thr	Leu	Val	Cys	His	Phe	Phe	Ala	Val	Ala	Val	Tyr	Gly	Val
		130				135					140				
Ile	Arg	Leu	Leu	Ile	Pro	Phe	Pro	Ser	Pro	Lys	Arg	Ile	Trp	Leu	Gly
145					150					155					160
Ala	Lys	Leu	Ile	Ser	Gly	Ala	Ser	Gly	Ile	Ile	Phe	Pro	Ile	Ile	Lys
			165					170						175	
Ala	Glu	Gly	Val	Arg	Gln	Met	Phe	Phe	Pro	Ala	Thr	Val	Pro	Ala	Tyr
			180					185					190		
Tyr	Tyr	Lys	Ala	Pro	Thr	Val	Gly	Glu	Thr	Lys	Cys	Ser			
		195				200						205			

(2) INFORMATION FOR SEQ ID NO:854:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 200 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..200

(D) OTHER INFORMATION: / Ceres Seq. ID 1499091

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:854:

Met	Pro	Ala	Ser	Pro	Tyr	Pro	Thr	Pro	Gly	Ala	Leu	Leu	Met	Gly	Asp
1				5					10					15	
Ala	Phe	Asn	Met	Arg	His	Pro	Leu	Thr	Gly	Gly	Gly	Met	Thr	Val	Ala
			20					25					30		
Leu	Ala	Asp	Ile	Val	Val	Leu	Arg	Asn	Leu	Leu	Arg	Pro	Leu	Arg	Asp
		35					40					45			
Leu	Ser	Asp	Gly	Ala	Ser	Leu	Cys	Lys	Tyr	Leu	Glu	Ser	Phe	Tyr	Thr
		50				55					60				
Leu	Arg	Lys	Pro	Val	Ala	Ala	Thr	Ile	Asn	Thr	Leu	Ala	Asn	Ala	Leu
65					70					75					80
Tyr	Gln	Val	Phe	Cys	Ser	Ser	Glu	Asn	Glu	Ala	Arg	Asn	Glu	Met	Arg
			85					90						95	
Glu	Ala	Cys	Phe	Asp	Tyr	Leu	Gly	Leu	Gly	Gly	Met	Cys	Thr	Ser	Gly
		100					105					110			
Pro	Val	Ser	Leu	Leu	Ser	Gly	Leu	Asn	Pro	Arg	Pro	Leu	Thr	Leu	Val
		115					120					125			
Cys	His	Phe	Phe	Ala	Val	Ala	Val	Tyr	Gly	Val	Ile	Arg	Leu	Leu	Ile
		130					135					140			

Pro Phe Pro Ser Pro Lys Arg Ile Trp Leu Gly Ala Lys Leu Ile Ser
145 150 155 160
Gly Ala Ser Gly Ile Phe Pro Ile Ile Lys Ala Glu Gly Val Arg
165 170 175
Gln Met Phe Phe Pro Ala Thr Val Pro Ala Tyr Tyr Tyr Lys Ala Pro
180 185 190
Thr Val Gly Glu Thr Lys Cys Ser
195 200

(2) INFORMATION FOR SEQ ID NO:855:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1146 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1146
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499092

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:855:

aattgcaa	aatggatc	gtcttaag	cttatttc	tcctgttt	gtgtttct	ttgtttct	60
tatcgtct	cggttcgt	ctgatgtc	aaacggcg	gatctcgt	gatacag	gttcaggt	120
ggttggtg	gacgagcc	aggttttg	ctcagagg	gacttttc	tttcaagg	cggtttg	180
gaagttcg	gaagttct	cttccaac	gagcatga	tatagatt	ctcggttg	gagttg	240
tccgtaag	gcacttgg	gtagaagt	gctttaag	tcctaaag	gccaaca	gaaggt	300
ctccgatt	ccctaccg	aatctcc	aggatttt	ttggagag	catggcg	cccggt	360
ttactccc	gaaaatca	ggatcttg	gctcttgc	gagtttc	gcccact	ggaggt	420
ctttgga	tgctaact	ctcgctac	gcagactc	cagcctca	gaacaac	gacgag	480
tcgtcgac	tgatcacg	tgatcccc	aggaggca	tttcctgc	ctctggt	gttcgt	540
aatggtgg	taatgaac	cgcttttg	tacaccct	aaaccgg	gctcatga	aaaggt	600
gaagaaga	atccttac	cggaaagg	ggcaagac	gcaagcta	caagtcca	gaaggt	660
atcgttgc	ctgtctcc	cttcagtg	atctccat	atgaaga	gattgct	gcaagt	720
aaccttgt	agaacgg	cttgcgtg	gccatcaa	ctggctat	gcagact	tacagt	780
attggagg	tctcatgc	ttacatgc	accaggag	tcaaccag	tgtcttat	tggttat	840
gttggtat	gagcggca	ttacgctc	gctaggtt	aggagaag	ttactgg	atcggat	900
atcaaga	actcgtgg	gagggg	gaaatggt	tctacaaa	ctgcaaa	ggcggt	960
cgtaacat	ttgtggt	tcagtggt	tcactgtt	cagccacc	ctcaacc	accggt	1020
gcccatta	agcatctc	gtcattta	attacttt	tgatttgt	gagcgag	ctcgtc	1080
tccttgcg	ctgtactc	tctatttc	tctgtctt	gcttgtaa	aaaatgc	gttctt	1140
ctattg							

(2) INFORMATION FOR SEQ ID NO:856:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 246 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..246
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499093

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:856:

Met	Pro	Thr	Arg	Leu	Arg	Phe	Ser	Leu	Pro	Lys	Ile	Ser	Leu	Arg	Ile
1				5					10					15	
Leu	Ile	Gly	Glu	Ile	Met	Ala	Pro	Leu	Pro	Ser	Lys	Ile	Arg	Asp	
			20					25				30			
Leu	Ala	Ala	Leu	Ala	Gly	Val	Ser	Ala	Pro	Leu	Glu	Leu	Trp	Lys	Val
		35					40				45				
Leu	Thr	Ser	Ser	Leu	Pro	Ala	Asp	Ser	Ser	Ala	Ser	Ala	Asn	Asn	Ser
	50					55				60					
Ser	Ser	Thr	Val	Ile	Thr	Ser	Val	Ile	Pro	Arg	Arg	Gln	Ile	Ser	Cys

65		70		75		80									
Asp	Ser	Gly	Cys	Asn	Gly	Gly	Leu	Met	Asn	Ser	Ala	Phe	Glu	Tyr	Thr
				85					90					95	
Leu	Lys	Thr	Gly	Gly	Leu	Met	Lys	Glu	Asp	Tyr	Pro	Tyr	Thr	Gly	
			100					105					110		
Lys	Asp	Gly	Lys	Thr	Cys	Lys	Leu	Asp	Lys	Ser	Lys	Ile	Val	Ala	Ser
		115					120					125			
Val	Ser	Asn	Phe	Ser	Val	Ile	Ser	Ile	Asp	Glu	Glu	Gln	Ile	Ala	Ala
	130					135					140				
Asn	Leu	Val	Lys	Asn	Gly	Pro	Leu	Ala	Val	Ala	Ile	Asn	Ala	Gly	Tyr
145					150					155					160
Met	Gln	Thr	Tyr	Ile	Gly	Gly	Val	Ser	Cys	Pro	Tyr	Ile	Cys	Thr	Arg
				165					170					175	
Arg	Leu	Asn	His	Gly	Val	Leu	Leu	Val	Gly	Tyr	Gly	Ala	Ala	Gly	Tyr
			180					185					190		
Ala	Pro	Ala	Arg	Phe	Lys	Glu	Lys	Pro	Tyr	Trp	Ile	Ile	Lys	Asn	Ser
		195					200					205			
Trp	Gly	Glu	Thr	Trp	Gly	Glu	Asn	Gly	Phe	Tyr	Lys	Ile	Cys	Lys	Gly
	210				215						220				
Arg	Asn	Ile	Cys	Gly	Val	Asp	Ser	Met	Val	Ser	Thr	Val	Ala	Ala	Thr
225					230					235					240
Val	Ser	Thr	Thr	Ala	His										
				245											

(2) INFORMATION FOR SEQ ID NO:857:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 225 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..225

(D) OTHER INFORMATION: / Ceres Seq. ID 1499094

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:857:

Met	Ala	Pro	Leu	Leu	Pro	Ser	Lys	Ile	Arg	Asp	Leu	Ala	Ala	Leu	Ala
1			5					10						15	
Gly	Val	Ser	Ala	Pro	Leu	Glu	Leu	Trp	Lys	Val	Leu	Thr	Ser	Ser	Leu
		20						25				30			
Pro	Ala	Asp	Ser	Ser	Ala	Ser	Ala	Asn	Asn	Ser	Ser	Ser	Thr	Val	Ile
		35					40					45			
Thr	Ser	Val	Ile	Pro	Arg	Arg	Gln	Ile	Ser	Cys	Asp	Ser	Gly	Cys	Asn
	50					55				60					
Gly	Gly	Leu	Met	Asn	Ser	Ala	Phe	Glu	Tyr	Thr	Leu	Lys	Thr	Gly	Gly
65				70				75						80	
Leu	Met	Lys	Glu	Glu	Asp	Tyr	Pro	Tyr	Thr	Gly	Lys	Asp	Gly	Lys	Thr
			85					90					95		
Cys	Lys	Leu	Asp	Lys	Ser	Lys	Ile	Val	Ala	Ser	Val	Ser	Asn	Phe	Ser
		100						105					110		
Val	Ile	Ser	Ile	Asp	Glu	Glu	Gln	Ile	Ala	Ala	Asn	Leu	Val	Lys	Asn
		115					120					125			
Gly	Pro	Leu	Ala	Val	Ala	Ile	Asn	Ala	Gly	Tyr	Met	Gln	Thr	Tyr	Ile
	130					135					140				
Gly	Gly	Val	Ser	Cys	Pro	Tyr	Ile	Cys	Thr	Arg	Leu	Asn	His	Gly	
145					150					155				160	
Val	Leu	Leu	Val	Gly	Tyr	Gly	Ala	Ala	Gly	Tyr	Ala	Pro	Ala	Arg	Phe
			165						170					175	
Lys	Glu	Lys	Pro	Tyr	Trp	Ile	Ile	Lys	Asn	Ser	Trp	Gly	Glu	Thr	Trp
			180					185					190		
Gly	Glu	Asn	Gly	Phe	Tyr	Lys	Ile	Cys	Lys	Gly	Arg	Asn	Ile	Cys	Gly
		195					200						205		

Val Asp Ser Met Val Ser Thr Val Val Ala Ala Thr Val Ser Thr Thr Ala
210 215 220

His
225

(2) INFORMATION FOR SEQ ID NO:858:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 158 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..158
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499095

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:858:

Met Asn Ser Ala Phe Glu Tyr Thr Leu Lys Thr Gly Gly Leu Met Lys
1 5 10 15
Glu Glu Asp Tyr Pro Tyr Thr Gly Lys Asp Gly Lys Thr Cys Lys Leu
20 25 30
Asp Lys Ser Lys Ile Val Ala Ser Val Ser Asn Phe Ser Val Ile Ser
35 40 45
Ile Asp Glu Glu Gln Ile Ala Ala Asn Leu Val Lys Asn Gly Pro Leu
50 55 60
Ala Val Ala Ile Asn Ala Gly Tyr Met Gln Thr Tyr Ile Gly Gly Val
65 70 75 80
Ser Cys Pro Tyr Ile Cys Thr Arg Arg Leu Asn His Gly Val Leu Leu
85 90 95
Val Gly Tyr Gly Ala Ala Gly Tyr Ala Pro Ala Arg Phe Lys Glu Lys
100 105 110
Pro Tyr Trp Ile Ile Lys Asn Ser Trp Gly Glu Thr Trp Gly Glu Asn
115 120 125
Gly Phe Tyr Lys Ile Cys Lys Gly Arg Asn Ile Cys Gly Val Asp Ser
130 135 140
Met Val Ser Thr Val Ala Ala Thr Val Ser Thr Thr Ala His
145 150 155

(2) INFORMATION FOR SEQ ID NO:859:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1854 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1854
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499100

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:859:

aattcacctt cctccgtccc cttcccctaa tccccaaaac acacagataa aaatctctcc 60
ttttttcatc gaagcatata acacaacacc gacaaggaga ttcctttaac tatggcgaag 120
aaagcaagaa ttgttataat cggagctgga atggctggtc tcacggcggc gaacaagctc 180
tacacaagct ccaacaacac cttcgagctc tcagtcgctg aaggcggttc tagaatcggc 240
ggtaggatca atacctctga gttctcatca gagaagattg agatgggtgc cacgtggatc 300
cacggaatcg gtggaagccc tgtttataga atcgctaaag agactggttc tttagtctct 360
gatgagccat gggagtgtat ggattccacc attgataaag ctaagacctt tgctgaaggt 420
gggttcgaga ttgagccttc cattgttgaa tccatctctg gtttgttcac tgctctcatg 480
gaattagctc aggggaaaga gatctctcaa tccgacgccg atttgagtcg tttggctcat 540
atttacgaaa ctgccactag ggtttgctct aagggaagta gtactagtgt tgggtcgttt 600
ttgaaatctg ggtttgatgc ttattgggat tcaatcagca atggaggaga agaaggagtt 660
aaagggtatg ggaaatggag taggaagtca cttgaagaag ccattttttac gatgtttagt 720
aacacacaga ggacttacac atctgctgat gaactctcga cgcttgattt cgcggcggag 780

agtgagtatc	agatgtttcc	aggagaagaa	atcactatag	ctaaaggcta	tcttagtggt	840
attcatcatt	tggcatctgt	gcttcctcaa	ggtgttatcc	aattgaatcg	aaaggtcacg	900
aagatcgagt	ggcagagtaa	tgaagtgaag	ctgcatttct	cagatgggtc	tggtgttttt	960
gcagatcatg	ttattgttac	tgtctcttta	ggtgtgctta	aagcagggat	tgagactgat	1020
gctgaattgt	ttagtcctcc	tttgccctgat	ttcaaactcag	acgctattag	aagactaggc	1080
tatggagttg	tcaacaagct	gttcgtcgag	atgtctcaaa	gaaagttccc	ctctttgcag	1140
cttgtgtttg	accgggagga	ttccgagttt	aggttcgtga	aaattccatg	gtggatgaga	1200
agaaccgcga	ccattacccc	aatccatagc	aattcaaagg	tcttgctttc	ttggtttgca	1260
ggcaaagaag	ctctcgagct	tgagaaactt	accgatgagg	agatcaaaga	cgctgtcatg	1320
accactatct	cttgcttgac	aggcaaggaa	gttaagaatg	ataccgcaa	gcccttgacc	1380
aatggctcat	tgaatgatga	tgatgaagcc	atgaagatta	caaaggtctt	gaagagcaaa	1440
tggggaagtg	atcctctggt	cagaggctcc	tattcgtatg	tagcggttgg	atcaagcggg	1500
gatgacctag	acgcaatggc	tgagccattg	ccaaagatta	ataagaaggt	tggtcaggtc	1560
aatggtcatg	atcaagccaa	ggttcatgag	cttcaagtca	tgtttgacag	ggaagcaaca	1620
catagaaccc	attactccac	aactcatggg	gcctactata	gtggtttaag	ggaagccaat	1680
aggcttctca	agcattacaa	atgtaatttt	tgagtgttaa	tttttaaaat	atgttctggt	1740
tttttttttt	ggggtaatgt	gtttagagaa	gcataattag	ttttgtaaga	ttttttaatt	1800
gtttaacttc	aatttttttt	ttactgtttt	ttactttttc	ttaactacaa	attc	

(2) INFORMATION FOR SEQ ID NO:860:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 533 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..533

(D) OTHER INFORMATION: / Ceres Seq. ID 1499101

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:860:

Met	Ala	Lys	Lys	Ala	Arg	Ile	Val	Ile	Ile	Gly	Ala	Gly	Met	Ala	Gly
1				5						10				15	
Leu	Thr	Ala	Ala	Asn	Lys	Leu	Tyr	Thr	Ser	Ser	Asn	Asn	Thr	Phe	Glu
				20						25				30	
Leu	Ser	Val	Val	Glu	Gly	Gly	Ser	Arg	Ile	Gly	Gly	Arg	Ile	Asn	Thr
				35						40				45	
Ser	Glu	Phe	Ser	Ser	Glu	Lys	Ile	Glu	Met	Gly	Ala	Thr	Trp	Ile	His
				50						55				60	
Gly	Ile	Gly	Gly	Ser	Pro	Val	Tyr	Arg	Ile	Ala	Lys	Glu	Thr	Gly	Ser
65						70				75				80	
Leu	Val	Ser	Asp	Glu	Pro	Trp	Glu	Cys	Met	Asp	Ser	Thr	Ile	Asp	Lys
				85						90				95	
Ala	Lys	Thr	Phe	Ala	Glu	Gly	Gly	Phe	Glu	Ile	Glu	Pro	Ser	Ile	Val
				100						105				110	
Glu	Ser	Ile	Ser	Gly	Leu	Phe	Thr	Ala	Leu	Met	Glu	Leu	Ala	Gln	Gly
				115						120				125	
Lys	Glu	Ile	Ser	Gln	Ser	Asp	Ala	Asp	Leu	Ser	Arg	Leu	Ala	His	Ile
				130						135				140	
Tyr	Glu	Thr	Ala	Thr	Arg	Val	Cys	Ser	Lys	Gly	Ser	Ser	Thr	Ser	Val
145						150				155				160	
Gly	Ser	Phe	Leu	Lys	Ser	Gly	Phe	Asp	Ala	Tyr	Trp	Asp	Ser	Ile	Ser
				165						170				175	
Asn	Gly	Gly	Glu	Glu	Gly	Val	Lys	Gly	Tyr	Gly	Lys	Trp	Ser	Arg	Lys
				180						185				190	
Ser	Leu	Glu	Glu	Ala	Ile	Phe	Thr	Met	Phe	Ser	Asn	Thr	Gln	Arg	Thr
				195						200				205	
Tyr	Thr	Ser	Ala	Asp	Glu	Leu	Ser	Thr	Leu	Asp	Phe	Ala	Ala	Glu	Ser
				210						215				220	
Glu	Tyr	Gln	Met	Phe	Pro	Gly	Glu	Glu	Ile	Thr	Ile	Ala	Lys	Gly	Tyr
225						230				235				240	
Leu	Ser	Val	Ile	His	His	Leu	Ala	Ser	Val	Leu	Pro	Gln	Gly	Val	Ile

Gln	Leu	Asn	Arg	Lys	Val	Thr	Lys	Ile	Glu	Trp	Gln	Ser	Asn	Glu	Val
			260					265					270		
Lys	Leu	His	Phe	Ser	Asp	Gly	Ser	Val	Val	Phe	Ala	Asp	His	Val	Ile
		275					280					285			
Val	Thr	Val	Ser	Leu	Gly	Val	Leu	Lys	Ala	Gly	Ile	Glu	Thr	Asp	Ala
	290					295					300				
Glu	Leu	Phe	Ser	Pro	Pro	Leu	Pro	Asp	Phe	Lys	Ser	Asp	Ala	Ile	Arg
305					310					315					320
Arg	Leu	Gly	Tyr	Gly	Val	Val	Asn	Lys	Leu	Phe	Val	Glu	Met	Ser	Gln
			325						330					335	
Arg	Lys	Phe	Pro	Ser	Leu	Gln	Leu	Val	Phe	Asp	Arg	Glu	Asp	Ser	Glu
			340					345					350		
Phe	Arg	Phe	Val	Lys	Ile	Pro	Trp	Trp	Met	Arg	Arg	Thr	Ala	Thr	Ile
	355						360					365			
Thr	Pro	Ile	His	Ser	Asn	Ser	Lys	Val	Leu	Leu	Ser	Trp	Phe	Ala	Gly
	370					375					380				
Lys	Glu	Ala	Leu	Glu	Leu	Glu	Lys	Leu	Thr	Asp	Glu	Glu	Ile	Lys	Asp
385					390					395					400
Ala	Val	Met	Thr	Thr	Ile	Ser	Cys	Leu	Thr	Gly	Lys	Glu	Val	Lys	Asn
			405						410					415	
Asp	Thr	Ala	Lys	Pro	Leu	Thr	Asn	Gly	Ser	Leu	Asn	Asp	Asp	Asp	Glu
		420						425					430		
Ala	Met	Lys	Ile	Thr	Lys	Val	Leu	Lys	Ser	Lys	Trp	Gly	Ser	Asp	Pro
	435					440					445				
Leu	Phe	Arg	Gly	Ser	Tyr	Ser	Tyr	Val	Ala	Val	Gly	Ser	Ser	Gly	Asp
	450					455					460				
Asp	Leu	Asp	Ala	Met	Ala	Glu	Pro	Leu	Pro	Lys	Ile	Asn	Lys	Lys	Val
465					470					475					480
Gly	Gln	Val	Asn	Gly	His	Asp	Gln	Ala	Lys	Val	His	Glu	Leu	Gln	Val
			485						490					495	
Met	Phe	Ala	Gly	Glu	Ala	Thr	His	Arg	Thr	His	Tyr	Ser	Thr	Thr	His
		500						505					510		
Gly	Ala	Tyr	Tyr	Ser	Gly	Leu	Arg	Glu	Ala	Asn	Arg	Leu	Leu	Lys	His
		515				520						525			
Tyr	Lys	Cys	Asn	Phe											
	530														

(2) INFORMATION FOR SEQ ID NO:861:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 520 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..520
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499102

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:861:

Met	Ala	Gly	Leu	Thr	Ala	Ala	Asn	Lys	Leu	Tyr	Thr	Ser	Ser	Asn	Asn
1			5						10					15	
Thr	Phe	Glu	Leu	Ser	Val	Val	Glu	Gly	Gly	Ser	Arg	Ile	Gly	Gly	Arg
			20					25					30		
Ile	Asn	Thr	Ser	Glu	Phe	Ser	Ser	Glu	Lys	Ile	Glu	Met	Gly	Ala	Thr
		35				40					45				
Trp	Ile	His	Gly	Ile	Gly	Gly	Ser	Pro	Val	Tyr	Arg	Ile	Ala	Lys	Glu
	50					55				60					
Thr	Gly	Ser	Leu	Val	Ser	Asp	Glu	Pro	Trp	Glu	Cys	Met	Asp	Ser	Thr
65					70				75					80	
Ile	Asp	Lys	Ala	Lys	Thr	Phe	Ala	Glu	Gly	Gly	Phe	Glu	Ile	Glu	Pro
			85					90						95	

Ser Ile Val Glu Ser Ile Ser Gly Leu Phe Thr Ala Leu Met Glu Leu
100 105 110
Ala Gln Gly Lys Glu Ile Ser Gln Ser Asp Ala Asp Leu Ser Arg Leu
115 120 125
Ala His Ile Tyr Glu Thr Ala Thr Arg Val Cys Ser Lys Gly Ser Ser
130 135 140
Thr Ser Val Gly Ser Phe Leu Lys Ser Gly Phe Asp Ala Tyr Trp Asp
145 150 155 160
Ser Ile Ser Asn Gly Gly Glu Glu Gly Val Lys Gly Tyr Gly Lys Trp
165 170 175
Ser Arg Lys Ser Leu Glu Glu Ala Ile Phe Thr Met Phe Ser Asn Thr
180 185 190
Gln Arg Thr Tyr Thr Ser Ala Asp Glu Leu Ser Thr Leu Asp Phe Ala
195 200 205
Ala Glu Ser Glu Tyr Gln Met Phe Pro Gly Glu Glu Ile Thr Ile Ala
210 215 220
Lys Gly Tyr Leu Ser Val Ile His His Leu Ala Ser Val Leu Pro Gln
225 230 235 240
Gly Val Ile Gln Leu Asn Arg Lys Val Thr Lys Ile Glu Trp Gln Ser
245 250 255
Asn Glu Val Lys Leu His Phe Ser Asp Gly Ser Val Val Phe Ala Asp
260 265 270
His Val Ile Val Thr Val Ser Leu Gly Val Leu Lys Ala Gly Ile Glu
275 280 285
Thr Asp Ala Glu Leu Phe Ser Pro Pro Leu Pro Asp Phe Lys Ser Asp
290 295 300
Ala Ile Arg Arg Leu Gly Tyr Gly Val Val Asn Lys Leu Phe Val Glu
305 310 315 320
Met Ser Gln Arg Lys Phe Pro Ser Leu Gln Leu Val Phe Asp Arg Glu
325 330 335
Asp Ser Glu Phe Arg Phe Val Lys Ile Pro Trp Trp Met Arg Arg Thr
340 345 350
Ala Thr Ile Thr Pro Ile His Ser Asn Ser Lys Val Leu Ser Trp
355 360 365
Phe Ala Gly Lys Glu Ala Leu Glu Leu Glu Lys Leu Thr Asp Glu Glu
370 375 380
Ile Lys Asp Ala Val Met Thr Thr Ile Ser Cys Leu Thr Gly Lys Glu
385 390 395 400
Val Lys Asn Asp Thr Ala Lys Pro Leu Thr Asn Gly Ser Leu Asn Asp
405 410 415
Asp Asp Glu Ala Met Lys Ile Thr Lys Val Leu Lys Ser Lys Trp Gly
420 425 430
Ser Asp Pro Leu Phe Arg Gly Ser Tyr Ser Tyr Val Ala Val Gly Ser
435 440 445
Ser Gly Asp Asp Leu Asp Ala Met Ala Glu Pro Leu Pro Lys Ile Asn
450 455 460
Lys Lys Val Gly Gln Val Asn Gly His Asp Gln Ala Lys Val His Glu
465 470 475 480
Leu Gln Val Met Phe Ala Gly Glu Ala Thr His Arg Thr His Tyr Ser
485 490 495
Thr Thr His Gly Ala Tyr Tyr Ser Gly Leu Arg Glu Ala Asn Arg Leu
500 505 510
Leu Lys His Tyr Lys Cys Asn Phe
515 520

(2) INFORMATION FOR SEQ ID NO:862:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 476 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..476

(D) OTHER INFORMATION: / Ceres Seq. ID 1499103

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:862:

Met	Gly	Ala	Thr	Trp	Ile	His	Gly	Ile	Gly	Gly	Ser	Pro	Val	Tyr	Arg
1				5					10					15	
Ile	Ala	Lys	Glu	Thr	Gly	Ser	Leu	Val	Ser	Asp	Glu	Pro	Trp	Glu	Cys
			20					25					30		
Met	Asp	Ser	Thr	Ile	Asp	Lys	Ala	Lys	Thr	Phe	Ala	Glu	Gly	Gly	Phe
		35				40						45			
Glu	Ile	Glu	Pro	Ser	Ile	Val	Glu	Ser	Ile	Ser	Gly	Leu	Phe	Thr	Ala
	50					55					60				
Leu	Met	Glu	Leu	Ala	Gln	Gly	Lys	Glu	Ile	Ser	Gln	Ser	Asp	Ala	Asp
65					70					75				80	
Leu	Ser	Arg	Leu	Ala	His	Ile	Tyr	Glu	Thr	Ala	Thr	Arg	Val	Cys	Ser
				85					90					95	
Lys	Gly	Ser	Ser	Thr	Ser	Val	Gly	Ser	Phe	Leu	Lys	Ser	Gly	Phe	Asp
			100					105					110		
Ala	Tyr	Trp	Asp	Ser	Ile	Ser	Asn	Gly	Gly	Glu	Glu	Gly	Val	Lys	Gly
		115					120					125			
Tyr	Gly	Lys	Trp	Ser	Arg	Lys	Ser	Leu	Glu	Glu	Ala	Ile	Phe	Thr	Met
	130					135					140				
Phe	Ser	Asn	Thr	Gln	Arg	Thr	Tyr	Thr	Ser	Ala	Asp	Glu	Leu	Ser	Thr
145					150					155				160	
Leu	Asp	Phe	Ala	Ala	Glu	Ser	Glu	Tyr	Gln	Met	Phe	Pro	Gly	Glu	Glu
				165					170					175	
Ile	Thr	Ile	Ala	Lys	Gly	Tyr	Leu	Ser	Val	Ile	His	His	Leu	Ala	Ser
			180					185					190		
Val	Leu	Pro	Gln	Gly	Val	Ile	Gln	Leu	Asn	Arg	Lys	Val	Thr	Lys	Ile
		195					200					205			
Glu	Trp	Gln	Ser	Asn	Glu	Val	Lys	Leu	His	Phe	Ser	Asp	Gly	Ser	Val
	210					215					220				
Val	Phe	Ala	Asp	His	Val	Ile	Val	Thr	Val	Ser	Leu	Gly	Val	Leu	Lys
225					230					235				240	
Ala	Gly	Ile	Glu	Thr	Asp	Ala	Glu	Leu	Phe	Ser	Pro	Pro	Leu	Pro	Asp
				245					250					255	
Phe	Lys	Ser	Asp	Ala	Ile	Arg	Arg	Leu	Gly	Tyr	Gly	Val	Val	Asn	Lys
			260					265					270		
Leu	Phe	Val	Glu	Met	Ser	Gln	Arg	Lys	Phe	Pro	Ser	Leu	Gln	Leu	Val
		275					280					285			
Phe	Asp	Arg	Glu	Asp	Ser	Glu	Phe	Arg	Phe	Val	Lys	Ile	Pro	Trp	Trp
	290					295					300				
Met	Arg	Arg	Thr	Ala	Thr	Ile	Thr	Pro	Ile	His	Ser	Asn	Ser	Lys	Val
305					310					315				320	
Leu	Leu	Ser	Trp	Phe	Ala	Gly	Lys	Glu	Ala	Leu	Glu	Leu	Glu	Lys	Leu
				325					330					335	
Thr	Asp	Glu	Glu	Ile	Lys	Asp	Ala	Val	Met	Thr	Thr	Ile	Ser	Cys	Leu
		340						345					350		
Thr	Gly	Lys	Glu	Val	Lys	Asn	Asp	Thr	Ala	Lys	Pro	Leu	Thr	Asn	Gly
		355					360					365			
Ser	Leu	Asn	Asp	Asp	Asp	Glu	Ala	Met	Lys	Ile	Thr	Lys	Val	Leu	Lys
	370					375					380				
Ser	Lys	Trp	Gly	Ser	Asp	Pro	Leu	Phe	Arg	Gly	Ser	Tyr	Ser	Tyr	Val
385					390					395				400	
Ala	Val	Gly	Ser	Ser	Gly	Asp	Asp	Leu	Asp	Ala	Met	Ala	Glu	Pro	Leu
				405					410					415	
Pro	Lys	Ile	Asn	Lys	Lys	Val	Gly	Gln	Val	Asn	Gly	His	Asp	Gln	Ala
			420					425					430		
Lys	Val	His	Glu	Leu	Gln	Val	Met	Phe	Ala	Gly	Glu	Ala	Thr	His	Arg
		435					440					445			

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Thr His Tyr Ser Thr Thr His Gly Ala Tyr Tyr Ser Gly Leu Arg Glu
450 455 460
Ala Asn Arg Leu Leu Lys His Tyr Lys Cys Asn Phe
465 470 475

(2) INFORMATION FOR SEQ ID NO:863:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1618 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1618
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499108

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:863:

```
aaatacacagag cagaaacctt taagagaaga tctaataaga aagaagagga aaaaaaagga      60
tggtttttctc agtttccatt tttgcctctc tcgctccgta cttagtctct tcgttactac      120
tcttctttct catcgagcag ctctcttacc tcgtcaagaa acgtaacctc cctggctctc      180
tctttgtccc tccgatcatc ggaaacgcca tttcactcgt ccgtgatcct acttccttct      240
ggttcaagca atccgacacg gcaggcactt cccctggcct cgctgctaac tacctcatcg      300
gcaaattcat catctacatc agagacacag agctttctca tcaaatattc tccaacgttc      360
gtcttgaagc ttttcacct ctaggacatc cttttggcaa acaactattc ggtgatcata      420
gcctaatacta cttgtttggg gaggatcaca aaactgttcg ccgtcacctt gctcctaact      480
tcacccccaa ggcactctcc acttactctg atctccaaca aatagttatg ctccgtcatc      540
tacgacagtg ggaggaaagt ttctccggcg gaactaagcc ggtttctatg cgagaccttg      600
tccgtgaact caatcttgag acttctcaaa cggttttcgt tggacctac cttgacaagg      660
aagctaggaa cacgttctgt actgattaca atctgttcaa tctcggatct atggcgctcc      720
cgatcaacct gcccggttt gcgttcaaca aggctcgccg ggcggtaatg aacctggaga      780
agacgctctc cgtctgtcgc gctctgtcca aaaagaggat ggctacagga gaggagccaa      840
catgcttaat cgatttttgg atgcatgcat tcgtcacgga gatagaatcc ggtaatccac      900
cgccgcttca ctccgaagac gaagccatcg gcggtttgct cttcgatttt ctctttgcgc      960
cacaagacgc gtcgacgtca tcaactcctt gggcggtgac gtttctagaa tctcatccga      1020
aagtgtctgag caaagtgagg gaggaagtgg ccaagatttg gtcacctcag tctggccatc      1080
tgatcacggc cgatcagctc gcggagatga agtatactcg cgctgtggca cgtgaggtgg      1140
tgagatatcg accaccggca actatggctc cacacattgc tactaatgat ttccctctta      1200
cagaatcgta cactatccca aaaggtacaa tagtgtttcc ctcggttttc gacgcctcgt      1260
ttcaagggtt tactgaaccg aaccggttcg atccggaccg gtttagtgag acaaggcaag      1320
aggatcaagt gttcaaacga aactacctag cttttggatg ggggtgcacac caatgcgtag      1380
gccagcgta cgcattgaac cacctcgtgc tcttcacgcg tatgttctca tcgttggttg      1440
atttcaagag acttcaatcg gacggttgcg atgacatcat atactgtccc acgatatcgc      1500
caaaggacgg gtgcacggtg ttcttgtcta agcgcacatg aacgtatccg aacctctgat      1560
ttggattttt gttacaaatt attggtgatc aaagtcaata ctcatgagtg tgattact
```

(2) INFORMATION FOR SEQ ID NO:864:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 499 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..499
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499109

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:864:

Met Val Phe Ser Val Ser Ile Phe Ala Ser Leu Ala Pro Tyr Leu Val
1 5 10 15
Ser Ser Leu Leu Leu Phe Phe Leu Ile Glu Gln Leu Ser Tyr Leu Val
20 25 30
Lys Lys Arg Asn Leu Pro Gly Pro Leu Phe Val Pro Pro Ile Ile Gly
35 40 45

Asn	Ala	Ile	Ser	Leu	Val	Arg	Asp	Pro	Thr	Ser	Phe	Trp	Phe	Lys	Gln
50						55					60				
Ser	Asp	Thr	Ala	Gly	Thr	Ser	Pro	Gly	Leu	Ala	Asn	Tyr	Leu	Ile	
65					70				75					80	
Gly	Lys	Phe	Ile	Ile	Tyr	Ile	Arg	Asp	Thr	Glu	Leu	Ser	His	Gln	Ile
			85						90					95	
Phe	Ser	Asn	Val	Arg	Leu	Glu	Ala	Phe	His	Pro	Leu	Gly	His	Pro	Phe
			100					105					110		
Gly	Lys	Gln	Leu	Phe	Gly	Asp	His	Ser	Leu	Ile	Tyr	Leu	Phe	Gly	Glu
		115					120						125		
Asp	His	Lys	Thr	Val	Arg	Arg	His	Leu	Ala	Pro	Asn	Phe	Thr	Pro	Lys
		130				135					140				
Ala	Leu	Ser	Thr	Tyr	Ser	Asp	Leu	Gln	Gln	Ile	Val	Met	Leu	Arg	His
145					150					155					160
Leu	Arg	Gln	Trp	Glu	Glu	Ser	Phe	Ser	Gly	Gly	Thr	Lys	Pro	Val	Ser
			165						170					175	
Met	Arg	Asp	Leu	Val	Arg	Glu	Leu	Asn	Leu	Glu	Thr	Ser	Gln	Thr	Val
			180					185					190		
Phe	Val	Gly	Pro	Tyr	Leu	Asp	Lys	Glu	Ala	Arg	Asn	Thr	Phe	Cys	Thr
		195					200					205			
Asp	Tyr	Asn	Leu	Phe	Asn	Leu	Gly	Ser	Met	Ala	Leu	Pro	Ile	Asn	Leu
		210				215					220				
Pro	Gly	Phe	Ala	Phe	Asn	Lys	Ala	Arg	Arg	Ala	Val	Met	Asn	Leu	Glu
225					230					235					240
Lys	Thr	Leu	Ser	Val	Cys	Ala	Gly	Lys	Ser	Lys	Lys	Arg	Met	Ala	Thr
			245						250					255	
Gly	Glu	Glu	Pro	Thr	Cys	Leu	Ile	Asp	Phe	Trp	Met	His	Ala	Phe	Val
			260					265					270		
Thr	Glu	Ile	Glu	Ser	Gly	Asn	Pro	Pro	Pro	Leu	His	Ser	Glu	Asp	Glu
		275					280						285		
Ala	Ile	Gly	Gly	Leu	Leu	Phe	Asp	Phe	Leu	Phe	Ala	Ala	Gln	Asp	Ala
		290				295					300				
Ser	Thr	Ser	Ser	Leu	Leu	Trp	Ala	Val	Thr	Phe	Leu	Glu	Ser	His	Pro
305				310						315					320
Lys	Val	Leu	Ser	Lys	Val	Arg	Glu	Glu	Val	Ala	Lys	Ile	Trp	Ser	Pro
			325						330					335	
Gln	Ser	Gly	His	Leu	Ile	Thr	Ala	Asp	Gln	Leu	Ala	Glu	Met	Lys	Tyr
			340					345					350		
Thr	Arg	Ala	Val	Ala	Arg	Glu	Val	Val	Arg	Tyr	Arg	Pro	Pro	Ala	Thr
		355					360						365		
Met	Val	Pro	His	Ile	Ala	Thr	Asn	Asp	Phe	Pro	Leu	Thr	Glu	Ser	Tyr
		370				375					380				
Thr	Ile	Pro	Lys	Gly	Thr	Ile	Val	Phe	Pro	Ser	Val	Phe	Asp	Ala	Ser
385					390					395					400
Phe	Gln	Gly	Phe	Thr	Glu	Pro	Asn	Arg	Phe	Asp	Pro	Asp	Arg	Phe	Ser
			405						410					415	
Glu	Thr	Arg	Gln	Glu	Asp	Gln	Val	Phe	Lys	Arg	Asn	Tyr	Leu	Ala	Phe
			420					425					430		
Gly	Trp	Gly	Ala	His	Gln	Cys	Val	Gly	Gln	Arg	Tyr	Ala	Leu	Asn	His
		435					440					445			
Leu	Val	Leu	Phe	Ile	Ala	Met	Phe	Ser	Ser	Leu	Phe	Asp	Phe	Lys	Arg
		450				455					460				
Leu	Gln	Ser	Asp	Gly	Cys	Asp	Asp	Ile	Ile	Tyr	Cys	Pro	Thr	Ile	Ser
465					470					475					480
Pro	Lys	Asp	Gly	Cys	Thr	Val	Phe	Leu	Ser	Lys	Arg	Ile	Val	Thr	Tyr
			485						490					495	

Pro Asn Leu

(2) INFORMATION FOR SEQ ID NO:865:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 343 amino acids

(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..343
(D) OTHER INFORMATION: / Ceres Seq. ID 1499110
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:865:

Met	Leu	Arg	His	Leu	Arg	Gln	Trp	Glu	Glu	Ser	Phe	Ser	Gly	Gly	Thr
1				5				10					15		
Lys	Pro	Val	Ser	Met	Arg	Asp	Leu	Val	Arg	Glu	Leu	Asn	Leu	Glu	Thr
				20				25					30		
Ser	Gln	Thr	Val	Phe	Val	Gly	Pro	Tyr	Leu	Asp	Lys	Glu	Ala	Arg	Asn
				35				40					45		
Thr	Phe	Cys	Thr	Asp	Tyr	Asn	Leu	Phe	Asn	Leu	Gly	Ser	Met	Ala	Leu
				50				55					60		
Pro	Ile	Asn	Leu	Pro	Gly	Phe	Ala	Phe	Asn	Lys	Ala	Arg	Arg	Ala	Val
65															
Met	Asn	Leu	Glu	Lys	Thr	Leu	Ser	Val	Cys	Ala	Gly	Lys	Ser	Lys	Lys
				85											
Arg	Met	Ala	Thr	Gly	Glu	Glu	Pro	Thr	Cys	Leu	Ile	Asp	Phe	Trp	Met
				100				105							
His	Ala	Phe	Val	Thr	Glu	Ile	Glu	Ser	Gly	Asn	Pro	Pro	Pro	Leu	His
				115				120							
Ser	Glu	Asp	Glu	Ala	Ile	Gly	Gly	Leu	Leu	Phe	Asp	Phe	Leu	Phe	Ala
				130				135							
Ala	Gln	Asp	Ala	Ser	Thr	Ser	Ser	Leu	Leu	Trp	Ala	Val	Thr	Phe	Leu
145															
Glu	Ser	His	Pro	Lys	Val	Leu	Ser	Lys	Val	Arg	Glu	Glu	Val	Ala	Lys
				165											
Ile	Trp	Ser	Pro	Gln	Ser	Gly	His	Leu	Ile	Thr	Ala	Asp	Gln	Leu	Ala
				180				185							
Glu	Met	Lys	Tyr	Thr	Arg	Ala	Val	Ala	Arg	Glu	Val	Val	Arg	Tyr	Arg
				195				200							
Pro	Pro	Ala	Thr	Met	Val	Pro	His	Ile	Ala	Thr	Asn	Asp	Phe	Pro	Leu
				210				215							
Thr	Glu	Ser	Tyr	Thr	Ile	Pro	Lys	Gly	Thr	Ile	Val	Phe	Pro	Ser	Val
225															
Phe	Asp	Ala	Ser	Phe	Gln	Gly	Phe	Thr	Glu	Pro	Asn	Arg	Phe	Asp	Pro
				245											
Asp	Arg	Phe	Ser	Glu	Thr	Arg	Gln	Glu	Asp	Gln	Val	Phe	Lys	Arg	Asn
				260				265							
Tyr	Leu	Ala	Phe	Gly	Trp	Gly	Ala	His	Gln	Cys	Val	Gly	Gln	Arg	Tyr
				275				280							
Ala	Leu	Asn	His	Leu	Val	Leu	Phe	Ile	Ala	Met	Phe	Ser	Ser	Leu	Phe
				290				295							
Asp	Phe	Lys	Arg	Leu	Gln	Ser	Asp	Gly	Cys	Asp	Asp	Ile	Ile	Tyr	Cys
305															
Pro	Thr	Ile	Ser	Pro	Lys	Asp	Gly	Cys	Thr	Val	Phe	Leu	Ser	Lys	Arg
				325											
Ile	Val	Thr	Tyr	Pro	Asn	Leu									
				340											

(2) INFORMATION FOR SEQ ID NO:866:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 323 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:

(A) NAME/KEY: peptide
(B) LOCATION: 1..323
(D) OTHER INFORMATION: / Ceres Seq. ID 1499111

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:866:

Met Arg Asp Leu Val Arg Glu Leu Asn Leu Glu Thr Ser Gln Thr Val
1 5 10 15
Phe Val Gly Pro Tyr Leu Asp Lys Glu Ala Arg Asn Thr Phe Cys Thr
20 25 30
Asp Tyr Asn Leu Phe Asn Leu Gly Ser Met Ala Leu Pro Ile Asn Leu
35 40 45
Pro Gly Phe Ala Phe Asn Lys Ala Arg Arg Ala Val Met Asn Leu Glu
50 55 60
Lys Thr Leu Ser Val Cys Ala Gly Lys Ser Lys Lys Arg Met Ala Thr
65 70 75 80
Gly Glu Glu Pro Thr Cys Leu Ile Asp Phe Trp Met His Ala Phe Val
85 90 95
Thr Glu Ile Glu Ser Gly Asn Pro Pro Leu His Ser Glu Asp Glu
100 105 110
Ala Ile Gly Gly Leu Leu Phe Asp Phe Leu Phe Ala Ala Gln Asp Ala
115 120 125
Ser Thr Ser Ser Leu Leu Trp Ala Val Thr Phe Leu Glu Ser His Pro
130 135 140
Lys Val Leu Ser Lys Val Arg Glu Glu Val Ala Lys Ile Trp Ser Pro
145 150 155 160
Gln Ser Gly His Leu Ile Thr Ala Asp Gln Leu Ala Glu Met Lys Tyr
165 170 175
Thr Arg Ala Val Ala Arg Glu Val Val Arg Tyr Arg Pro Pro Ala Thr
180 185 190
Met Val Pro His Ile Ala Thr Asn Asp Phe Pro Leu Thr Glu Ser Tyr
195 200 205
Thr Ile Pro Lys Gly Thr Ile Val Phe Pro Ser Val Phe Asp Ala Ser
210 215 220
Phe Gln Gly Phe Thr Glu Pro Asn Arg Phe Asp Pro Asp Arg Phe Ser
225 230 235 240
Glu Thr Arg Gln Glu Asp Gln Val Phe Lys Arg Asn Tyr Leu Ala Phe
245 250 255
Gly Trp Gly Ala His Gln Cys Val Gly Gln Arg Tyr Ala Leu Asn His
260 265 270
Leu Val Leu Phe Ile Ala Met Phe Ser Ser Leu Phe Asp Phe Lys Arg
275 280 285
Leu Gln Ser Asp Gly Cys Asp Asp Ile Ile Tyr Cys Pro Thr Ile Ser
290 295 300
Pro Lys Asp Gly Cys Thr Val Phe Leu Ser Lys Arg Ile Val Thr Tyr
305 310 315 320
Pro Asn Leu

(2) INFORMATION FOR SEQ ID NO:867:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1451 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -
(B) LOCATION: 1..1451
(D) OTHER INFORMATION: / Ceres Seq. ID 1499112

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:867:

actcaactta aactctttta gtaacaatgg tttcttcttc tttaaccaag cttgtgttct 60
ttggttgtct cctcctgctc acattcacgg acaaccttgt ggctggaaaa tctggcaaag 120
tgaagctcaa tctttactac gaatcacttt gtcccggttg tcaggaattc atcgctcgatg 180

acctaggtaa aatctttgac tacgatctct acacaatcac tgatctcaag ctgtttccat 240
ttggtaatgc cgaactctcc gataatctga ctgtcacttt tttttttttt ttttttgaga 300
gaaacaaagg caatggatat gaacagacaa gcacaccaca tgagcttggt gattacaaac 360
acaagcttct ttttcgcctt ctgctcaatc acaacaactg aagtctgcac cacaacaaca 420
gctaaggata taaacagtgc caagctgtca aagatgaaga agaccagaaa cggtgctttg 480
tttgctatat gagcttggtc tagcaactct cctttcgacc ggtcctcttc gtactgaccg 540
ggtattgtga agattgctgc gaaagccact gtggcaataa gcaactgccac aacagttgct 600
gagtttatag cgttggttag accactaatg ttagctttct tgagtctttt tgctatcttc 660
tggactctta cacctggttg tctggattgc tgaagctgag attgtacttc atgtttgatg 720
tcgctgactg tttgcttcag ttgcttagct gggttctgag gctttccgag atctttagct 780
gtacgagctc ctgcttcctt cagaactgac acaagctctg cgtttcctat cttctcagag 840
acatcgagtg gcgtatctcc agctttgttt attgggttga ggtttatgcc ttcaaaagat 900
accaaaccac gtactatctt aatacgcccc ttgtttgtgg caataagaac ttggcccgat 960
cagaaatcac aatactcggt catacggtgc gtcgaaagcg atacgaaagg ctgggaatca 1020
tgtgttaaaa actctggacg tgagaaagca atcaatgatt gttacaatgg tgatctttct 1080
agaaagctga tacttgggta cgcaaccaa accaagaatt tgaagccgcc acatgaatac 1140
gtaccatggg tcacactcaa cggcaagcca ctcgatgaca gcgtacaaag tacggatgat 1200
ctcgtagctc aaatctgcaa agcatacaaa ggaaagggtg ctctcccaaa agtttgcaat 1260
tcacccgctt caatgtctaa gtcgcctgag aggaaatgga agcttcaagt ctcttatgcc 1320
ataaaagcta ccaattatta agttaactat caaacttcgt attgaactaa gatggattta 1380
agctttatgt tataagtgga atgatgaata aaggcctggt cttaaactttt atgggttacga 1440
attgatgtat t

(2) INFORMATION FOR SEQ ID NO:868:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 124 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..124

(D) OTHER INFORMATION: / Ceres Seq. ID 1499113

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:868:

Met Val Ser Ser Leu Thr Lys Leu Val Phe Phe Gly Cys Leu Leu
1 5 10 15
Leu Leu Thr Phe Thr Asp Asn Leu Val Ala Gly Lys Ser Gly Lys Val
20 25 30
Lys Leu Asn Leu Tyr Tyr Glu Ser Leu Cys Pro Gly Cys Gln Glu Phe
35 40 45
Ile Val Asp Asp Leu Gly Lys Ile Phe Asp Tyr Asp Leu Tyr Thr Ile
50 55 60
Thr Asp Leu Lys Leu Phe Pro Phe Gly Asn Ala Glu Leu Ser Asp Asn
65 70 75 80
Leu Thr Val Thr Phe Phe Phe Phe Phe Glu Arg Asn Lys Gly Asn
85 90 95
Gly Tyr Glu Gln Thr Ser Thr Pro His Glu Leu Val Asp Tyr Lys His
100 105 110
Lys Leu Leu Phe Arg Leu Leu Leu Asn His Asn Asn
115 120

(2) INFORMATION FOR SEQ ID NO:869:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 151 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..151

(D) OTHER INFORMATION: / Ceres Seq. ID 1499114

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:869:

Met Pro Ser Lys Asp Thr Lys His Arg Thr Ile Leu Ile Arg Pro Leu
1 5 10 15
Phe Val Ala Ile Arg Thr Trp Pro Asp Gln Lys Ser Gln Tyr Ser Phe
20 25 30
Ile Arg Cys Val Glu Ser Asp Thr Lys Gly Trp Glu Ser Cys Val Lys
35 40 45
Asn Ser Gly Arg Glu Lys Ala Ile Asn Asp Cys Tyr Asn Gly Asp Leu
50 55 60
Ser Arg Lys Leu Ile Leu Gly Tyr Ala Thr Lys Thr Lys Asn Leu Lys
65 70 75 80
Pro Pro His Glu Tyr Val Pro Trp Val Thr Leu Asn Gly Lys Pro Leu
85 90 95
Asp Asp Ser Val Gln Ser Thr Asp Asp Leu Val Ala Gln Ile Cys Lys
100 105 110
Ala Tyr Lys Gly Lys Val Ala Leu Pro Lys Val Cys Asn Ser Ser Ala
115 120 125
Ser Met Ser Lys Ser Pro Glu Arg Lys Trp Lys Leu Gln Val Ser Tyr
130 135 140
Ala Asn Lys Ala Thr Asn Tyr
145 150

(2) INFORMATION FOR SEQ ID NO:870:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1905 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1905
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499115

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:870:

acacaaaccg acccgacccg aatctggccg gtgagaaaat ggaggtccaa agcagcagca 60
acaatggtgg tcaactcttct ttctccagtc tccgcgtcta cctcaactct ctttccgcga 120
cgccttctcg cttatcccgc cgcgctatatt ccgtctccac ctcttccgac gagatgagtc 180
gcgtccgcgc cgtctccggc gaacagatgc gccgtactct ccggtggtac gatctcattg 240
gactcggaat cgggggaatg gtcggcgccg gtgtctttgt caccaccggc cgtgctagtc 300
gtctcgacgc cggtccttca attgtcgtct cttacgccat cgcggggctc tgcgtctctc 360
tctccgcttt ctgttacacc gaattcgccg tccatctccc ggtcgccggc ggtgccttca 420
gctacatccg tatcacattc ggtgaatttc cagcattttt caccggagca aatcttgtaa 480
tggtattacgt aatgtcaaac gcggccggtt cgagaagctt caccgcttat ttaggaacag 540
ctttcgggat ctcaacttcc aagtggcgat tcgtcgtctc cggtttaccg aaaggattca 600
acgagattga tccagtcgca gttctcgtcg tcctcgtaat cacagtcatc atctgttgca 660
gtacaagaga gagttccaaa gtgaacatga taatgactgc atttcacatc gcattcatat 720
tcttcgtgat cgtgatggga ttcataaaag gagattcaaa gaatctatcc tcaccggcga 780
atccagagca cccctcgga ttttttccgt tcggcgccggc gggagttttc aacggagctg 840
ccatggttta cttaagctac ataggatacg acgccgtttc aaccatggcg gaagaagttg 900
aaaatccggc caaagatata cccgtcggtg tttccggctc cgtcgcaatc gtcaccgttc 960
tttactgtct catggcagtc tctatgtcaa tgcttctgcc atacgatctg atagatccgg 1020
aggcgccggt ttccgcggcg ttcagaggat cgaacggctg ggaatgggtg acgaaagtgg 1080
tggtggatagg agcaagcttt gggatattaa catcactttt ggtggcaatg ttaggtcagg 1140
ctcgctacat gtgtgtcatc ggacggtcca gagtgggtccc cttttgggtc gctaagattc 1200
atcccaaaac atctacgcca gtcaacgcct ccacttttct tggcattttc acggcggtc 1260
ttgcgctttt caccgacctt aacgtcctcc taaacctcgt atccattgga acactatttg 1320
tcttctacat ggtcgcaaac gctctcatct tcagacgtta cgtcccgggt ggaccaccca 1380
agccgtggcc cacactctgc ttccctcacac tatttccat aacctctctc gtcttcaccc 1440
tcacttgga aacttgtccg gaaggtaagc ctaaagcttt catgctcggt gccagtgcgg 1500
tggtggctat agccatcggt gaagcgtttc agtgcgtggt tccccaggct aggaaacctg 1560
agttgtgggg agtcccgttc atgccgtgga ccccgtgcgt gtcgatattc ttgaacattt 1620
ttttgcttgg ttcggttgac gcacctctt acgtccggtt tggattcttc tccggtttga 1680

tcgtgctcgt gtatttggtt tatggcgctt atgcgagttc tgatgctgaa gcgaatggat 1740
cttttggtgt gaaagatgga caagtcataa aagagctaata tgaagtgtga aaagtattta 1800
tttagtttag ttttctaaag catcatgaac caaaatgtaa ttaaactctc taattttttt 1860
tctacatgag ggggtttgaa atattaatga gaaaatatta aatgc

(2) INFORMATION FOR SEQ ID NO:871:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 595 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..595

(D) OTHER INFORMATION: / Ceres Seq. ID 1499116

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:871:

Thr	Asn	Arg	Pro	Asp	Pro	Asn	Leu	Ala	Gly	Glu	Lys	Met	Glu	Val	Gln
1				5					10					15	
Ser	Ser	Ser	Asn	Asn	Gly	Gly	His	Ser	Ser	Phe	Ser	Ser	Leu	Arg	Val
			20					25					30		
Tyr	Leu	Asn	Ser	Leu	Ser	Ala	Thr	Pro	Ser	Arg	Leu	Ser	Arg	Arg	Ala
		35					40					45			
Ile	Ser	Val	Ser	Thr	Ser	Ser	Asp	Glu	Met	Ser	Arg	Val	Arg	Ala	Val
	50					55					60				
Ser	Gly	Glu	Gln	Met	Arg	Arg	Thr	Leu	Arg	Trp	Tyr	Asp	Leu	Ile	Gly
65					70					75				80	
Leu	Gly	Ile	Gly	Gly	Met	Val	Gly	Ala	Gly	Val	Phe	Val	Thr	Thr	Gly
			85						90					95	
Arg	Ala	Ser	Arg	Leu	Asp	Ala	Gly	Pro	Ser	Ile	Val	Val	Ser	Tyr	Ala
			100					105						110	
Ile	Ala	Gly	Leu	Cys	Ala	Leu	Leu	Ser	Ala	Phe	Cys	Tyr	Thr	Glu	Phe
		115					120					125			
Ala	Val	His	Leu	Pro	Val	Ala	Gly	Gly	Ala	Phe	Ser	Tyr	Ile	Arg	Ile
	130					135						140			
Thr	Phe	Gly	Glu	Phe	Pro	Ala	Phe	Phe	Thr	Gly	Ala	Asn	Leu	Val	Met
145					150					155				160	
Asp	Tyr	Val	Met	Ser	Asn	Ala	Ala	Val	Ser	Arg	Ser	Phe	Thr	Ala	Tyr
			165						170					175	
Leu	Gly	Thr	Ala	Phe	Gly	Ile	Ser	Thr	Ser	Lys	Trp	Arg	Phe	Val	Val
			180					185					190		
Ser	Gly	Leu	Pro	Lys	Gly	Phe	Asn	Glu	Ile	Asp	Pro	Val	Ala	Val	Leu
		195					200					205			
Val	Val	Leu	Val	Ile	Thr	Val	Ile	Ile	Cys	Cys	Ser	Thr	Arg	Glu	Ser
	210					215					220				
Ser	Lys	Val	Asn	Met	Ile	Met	Thr	Ala	Phe	His	Ile	Ala	Phe	Ile	Phe
225					230					235				240	
Phe	Val	Ile	Val	Met	Gly	Phe	Ile	Lys	Gly	Asp	Ser	Lys	Asn	Leu	Ser
			245						250					255	
Ser	Pro	Ala	Asn	Pro	Glu	His	Pro	Ser	Gly	Phe	Phe	Pro	Phe	Gly	Ala
			260					265					270		
Ala	Gly	Val	Phe	Asn	Gly	Ala	Ala	Met	Val	Tyr	Leu	Ser	Tyr	Ile	Gly
		275				280						285			
Tyr	Asp	Ala	Val	Ser	Thr	Met	Ala	Glu	Glu	Val	Glu	Asn	Pro	Val	Lys
	290					295					300				
Asp	Ile	Pro	Val	Gly	Val	Ser	Gly	Ser	Val	Ala	Ile	Val	Thr	Val	Leu
305					310					315				320	
Tyr	Cys	Leu	Met	Ala	Val	Ser	Met	Ser	Met	Leu	Leu	Pro	Tyr	Asp	Leu
			325						330				335		
Ile	Asp	Pro	Glu	Ala	Pro	Phe	Ser	Ala	Ala	Phe	Arg	Gly	Ser	Asn	Gly
			340					345					350		
Trp	Glu	Trp	Val	Thr	Lys	Val	Val	Gly	Ile	Gly	Ala	Ser	Phe	Gly	Ile

355	360	365
Leu Thr Ser Leu Leu Val Ala Met Leu Gly Gln Ala Arg Tyr Met Cys		
370	375	380
Val Ile Gly Arg Ser Arg Val Val Pro Phe Trp Phe Ala Lys Ile His		
385	390	395
Pro Lys Thr Ser Thr Pro Val Asn Ala Ser Thr Phe Leu Gly Ile Phe		400
	405	410
Thr Ala Ala Leu Ala Leu Phe Thr Asp Leu Asn Val Leu Leu Asn Leu		415
	420	425
Val Ser Ile Gly Thr Leu Phe Val Phe Tyr Met Val Ala Asn Ala Leu		430
	435	440
Ile Phe Arg Arg Tyr Val Pro Val Gly Pro Thr Lys Pro Trp Pro Thr		445
450	455	460
Leu Cys Phe Leu Thr Leu Phe Ser Ile Thr Ser Leu Val Phe Thr Leu		
465	470	475
Ile Trp Lys Leu Val Pro Glu Gly Lys Pro Lys Ala Phe Met Leu Gly		480
	485	490
Ala Ser Ala Val Val Ala Ile Ala Ile Val Leu Ser Phe Gln Cys Val		495
	500	505
Val Pro Gln Ala Arg Lys Pro Glu Leu Trp Gly Val Pro Phe Met Pro		510
	515	520
Trp Thr Pro Cys Val Ser Ile Phe Leu Asn Ile Phe Leu Leu Gly Ser		525
	530	535
Leu Asp Ala Pro Ser Tyr Val Arg Phe Gly Phe Phe Ser Gly Leu Ile		540
545	550	555
Val Leu Val Tyr Leu Phe Tyr Gly Val His Ala Ser Ser Asp Ala Glu		560
	565	570
Ala Asn Gly Ser Phe Gly Val Lys Asp Gly Gln Val Met Lys Glu Leu		575
	580	585
Ile Glu Val		590
595		

(2) INFORMATION FOR SEQ ID NO:872:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 583 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..583

(D) OTHER INFORMATION: / Ceres Seq. ID 1499117

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:872:

Met Glu Val Gln Ser Ser Ser Asn Asn Gly Gly His Ser Ser Phe Ser		
1	5	10
Ser Leu Arg Val Tyr Leu Asn Ser Leu Ser Ala Thr Pro Ser Arg Leu		15
	20	25
Ser Arg Arg Ala Ile Ser Val Ser Thr Ser Ser Asp Glu Met Ser Arg		30
	35	40
Val Arg Ala Val Ser Gly Glu Gln Met Arg Arg Thr Leu Arg Trp Tyr		45
	50	55
Asp Leu Ile Gly Leu Gly Ile Gly Gly Met Val Gly Ala Gly Val Phe		60
65	70	75
Val Thr Thr Gly Arg Ala Ser Arg Leu Asp Ala Gly Pro Ser Ile Val		80
	85	90
Val Ser Tyr Ala Ile Ala Gly Leu Cys Ala Leu Leu Ser Ala Phe Cys		95
	100	105
Tyr Thr Glu Phe Ala Val His Leu Pro Val Ala Gly Gly Ala Phe Ser		110
	115	120
Tyr Ile Arg Ile Thr Phe Gly Glu Phe Pro Ala Phe Phe Thr Gly Ala		125
130	135	140

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Asn Leu Val Met Asp Tyr Val Met Ser Asn Ala Ala Val Ser Arg Ser
145          150          155          160
Phe Thr Ala Tyr Leu Gly Thr Ala Phe Gly Ile Ser Thr Ser Lys Trp
          165          170          175
Arg Phe Val Val Ser Gly Leu Pro Lys Gly Phe Asn Glu Ile Asp Pro
          180          185          190
Val Ala Val Leu Val Val Leu Val Ile Thr Val Ile Ile Cys Cys Ser
          195          200          205
Thr Arg Glu Ser Ser Lys Val Asn Met Ile Met Thr Ala Phe His Ile
          210          215          220
Ala Phe Ile Phe Phe Val Ile Val Met Gly Phe Ile Lys Gly Asp Ser
225          230          235          240
Lys Asn Leu Ser Ser Pro Ala Asn Pro Glu His Pro Ser Gly Phe Phe
          245          250          255
Pro Phe Gly Ala Ala Gly Val Phe Asn Gly Ala Ala Met Val Tyr Leu
          260          265          270
Ser Tyr Ile Gly Tyr Asp Ala Val Ser Thr Met Ala Glu Glu Val Glu
          275          280          285
Asn Pro Val Lys Asp Ile Pro Val Gly Val Ser Gly Ser Val Ala Ile
          290          295          300
Val Thr Val Leu Tyr Cys Leu Met Ala Val Ser Met Ser Met Leu Leu
305          310          315          320
Pro Tyr Asp Leu Ile Asp Pro Glu Ala Pro Phe Ser Ala Ala Phe Arg
          325          330          335
Gly Ser Asn Gly Trp Glu Trp Val Thr Lys Val Val Gly Ile Gly Ala
          340          345          350
Ser Phe Gly Ile Leu Thr Ser Leu Val Ala Met Leu Gly Gln Ala
          355          360          365
Arg Tyr Met Cys Val Ile Gly Arg Ser Arg Val Val Pro Phe Trp Phe
          370          375          380
Ala Lys Ile His Pro Lys Thr Ser Thr Pro Val Asn Ala Ser Thr Phe
385          390          395          400
Leu Gly Ile Phe Thr Ala Ala Leu Ala Leu Phe Thr Asp Leu Asn Val
          405          410          415
Leu Leu Asn Leu Val Ser Ile Gly Thr Leu Phe Val Phe Tyr Met Val
          420          425          430
Ala Asn Ala Leu Ile Phe Arg Arg Tyr Val Pro Val Gly Pro Thr Lys
          435          440          445
Pro Trp Pro Thr Leu Cys Phe Leu Thr Leu Phe Ser Ile Thr Ser Leu
          450          455          460
Val Phe Thr Leu Ile Trp Lys Leu Val Pro Glu Gly Lys Pro Lys Ala
465          470          475          480
Phe Met Leu Gly Ala Ser Ala Val Val Ala Ile Ala Ile Val Leu Ser
          485          490          495
Phe Gln Cys Val Val Pro Gln Ala Arg Lys Pro Glu Leu Trp Gly Val
          500          505          510
Pro Phe Met Pro Trp Thr Pro Cys Val Ser Ile Phe Leu Asn Ile Phe
          515          520          525
Leu Leu Gly Ser Leu Asp Ala Pro Ser Tyr Val Arg Phe Gly Phe Phe
          530          535          540
Ser Gly Leu Ile Val Leu Val Tyr Leu Phe Tyr Gly Val His Ala Ser
545          550          555          560
Ser Asp Ala Glu Ala Asn Gly Ser Phe Gly Val Lys Asp Gly Gln Val
          565          570          575
Met Lys Glu Leu Ile Glu Val
          580

```

(2) INFORMATION FOR SEQ ID NO:873:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 538 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

- (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..538
 (D) OTHER INFORMATION: / Ceres Seq. ID 1499118
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:873:

Met	Ser	Arg	Val	Arg	Ala	Val	Ser	Gly	Glu	Gln	Met	Arg	Arg	Thr	Leu
1			5					10						15	
Arg	Trp	Tyr	Asp	Leu	Ile	Gly	Leu	Gly	Ile	Gly	Gly	Met	Val	Gly	Ala
			20				25						30		
Gly	Val	Phe	Val	Thr	Thr	Gly	Arg	Ala	Ser	Arg	Leu	Asp	Ala	Gly	Pro
		35				40						45			
Ser	Ile	Val	Val	Ser	Tyr	Ala	Ile	Ala	Gly	Leu	Cys	Ala	Leu	Leu	Ser
	50					55					60				
Ala	Phe	Cys	Tyr	Thr	Glu	Phe	Ala	Val	His	Leu	Pro	Val	Ala	Gly	Gly
65					70					75					80
Ala	Phe	Ser	Tyr	Ile	Arg	Ile	Thr	Phe	Gly	Glu	Phe	Pro	Ala	Phe	Phe
			85						90					95	
Thr	Gly	Ala	Asn	Leu	Val	Met	Asp	Tyr	Val	Met	Ser	Asn	Ala	Ala	Val
			100					105					110		
Ser	Arg	Ser	Phe	Thr	Ala	Tyr	Leu	Gly	Thr	Ala	Phe	Gly	Ile	Ser	Thr
		115					120					125			
Ser	Lys	Trp	Arg	Phe	Val	Val	Ser	Gly	Leu	Pro	Lys	Gly	Phe	Asn	Glu
	130					135					140				
Ile	Asp	Pro	Val	Ala	Val	Leu	Val	Val	Leu	Val	Ile	Thr	Val	Ile	Ile
145					150					155					160
Cys	Cys	Ser	Thr	Arg	Glu	Ser	Ser	Lys	Val	Asn	Met	Ile	Met	Thr	Ala
			165						170					175	
Phe	His	Ile	Ala	Phe	Ile	Phe	Phe	Val	Ile	Val	Met	Gly	Phe	Ile	Lys
			180					185					190		
Gly	Asp	Ser	Lys	Asn	Leu	Ser	Ser	Pro	Ala	Asn	Pro	Glu	His	Pro	Ser
		195					200					205			
Gly	Phe	Phe	Pro	Phe	Gly	Ala	Ala	Gly	Val	Phe	Asn	Gly	Ala	Ala	Met
	210					215					220				
Val	Tyr	Leu	Ser	Tyr	Ile	Gly	Tyr	Asp	Ala	Val	Ser	Thr	Met	Ala	Glu
225					230					235					240
Glu	Val	Glu	Asn	Pro	Val	Lys	Asp	Ile	Pro	Val	Gly	Val	Ser	Gly	Ser
			245						250					255	
Val	Ala	Ile	Val	Thr	Val	Leu	Tyr	Cys	Leu	Met	Ala	Val	Ser	Met	Ser
		260						265					270		
Met	Leu	Leu	Pro	Tyr	Asp	Leu	Ile	Asp	Pro	Glu	Ala	Pro	Phe	Ser	Ala
		275					280						285		
Ala	Phe	Arg	Gly	Ser	Asn	Gly	Trp	Glu	Trp	Val	Thr	Lys	Val	Val	Gly
	290					295					300				
Ile	Gly	Ala	Ser	Phe	Gly	Ile	Leu	Thr	Ser	Leu	Leu	Val	Ala	Met	Leu
305					310					315					320
Gly	Gln	Ala	Arg	Tyr	Met	Cys	Val	Ile	Gly	Arg	Ser	Arg	Val	Val	Pro
			325						330					335	
Phe	Trp	Phe	Ala	Lys	Ile	His	Pro	Lys	Thr	Ser	Thr	Pro	Val	Asn	Ala
		340						345					350		
Ser	Thr	Phe	Leu	Gly	Ile	Phe	Thr	Ala	Ala	Leu	Ala	Leu	Phe	Thr	Asp
		355					360					365			
Leu	Asn	Val	Leu	Leu	Asn	Leu	Val	Ser	Ile	Gly	Thr	Leu	Phe	Val	Phe
	370					375					380				
Tyr	Met	Val	Ala	Asn	Ala	Leu	Ile	Phe	Arg	Arg	Tyr	Val	Pro	Val	Gly
385					390					395					400
Pro	Thr	Lys	Pro	Trp	Pro	Thr	Leu	Cys	Phe	Leu	Thr	Leu	Phe	Ser	Ile
			405						410					415	
Thr	Ser	Leu	Val	Phe	Thr	Leu	Ile	Trp	Lys	Leu	Val	Pro	Glu	Gly	Lys
			420					425					430		

Pro Lys Ala Phe Met Leu Gly Ala Ser Ala Val Val Ala Ile Ala Ile
435 440 445
Val Leu Ser Phe Gln Cys Val Val Pro Gln Ala Arg Lys Pro Glu Leu
450 455 460
Trp Gly Val Pro Phe Met Pro Trp Thr Pro Cys Val Ser Ile Phe Leu
465 470 475 480
Asn Ile Phe Leu Leu Gly Ser Leu Asp Ala Pro Ser Tyr Val Arg Phe
485 490 495
Gly Phe Phe Ser Gly Leu Ile Val Leu Val Tyr Leu Phe Tyr Gly Val
500 505 510
His Ala Ser Ser Asp Ala Glu Ala Asn Gly Ser Phe Gly Val Lys Asp
515 520 525
Gly Gln Val Met Lys Glu Leu Ile Glu Val
530 535

(2) INFORMATION FOR SEQ ID NO:874:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1279 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1279
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499119

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:874:

aactgaattt	gaaagaaaaa	aaaaaaagaa	atcataaaat	gagaatcaat	atgttattca	60
tagtggcatt	ctcattttta	gtctctgttc	ggtcattacc	gatgagacca	actctaaagt	120
acgagtcaat	ctttaatttt	ggcgattcct	taagcgatac	cggaaacttt	ttattatccg	180
gtgatgttga	ctctccgaac	attggaagac	taccgtacgg	acaaaccttt	tttaaccggt	240
ccaccggctg	ttgctctgac	ggacgtctca	tcacgtattt	catcgctgag	gctagtggac	300
taccgtacat	tccaccgtat	ctccaaagct	tacggacgaa	tgattcggta	gatttcaaga	360
gaggtgcaaa	ttttgcggtg	gctggagcaa	cagcgaacga	atttagcttc	tttaaaaaca	420
gaggtctttc	agtaacattg	ttgacaaaca	agacactgga	tattcaactt	gattggttca	480
agaagttgaa	accttctctg	tgtaaaacca	agccagaatg	tgagcgatat	tttagaaaat	540
ctctattttc	cgtcggagaa	attagtggaa	acgattataa	ctaccctctt	ttggcattcc	600
gaagtttcaa	acatgctatg	gatttggtac	catttgttat	taacaaaatc	atggacgtca	660
caagtgcatt	gatagaggaa	ggtgccatga	cactaatagt	tccaggaaac	cttccaatcg	720
gttgttctgc	ggctctacta	gagcggttta	atgataatag	tgatgggctt	tatgactcga	780
ggaaccaatg	ctacatgcca	ttgaacaatt	tggctaagct	tcacaatgat	aagctcaaga	840
aaggcctcgc	ggctctaaga	aaaaagtacc	cttatgccaa	aattatatat	gctgattatt	900
acagttctgc	catgcaattc	ttcaactcac	cttccaaata	cggtttctact	ggaagtgtcc	960
taaaggcatg	ttgtggagga	ggagatggaa	gatacaacgt	gcaaccaaac	gtgcggtgcg	1020
gagaaaaggg	ttcaaccact	tgcgaaagatc	catcaacgta	cgcaaattgg	gacggaattc	1080
acctcactga	agcggcttac	cgccacattg	caactggctc	catctccggc	cgtttcacca	1140
tgcttactta	taattaataa	caattaagtt	actcataagt	tgtaactttt	tttttaacac	1200
acaaactttt	catataactc	ctaattgaaa	acctataaat	cgatcatatt	tatatcaagc	1260
tcgttcgaga	gcataagcc					

(2) INFORMATION FOR SEQ ID NO:875:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 384 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..384
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499120

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:875:

Leu Asn Leu Lys Glu Lys Lys Lys Arg Asn His Lys Met Arg Ile Asn

1	5	10	15
Met Leu Phe Ile Val Ala Phe Ser Phe Leu Val Ser Val Arg Ser Leu			
20	25	30	
Pro Met Arg Pro Thr Leu Lys Tyr Glu Ser Ile Phe Asn Phe Gly Asp			
35	40	45	
Ser Leu Ser Asp Thr Gly Asn Phe Leu Leu Ser Gly Asp Val Asp Ser			
50	55	60	
Pro Asn Ile Gly Arg Leu Pro Tyr Gly Gln Thr Phe Phe Asn Arg Ser			
65	70	75	80
Thr Gly Arg Cys Ser Asp Gly Arg Leu Ile Asp Phe Ile Ala Glu			
85	90	95	
Ala Ser Gly Leu Pro Tyr Ile Pro Pro Tyr Leu Gln Ser Leu Arg Thr			
100	105	110	
Asn Asp Ser Val Asp Phe Lys Arg Gly Ala Asn Phe Ala Val Ala Gly			
115	120	125	
Ala Thr Ala Asn Glu Phe Ser Phe Phe Lys Asn Arg Gly Leu Ser Val			
130	135	140	
Thr Leu Leu Thr Asn Lys Thr Leu Asp Ile Gln Leu Asp Trp Phe Lys			
145	150	155	160
Lys Leu Lys Pro Ser Leu Cys Lys Thr Lys Pro Glu Cys Glu Arg Tyr			
165	170	175	
Phe Arg Lys Ser Leu Phe Leu Val Gly Glu Ile Ser Gly Asn Asp Tyr			
180	185	190	
Asn Tyr Pro Leu Leu Ala Phe Arg Ser Phe Lys His Ala Met Asp Leu			
195	200	205	
Val Pro Phe Val Ile Asn Lys Ile Met Asp Val Thr Ser Ala Leu Ile			
210	215	220	
Glu Glu Gly Ala Met Thr Leu Ile Val Pro Gly Asn Leu Pro Ile Gly			
225	230	235	240
Cys Ser Ala Ala Leu Leu Glu Arg Phe Asn Asp Asn Ser Gly Trp Leu			
245	250	255	
Tyr Asp Ser Arg Asn Gln Cys Tyr Met Pro Leu Asn Asn Leu Ala Lys			
260	265	270	
Leu His Asn Asp Lys Leu Lys Lys Gly Leu Ala Ala Leu Arg Lys Lys			
275	280	285	
Tyr Pro Tyr Ala Lys Ile Ile Tyr Ala Asp Tyr Tyr Ser Ser Ala Met			
290	295	300	
Gln Phe Phe Asn Ser Pro Ser Lys Tyr Gly Phe Thr Gly Ser Val Leu			
305	310	315	320
Lys Ala Cys Cys Gly Gly Gly Asp Gly Arg Tyr Asn Val Gln Pro Asn			
325	330	335	
Val Arg Cys Gly Glu Lys Gly Ser Thr Thr Cys Glu Asp Pro Ser Thr			
340	345	350	
Tyr Ala Asn Trp Asp Gly Ile His Leu Thr Glu Ala Ala Tyr Arg His			
355	360	365	
Ile Ala Thr Gly Leu Ile Ser Gly Arg Phe Thr Met Pro Thr Tyr Asn			
370	375	380	

(2) INFORMATION FOR SEQ ID NO:876:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 372 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..372

(D) OTHER INFORMATION: / Ceres Seq. ID 1499121

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:876:

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Met Arg Ile Asn Met Leu Phe Ile Val Ala Phe Ser Phe Leu Val Ser
1      5      10      15
Val Arg Ser Leu Pro Met Arg Pro Thr Leu Lys Tyr Glu Ser Ile Phe
20      25      30
Asn Phe Gly Asp Ser Leu Ser Asp Thr Gly Asn Phe Leu Leu Ser Gly
35      40      45
Asp Val Asp Ser Pro Asn Ile Gly Arg Leu Pro Tyr Gly Gln Thr Phe
50      55      60
Phe Asn Arg Ser Thr Gly Arg Cys Ser Asp Gly Arg Leu Ile Ile Asp
65      70      75      80
Phe Ile Ala Glu Ala Ser Gly Leu Pro Tyr Ile Pro Pro Tyr Leu Gln
85      90      95
Ser Leu Arg Thr Asn Asp Ser Val Asp Phe Lys Arg Gly Ala Asn Phe
100     105     110
Ala Val Ala Gly Ala Thr Ala Asn Glu Phe Ser Phe Phe Lys Asn Arg
115     120     125
Gly Leu Ser Val Thr Leu Leu Thr Asn Lys Thr Leu Asp Ile Gln Leu
130     135     140
Asp Trp Phe Lys Lys Leu Lys Pro Ser Leu Cys Lys Thr Lys Pro Glu
145     150     155     160
Cys Glu Arg Tyr Phe Arg Lys Ser Leu Phe Leu Val Gly Glu Ile Ser
165     170     175
Gly Asn Asp Tyr Asn Tyr Pro Leu Leu Ala Phe Arg Ser Phe Lys His
180     185     190
Ala Met Asp Leu Val Pro Phe Val Ile Asn Lys Ile Met Asp Val Thr
195     200     205
Ser Ala Leu Ile Glu Glu Gly Ala Met Thr Leu Ile Val Pro Gly Asn
210     215     220
Leu Pro Ile Gly Cys Ser Ala Ala Leu Leu Glu Arg Phe Asn Asp Asn
225     230     235     240
Ser Gly Trp Leu Tyr Asp Ser Arg Asn Gln Cys Tyr Met Pro Leu Asn
245     250     255
Asn Leu Ala Lys Leu His Asn Asp Lys Leu Lys Lys Gly Leu Ala Ala
260     265     270
Leu Arg Lys Lys Tyr Pro Tyr Ala Lys Ile Ile Tyr Ala Asp Tyr Tyr
275     280     285
Ser Ser Ala Met Gln Phe Phe Asn Ser Pro Ser Lys Tyr Gly Phe Thr
290     295     300
Gly Ser Val Leu Lys Ala Cys Cys Gly Gly Gly Asp Gly Arg Tyr Asn
305     310     315     320
Val Gln Pro Asn Val Arg Cys Gly Glu Lys Gly Ser Thr Thr Cys Glu
325     330     335
Asp Pro Ser Thr Tyr Ala Asn Trp Asp Gly Ile His Leu Thr Glu Ala
340     345     350
Ala Tyr Arg His Ile Ala Thr Gly Leu Ile Ser Gly Arg Phe Thr Met
355     360     365
Pro Thr Tyr Asn
370

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(2) INFORMATION FOR SEQ ID NO:877:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 368 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..368
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499122

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:877:

Met Leu Phe Ile Val Ala Phe Ser Phe Leu Val Ser Val Arg Ser Leu

1	5	10	15
Pro Met Arg	Pro Thr Leu Lys Tyr Glu	Ser Ile Phe Asn	Phe Gly Asp
	20	25	30
Ser Leu Ser	Asp Thr Gly Asn Phe Leu	Leu Ser Gly Asp	Val Asp Ser
	35	40	45
Pro Asn Ile	Gly Arg Leu Pro Tyr Gly	Gln Thr Phe Phe	Asn Arg Ser
	50	55	60
Thr Gly Arg	Cys Ser Asp Gly Arg Leu	Ile Ile Asp Phe	Ile Ala Glu
	65	70	75
Ala Ser Gly	Leu Pro Tyr Ile Pro Pro	Tyr Leu Gln Ser	Leu Arg Thr
	85	90	95
Asn Asp Ser	Val Asp Phe Lys Arg Gly	Ala Asn Phe Ala	Val Ala Gly
	100	105	110
Ala Thr Ala	Asn Glu Phe Ser Phe Phe	Lys Asn Arg Gly	Leu Ser Val
	115	120	125
Thr Leu Leu	Thr Asn Lys Thr Leu Asp	Ile Gln Leu Asp	Trp Phe Lys
	130	135	140
Lys Leu Lys	Pro Ser Leu Cys Lys Thr	Lys Pro Glu Cys	Glu Arg Tyr
	145	150	155
Phe Arg Lys	Ser Leu Phe Leu Val Gly	Glu Ile Ser Gly	Asn Asp Tyr
	165	170	175
Asn Tyr Pro	Leu Leu Ala Phe Arg Ser	Phe Lys His Ala	Met Asp Leu
	180	185	190
Val Pro Phe	Val Ile Asn Lys Ile Met	Asp Val Thr Ser	Ala Leu Ile
	195	200	205
Glu Glu Gly	Ala Met Thr Leu Ile Val	Pro Gly Asn Leu	Pro Ile Gly
	210	215	220
Cys Ser Ala	Ala Leu Leu Glu Arg Phe	Asn Asp Asn Ser	Gly Trp Leu
	225	230	235
Tyr Asp Ser	Arg Asn Gln Cys Tyr Met	Pro Leu Asn Asn	Leu Ala Lys
	245	250	255
Leu His Asn	Asp Lys Leu Lys Lys Gly	Leu Ala Ala Leu	Arg Lys Lys
	260	265	270
Tyr Pro Tyr	Ala Lys Ile Ile Tyr Ala	Asp Tyr Tyr Ser	Ser Ala Met
	275	280	285
Gln Phe Phe	Asn Ser Pro Ser Lys Tyr	Gly Phe Thr Gly	Ser Val Leu
	290	295	300
Lys Ala Cys	Cys Gly Gly Asp Gly Arg	Tyr Asn Val Gln	Pro Asn
	305	310	315
Val Arg Cys	Gly Glu Lys Gly Ser Thr	Thr Cys Glu Asp	Pro Ser Thr
	325	330	335
Tyr Ala Asn	Trp Asp Gly Ile His Leu	Thr Glu Ala Ala	Tyr Arg His
	340	345	350
Ile Ala Thr	Gly Leu Ile Ser Gly Arg	Phe Thr Met Pro	Thr Tyr Asn
	355	360	365

(2) INFORMATION FOR SEQ ID NO:878:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1620 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1620
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499123

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:878:

ctctgcctct catctcttgt tctctccgcc catctctgct ctcttttatt ttcccagaaa
gtttttttttt tttcccgaat tccgtaatc tcattggggg ttccattgat agcaatggcg

60
120

11/11/2011 11:11:11

acggcctttcg	ctcccaactaa	gctcactgcc	acggttcctc	tgcattggatc	ccatgagaat	180
cgtctcttgc	tcccgatccg	attggctcct	ccttcttctt	tccctggatc	caccgcgttc	240
ctctcccttc	gcagactcaa	tcactccaac	gccacccgtc	gatctcccgt	cgtctctgtc	300
caggaagttg	tcaaggagaa	gcaatccacc	aataatacca	gcctggtgat	aaccaaagag	360
gaaggattgg	agttgtatga	agatatgata	ctaggtagat	ctttcgaaga	catgtgtgct	420
caaattgtatt	accgaggcaa	gatgtttggt	tttgttcaact	tgtacaatgg	ccaagaggct	480
gtttctactg	gctttatcaa	gctccttacc	aagtctgact	ctgtcggttag	tacctaccgt	540
gaccatgtcc	atgccctcag	caaagggtgc	tctgctcgtg	ctgttatgag	cgagctcttc	600
ggcaagggtta	ctggatgctg	cagaggccaa	ggtggatcca	tgcacatggt	ctccaaagaa	660
cacaacatgc	ttggtggcct	tgctttttatt	ggtgaaggca	ttcctgtcgc	cactggtgct	720
gccttttagct	ccaagtacag	gagggaaagtc	ttgaaacagg	attgtgatga	tgtcactgtc	780
gcctttttcg	gagatggaac	ttgtaacaac	ggacagttct	tcgagtgtct	caacatggct	840
gctctctata	aactgcctat	tatctttggt	gtcgagaata	acttgtgggc	cattgggatg	900
tctcacttga	gagccacttc	tgaccccgag	atttgaaga	aaggctcctgc	atttgggatg	960
cctggtgttc	atgttgacgg	tatggatgtc	ttgaagggtca	gggaagtcgc	ttaaaggaggct	1020
gtcactagag	ctagaagagg	agaagggtcca	accttggttg	aatgtgagac	ttatagattt	1080
agaggacact	ccttggtctga	tcccgatgag	ctccgtgatg	ctgctgagaa	agccaaatac	1140
gcggtctagag	acccaatcgc	agcattgaag	aagtatttga	tagagaacaa	gcttgcaaag	1200
gaagcagagc	taaagtcaat	agagaaaaag	atagacagtt	ggtggaggaa	gcggttgagt	1260
ttgcagacgc	tagtccacag	cccgttcgca	agcagttgct	agagaatgtg	tttctgtatc	1320
caaaaggatt	tggaattgga	cctgatggac	ggtacagatg	tgaggacccc	aagtttaccg	1380
aaggcacagc	tcaagtctga	gaagacaagt	ttaaccataa	gctgtctact	gtctcttcga	1440
tgtttctata	tatcttatta	agttaaattgc	tacagagaat	cagtttgaat	catttgcact	1500
ttttgctttt	tgtttggtgt	tactaaatta	tcacaagggt	cttcttgtag	ttcgttgggt	1560
tttcattggt	taccacttac	cagagaattg	tatttttttt	tttaaagata	attattttgc	1620

(2) INFORMATION FOR SEQ ID NO:879:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 433 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..433

(D) OTHER INFORMATION: / Ceres Seq. ID 1499124

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:879:

Leu	Cys	Leu	Ser	Ser	Leu	Val	Leu	Ser	Ala	His	Leu	Cys	Ser	Leu	Leu
1				5					10					15	
Phe	Ser	Gln	Lys	Val	Phe	Phe	Phe	Ser	Arg	Ile	Pro	Leu	Ile	Ser	Leu
			20					25					30		
Gly	Phe	Pro	Leu	Ile	Ala	Met	Ala	Thr	Ala	Phe	Ala	Pro	Thr	Lys	Leu
			35				40					45			
Thr	Ala	Thr	Val	Pro	Leu	His	Gly	Ser	His	Glu	Asn	Arg	Leu	Leu	Leu
	50					55					60				
Pro	Ile	Arg	Leu	Ala	Pro	Ser	Ser	Phe	Leu	Gly	Ser	Thr	Arg	Ser	
65					70				75					80	
Leu	Ser	Leu	Arg	Arg	Leu	Asn	His	Ser	Asn	Ala	Thr	Arg	Arg	Ser	Pro
			85						90					95	
Val	Val	Ser	Val	Gln	Glu	Val	Val	Lys	Glu	Lys	Gln	Ser	Thr	Asn	Asn
			100					105					110		
Thr	Ser	Leu	Leu	Ile	Thr	Lys	Glu	Glu	Gly	Leu	Glu	Leu	Tyr	Glu	Asp
		115				120					125				
Met	Ile	Leu	Gly	Arg	Ser	Phe	Glu	Asp	Met	Cys	Ala	Gln	Met	Tyr	Tyr
	130					135					140				
Arg	Gly	Lys	Met	Phe	Gly	Phe	Val	His	Leu	Tyr	Asn	Gly	Gln	Glu	Ala
145					150				155					160	
Val	Ser	Thr	Gly	Phe	Ile	Lys	Leu	Leu	Thr	Lys	Ser	Asp	Ser	Val	Val
			165					170					175		
Ser	Thr	Tyr	Arg	Asp	His	Val	His	Ala	Leu	Ser	Lys	Gly	Val	Ser	Ala

Arg	Ala	Val	Met	Ser	Glu	Leu	Phe	Gly	Lys	Val	Thr	Gly	Cys	Cys	Arg
	195						200					205			
Gly	Gln	Gly	Gly	Ser	Met	His	Met	Phe	Ser	Lys	Glu	His	Asn	Met	Leu
	210					215					220				
Gly	Gly	Phe	Ala	Phe	Ile	Gly	Glu	Gly	Ile	Pro	Val	Ala	Thr	Gly	Ala
225					230					235					240
Ala	Phe	Ser	Ser	Lys	Tyr	Arg	Arg	Glu	Val	Leu	Lys	Gln	Asp	Cys	Asp
				245					250					255	
Asp	Val	Thr	Val	Ala	Phe	Phe	Gly	Asp	Gly	Thr	Cys	Asn	Asn	Gly	Gln
			260					265						270	
Phe	Phe	Glu	Cys	Leu	Asn	Met	Ala	Ala	Leu	Tyr	Lys	Leu	Pro	Ile	Ile
	275						280					285			
Phe	Val	Val	Glu	Asn	Asn	Leu	Trp	Ala	Ile	Gly	Met	Ser	His	Leu	Arg
	290					295				300					
Ala	Thr	Ser	Asp	Pro	Glu	Ile	Trp	Lys	Lys	Gly	Pro	Ala	Phe	Gly	Met
305					310					315					320
Pro	Gly	Val	His	Val	Asp	Gly	Met	Asp	Val	Leu	Lys	Val	Arg	Glu	Val
				325					330					335	
Ala	Lys	Glu	Ala	Val	Thr	Arg	Ala	Arg	Arg	Gly	Glu	Gly	Pro	Thr	Leu
			340				345						350		
Val	Glu	Cys	Glu	Thr	Tyr	Arg	Phe	Arg	Gly	His	Ser	Leu	Ala	Asp	Pro
	355						360					365			
Asp	Glu	Leu	Arg	Asp	Ala	Ala	Glu	Lys	Ala	Lys	Tyr	Ala	Ala	Arg	Asp
	370					375					380				
Pro	Ile	Ala	Ala	Leu	Lys	Lys	Tyr	Leu	Ile	Glu	Asn	Lys	Leu	Ala	Lys
385					390					395					400
Glu	Ala	Glu	Leu	Lys	Ser	Ile	Glu	Lys	Lys	Ile	Asp	Ser	Trp	Trp	Arg
				405				410						415	
Lys	Arg	Leu	Ser	Leu	Gln	Thr	Leu	Val	His	Ser	Pro	Val	Ala	Val	Ser
			420				425						430		
Cys															

(2) INFORMATION FOR SEQ ID NO:880:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 395 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..395
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499125

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:880:

Met	Ala	Thr	Ala	Phe	Ala	Pro	Thr	Lys	Leu	Thr	Ala	Thr	Val	Pro	Leu
1			5						10					15	
His	Gly	Ser	His	Glu	Asn	Arg	Leu	Leu	Leu	Pro	Ile	Arg	Leu	Ala	Pro
			20					25					30		
Pro	Ser	Ser	Phe	Leu	Gly	Ser	Thr	Arg	Ser	Leu	Ser	Leu	Arg	Arg	Leu
		35					40					45			
Asn	His	Ser	Asn	Ala	Thr	Arg	Arg	Ser	Pro	Val	Val	Ser	Val	Gln	Glu
	50					55					60				
Val	Val	Lys	Glu	Lys	Gln	Ser	Thr	Asn	Asn	Thr	Ser	Leu	Leu	Ile	Thr
65					70					75					80
Lys	Glu	Glu	Gly	Leu	Glu	Leu	Tyr	Glu	Asp	Met	Ile	Leu	Gly	Arg	Ser
			85					90						95	
Phe	Glu	Asp	Met	Cys	Ala	Gln	Met	Tyr	Tyr	Arg	Gly	Lys	Met	Phe	Gly
			100					105					110		
Phe	Val	His	Leu	Tyr	Asn	Gly	Gln	Glu	Ala	Val	Ser	Thr	Gly	Phe	Ile
			115				120						125		

Lys Leu Leu Thr Lys Ser Asp Ser Val Val Ser Thr Tyr Arg Asp His
130 135 140
Val His Ala Leu Ser Lys Gly Val Ser Ala Arg Ala Val Met Ser Glu
145 150 155 160
Leu Phe Gly Lys Val Thr Gly Cys Cys Arg Gly Gln Gly Gly Ser Met
165 170 175
His Met Phe Ser Lys Glu His Asn Met Leu Gly Gly Phe Ala Phe Ile
180 185 190
Gly Glu Gly Ile Pro Val Ala Thr Gly Ala Ala Phe Ser Ser Lys Tyr
195 200 205
Arg Arg Glu Val Leu Lys Gln Asp Cys Asp Asp Val Thr Val Ala Phe
210 215 220
Phe Gly Asp Gly Thr Cys Asn Asn Gly Gln Phe Phe Glu Cys Leu Asn
225 230 235 240
Met Ala Ala Leu Tyr Lys Leu Pro Ile Ile Phe Val Val Glu Asn Asn
245 250 255
Leu Trp Ala Ile Gly Met Ser His Leu Arg Ala Thr Ser Asp Pro Glu
260 265 270
Ile Trp Lys Lys Gly Pro Ala Phe Gly Met Pro Gly Val His Val Asp
275 280 285
Gly Met Asp Val Leu Lys Val Arg Glu Val Ala Lys Glu Ala Val Thr
290 295 300
Arg Ala Arg Arg Gly Glu Gly Pro Thr Leu Val Glu Cys Glu Thr Tyr
305 310 315 320
Arg Phe Arg Gly His Ser Leu Ala Asp Pro Asp Glu Leu Arg Asp Ala
325 330 335
Ala Glu Lys Ala Lys Tyr Ala Ala Arg Asp Pro Ile Ala Ala Leu Lys
340 345 350
Lys Tyr Leu Ile Glu Asn Lys Leu Ala Lys Glu Ala Glu Leu Lys Ser
355 360 365
Ile Glu Lys Lys Ile Asp Ser Trp Trp Arg Lys Arg Leu Ser Leu Gln
370 375 380
Thr Leu Val His Ser Pro Val Ala Val Ser Cys
385 390 395

(2) INFORMATION FOR SEQ ID NO:881:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 305 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..305

(D) OTHER INFORMATION: / Ceres Seq. ID 1499126

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:881:

Met Ile Leu Gly Arg Ser Phe Glu Asp Met Cys Ala Gln Met Tyr Tyr
1 5 10 15
Arg Gly Lys Met Phe Gly Phe Val His Leu Tyr Asn Gly Gln Glu Ala
20 25 30
Val Ser Thr Gly Phe Ile Lys Leu Leu Thr Lys Ser Asp Ser Val Val
35 40 45
Ser Thr Tyr Arg Asp His Val His Ala Leu Ser Lys Gly Val Ser Ala
50 55 60
Arg Ala Val Met Ser Glu Leu Phe Gly Lys Val Thr Gly Cys Cys Arg
65 70 75 80
Gly Gln Gly Gly Ser Met His Met Phe Ser Lys Glu His Asn Met Leu
85 90 95
Gly Gly Phe Ala Phe Ile Gly Glu Gly Ile Pro Val Ala Thr Gly Ala
100 105 110
Ala Phe Ser Ser Lys Tyr Arg Arg Glu Val Leu Lys Gln Asp Cys Asp

115	120	125
Asp Val Thr Val Ala Phe Phe Gly Asp Gly Thr Cys Asn Asn Gly Gln		
130	135	140
Phe Phe Glu Cys Leu Asn Met Ala Ala Leu Tyr Lys Leu Pro Ile Ile		
145	150	155
Phe Val Val Glu Asn Asn Leu Trp Ala Ile Gly Met Ser His Leu Arg		
165	170	175
Ala Thr Ser Asp Pro Glu Ile Trp Lys Lys Gly Pro Ala Phe Gly Met		
180	185	190
Pro Gly Val His Val Asp Gly Met Asp Val Leu Lys Val Arg Glu Val		
195	200	205
Ala Lys Glu Ala Val Thr Arg Ala Arg Arg Gly Glu Gly Pro Thr Leu		
210	215	220
Val Glu Cys Glu Thr Tyr Arg Phe Arg Gly His Ser Leu Ala Asp Pro		
225	230	235
Asp Glu Leu Arg Asp Ala Ala Glu Lys Ala Lys Tyr Ala Ala Arg Asp		
245	250	255
Pro Ile Ala Ala Leu Lys Lys Tyr Leu Ile Glu Asn Lys Leu Ala Lys		
260	265	270
Glu Ala Glu Leu Lys Ser Ile Glu Lys Lys Ile Asp Ser Trp Trp Arg		
275	280	285
Lys Arg Leu Ser Leu Gln Thr Leu Val His Ser Pro Val Ala Val Ser		
290	295	300

Cys
305

(2) INFORMATION FOR SEQ ID NO:882:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1253 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1253
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499127

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:882:

aaacacatga	cccctaaatc	gagaggcttc	gtaggagaaa	ggagaagcag	aagagtgttg	60
gttctcgatt	gtcgcgtc	acaatggcgt	agtctcccca	aaatgcgtca	acctcgagct	120
tctcctgccg	cgtatgttaa	ggatggctctg	atcattgtga	ttggagggttg	cagggtccaag	180
aatatcgaga	cttggggaga	gatttatgat	ctaaagacca	atacttgggg	gcgaataactg	240
ctccaatcac	atgatccccc	agttcaaaat	gcttacttga	atcgcttttaa	acctaaacttg	300
cagacgaatg	cttgctatgt	agagattgac	aaggtgtcgt	gcctgatatt	tttatccgat	360
gggaagctat	tttggcgtga	aacaaagcaa	ggttttgaga	ggtgtagtgt	tatataggga	420
gatgatgagc	aagtgtcctc	ttatcaactt	gtttcggttg	caaacgccgc	cggaggagga	480
agagtgcacg	tttgggtgaa	gtcgggggta	aaagttcttg	atctcttaag	tggcactgag	540
acttgggaat	gttacacaaa	tagtcgggtg	gcagagattt	cgtttgagag	aagaggttta	600
agagagcttt	ggggattcgt	tgaatggctc	agagaggtgt	ttaccggtga	tggatatgac	660
gatacttacg	atttcttttt	aaattctgct	attgtgacct	attgatcagt	gggactttat	720
cttacttgta	ctgtgggaat	tttgagtatg	attttaatag	ataaataaat	gtgatttgct	780
aacaacatta	caacatagat	ctaagcattc	aaggttggtg	tgggtgcctga	tggcttttga	840
tgaaggggag	gttttctact	ttgtatcaga	cttttgcttg	ctagtgaag	agagaataat	900
gggcacaaca	tttttggttac	tccatgggaa	agataatgta	gagtgggtctc	aaggaaaaaa	960
tgggtgtggag	agtgtgtcaag	ggacttggat	tgccaaacat	tgtgttttcag	tttgggtggtg	1020
tacaatgttg	gatcacccct	atggtcgtaa	agtgcagatt	tcgcagagct	ttccaaggga	1080
atcatagaat	cgtcaacgga	gttggtgttc	gaaccaaagg	atgtatattt	cgttccactt	1140
tcttcttgca	ctctgctaca	gtaacacatg	gatttgatg	ctctcatggg	agtgtacaaa	1200
ctcctagtga	ttgggtgttt	tatttgcctt	ttggaatgct	taaagaatga	tat	

(2) INFORMATION FOR SEQ ID NO:883:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 234 amino acids

- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..234
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1499128
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:883:

Lys His Met Thr Pro Lys Ser Arg Gly Phe Val Arg Arg Arg Arg Ser
1 5 10 15
Arg Arg Val Leu Val Leu Asp Cys Arg Ser Gln Gln Trp Arg Ser Leu
20 25 30
Pro Lys Met Arg Gln Pro Arg Ala Ser Pro Ala Ala Tyr Val Lys Asp
35 40 45
Gly Leu Ile Ile Val Ile Gly Gly Cys Arg Ser Lys Asn Ile Glu Thr
50 55 60
Trp Gly Glu Ile Tyr Asp Leu Lys Thr Asn Thr Trp Gly Arg Ile Leu
65 70 75 80
Leu Gln Ser His Asp Pro Thr Val Gln Asn Ala Tyr Leu Asn Arg Phe
85 90 95
Lys Pro Asn Leu Gln Thr Asn Ala Cys Tyr Val Glu Ile Asp Lys Val
100 105 110
Ser Cys Leu Ile Phe Leu Ser Asp Gly Lys Leu Phe Trp Arg Glu Thr
115 120 125
Lys Gln Gly Phe Glu Arg Cys Ser Val Ile Leu Gly Asp Asp Glu Gln
130 135 140
Val Ser Ser Tyr Gln Leu Val Ser Val Ala Asn Ala Ala Gly Gly Gly
145 150 155 160
Arg Val Thr Val Trp Trp Lys Ser Gly Leu Lys Val Leu Asp Leu Leu
165 170 175
Ser Gly Thr Glu Thr Trp Glu Cys Tyr Thr Asn Ser Arg Cys Ala Glu
180 185 190
Ile Ser Phe Glu Arg Arg Gly Leu Arg Glu Leu Trp Gly Phe Val Glu
195 200 205
Trp Ser Arg Glu Val Phe Thr Val Asp Gly Tyr Asp Asp Thr Tyr Asp
210 215 220
Phe Phe Leu Asn Ser Ala Ile Val Thr Tyr
225 230

(2) INFORMATION FOR SEQ ID NO:884:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 232 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..232
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1499129
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:884:

Met Thr Pro Lys Ser Arg Gly Phe Val Arg Arg Arg Arg Arg Ser Arg Arg
1 5 10 15
Val Leu Val Leu Asp Cys Arg Ser Gln Gln Trp Arg Ser Leu Pro Lys
20 25 30
Met Arg Gln Pro Arg Ala Ser Pro Ala Ala Tyr Val Lys Asp Gly Leu
35 40 45
Ile Ile Val Ile Gly Gly Cys Arg Ser Lys Asn Ile Glu Thr Trp Gly
50 55 60
Glu Ile Tyr Asp Leu Lys Thr Asn Thr Trp Gly Arg Ile Leu Leu Gln
65 70 75 80

Ser His Asp Pro Thr Val Gln Asn Ala Tyr Leu Asn Arg Phe Lys Pro
85 90 95
Asn Leu Gln Thr Asn Ala Cys Tyr Val Glu Ile Asp Lys Val Ser Cys
100 105 110
Leu Ile Phe Leu Ser Asp Gly Lys Leu Phe Trp Arg Glu Thr Lys Gln
115 120 125
Gly Phe Glu Arg Cys Ser Val Ile Leu Gly Asp Asp Glu Gln Val Ser
130 135 140
Ser Tyr Gln Leu Val Ser Val Ala Asn Ala Ala Gly Gly Gly Arg Val
145 150 155 160
Thr Val Trp Trp Lys Ser Gly Leu Lys Val Leu Asp Leu Leu Ser Gly
165 170 175
Thr Glu Thr Trp Glu Cys Tyr Thr Asn Ser Arg Cys Ala Glu Ile Ser
180 185 190
Phe Glu Arg Arg Gly Leu Arg Glu Leu Trp Gly Phe Val Glu Trp Ser
195 200 205
Arg Glu Val Phe Thr Val Asp Gly Tyr Asp Asp Thr Tyr Asp Phe Phe
210 215 220
Leu Asn Ser Ala Ile Val Thr Tyr
225 230

(2) INFORMATION FOR SEQ ID NO:885:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 200 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..200

(D) OTHER INFORMATION: / Ceres Seq. ID 1499130

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:885:

Met Arg Gln Pro Arg Ala Ser Pro Ala Tyr Val Lys Asp Gly Leu
1 5 10 15
Ile Ile Val Ile Gly Gly Cys Arg Ser Lys Asn Ile Glu Thr Trp Gly
20 25 30
Glu Ile Tyr Asp Leu Lys Thr Asn Thr Trp Gly Arg Ile Leu Leu Gln
35 40 45
Ser His Asp Pro Thr Val Gln Asn Ala Tyr Leu Asn Arg Phe Lys Pro
50 55 60
Asn Leu Gln Thr Asn Ala Cys Tyr Val Glu Ile Asp Lys Val Ser Cys
65 70 75 80
Leu Ile Phe Leu Ser Asp Gly Lys Leu Phe Trp Arg Glu Thr Lys Gln
85 90 95
Gly Phe Glu Arg Cys Ser Val Ile Leu Gly Asp Asp Glu Gln Val Ser
100 105 110
Ser Tyr Gln Leu Val Ser Val Ala Asn Ala Ala Gly Gly Arg Val
115 120 125
Thr Val Trp Trp Lys Ser Gly Leu Lys Val Leu Asp Leu Leu Ser Gly
130 135 140
Thr Glu Thr Trp Glu Cys Tyr Thr Asn Ser Arg Cys Ala Glu Ile Ser
145 150 155 160
Phe Glu Arg Arg Gly Leu Arg Glu Leu Trp Gly Phe Val Glu Trp Ser
165 170 175
Arg Glu Val Phe Thr Val Asp Gly Tyr Asp Asp Thr Tyr Asp Phe Phe
180 185 190
Leu Asn Ser Ala Ile Val Thr Tyr
195 200

(2) INFORMATION FOR SEQ ID NO:886:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1636 base pairs

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- (B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
(A) NAME/KEY: -
(B) LOCATION: 1..1636
(D) OTHER INFORMATION: / Ceres Seq. ID 1499135
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:886:

```
ggagagtaac atcgagacaa agaagaaaag ctaaaaaaga gaaccccaaa gaatcgaata      60
tttattattt cgccccgaag attctatttc tgatcattta caccacctaa aagagtagag      120
ctttcgtgaa gccaccatgt gtggaggagc tataatctcc gatttcatac ctccgccgag      180
gtccctccgc gtcactaacg agtttatctg gccggatctg aaaaacaaag tgaaagcttc      240
aaagaagaga tcgaataagc gatccgattt cttcgatctt gacgatgatt tcgaagctga      300
tttccaaggg tttaaggatg actcggcttt tgactgcgaa gacgatgatg atgtcttcgt      360
caatgttaag cttttcgtct tcaccgcaac tactaagccc gtagcttccg ctttcgtctc      420
cactgggtata tatttggtag gttcagcata tgccaagaaa actgtagagt ccgctgagca      480
agctgagaaa tcttctaaga ggaagaggaa gaatcagtac cgagggatta ggcagcgtcc      540
ttggggaaaa tgggctgcgg agatccgtga tccgagaaaa ggctcccagag aatggcttgg      600
aacattcgac actgctgagg aagcagcaag agcttatgat gctgcagcac gcagaatccg      660
tggcacgaaa gctaaggatg attttcccg ggaagaagaa cctagcgtcg tatcccagaa      720
acgtcctagt gctaagacta ataattctca gaaatcagtg gctaaaaccaa acaaaagcgt      780
aactttggtt cagcagccaa cacatctgag tcagcagtac tgcaacaact cttttgacaa      840
ctcttttggt gatatgagtt tcatggaaga gaagcctcag atgtacaaca atcagtttgg      900
gttaacaaac tcgttcgatg ctggaggtaa caatggatac cagtatttca gttccgatca      960
gggcagtaac tccttcgact gttctgagtt cgggtggagt gatcacggcc ctaaaacacc     1020
cgagatctct tcaatgcttg tcaataacaa cgaagcatca tttgttgaag aaaccaatgc     1080
agccaagaag ctcaaaccta actctgatga gtcagacgat ctgatggcat accttgacaa     1140
cgccctgtgg gacacccac tagaagtgaag agccatgctt ggcgagatg ctggtgctgt     1200
gactcaggaa gaggaaaacc cagtggagct atggagctta gatgagatca atttcatgct     1260
ggaaggagac ttttgaagtg atcgatggtt ccttagtttg taaataaagc tgtgttggat     1320
tttgctgttg ggggatggta caagtcacac ctcaagctct atgcattggt atctcatgag     1380
cctctcttcc atagagagtt tctcttttaa ttttgtcgaa ataaaaaagg tgtgatgaag     1440
taaataagagg tataataata tctatctatt aagtcttgtt ttgttctttc atttttgtat     1500
ttcttttcta tttaaaagac agtttattag tcttctgagc tctctttttg atctttgtta     1560
tagcgtatca tcaccctcga aagtgtaatg ttttgtacc ccaaacttgt ttagcattat     1620
aataaagtct ctttgg
```

(2) INFORMATION FOR SEQ ID NO:887:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 379 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..379
(D) OTHER INFORMATION: / Ceres Seq. ID 1499136
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:887:

```
Met Cys Gly Gly Ala Ile Ile Ser Asp Phe Ile Pro Pro Pro Arg Ser
1          5          10          15
Leu Arg Val Thr Asn Glu Phe Ile Trp Pro Asp Leu Lys Asn Lys Val
20          25          30
Lys Ala Ser Lys Lys Arg Ser Asn Lys Arg Ser Asp Phe Phe Asp Leu
35          40          45
Asp Asp Asp Phe Glu Ala Asp Phe Gln Gly Phe Lys Asp Asp Ser Ala
50          55          60
Phe Asp Cys Glu Asp Asp Asp Asp Val Phe Val Asn Val Lys Pro Phe
65          70          75          80
Val Phe Thr Ala Thr Thr Lys Pro Val Ala Ser Ala Phe Val Ser Thr
85          90          95
```

Gly Ile Tyr Leu Val Gly Ser Ala Tyr Ala Lys Lys Thr Val Glu Ser
100 105 110
Ala Glu Gln Ala Glu Lys Ser Ser Lys Arg Lys Arg Lys Asn Gln Tyr
115 120 125
Arg Gly Ile Arg Gln Arg Pro Trp Gly Lys Trp Ala Ala Glu Ile Arg
130 135 140
Asp Pro Arg Lys Gly Ser Arg Glu Trp Leu Gly Thr Phe Asp Thr Ala
145 150 155 160
Glu Glu Ala Ala Arg Ala Tyr Asp Ala Ala Arg Arg Ile Arg Gly
165 170 175
Thr Lys Ala Lys Val Asn Phe Pro Glu Glu Lys Asn Pro Ser Val Val
180 185 190
Ser Gln Lys Arg Pro Ser Ala Lys Thr Asn Asn Leu Gln Lys Ser Val
195 200 205
Ala Lys Pro Asn Lys Ser Val Thr Leu Val Gln Gln Pro Thr His Leu
210 215 220
Ser Gln Gln Tyr Cys Asn Asn Ser Phe Asp Asn Ser Phe Gly Asp Met
225 230 235 240
Ser Phe Met Glu Glu Lys Pro Gln Met Tyr Asn Asn Gln Phe Gly Leu
245 250 255
Thr Asn Ser Phe Asp Ala Gly Gly Asn Asn Gly Tyr Gln Tyr Phe Ser
260 265 270
Ser Asp Gln Gly Ser Asn Ser Phe Asp Cys Ser Glu Phe Gly Trp Ser
275 280 285
Asp His Gly Pro Lys Thr Pro Glu Ile Ser Ser Met Leu Val Asn Asn
290 295 300
Asn Glu Ala Ser Phe Val Glu Glu Thr Asn Ala Ala Lys Lys Leu Lys
305 310 315 320
Pro Asn Ser Asp Glu Ser Asp Asp Leu Met Ala Tyr Leu Asp Asn Ala
325 330 335
Leu Trp Asp Thr Pro Leu Glu Val Lys Ala Met Leu Gly Ala Asp Ala
340 345 350
Gly Ala Val Thr Gln Glu Glu Glu Asn Pro Val Glu Leu Trp Ser Leu
355 360 365
Asp Glu Ile Asn Phe Met Leu Glu Gly Asp Phe
370 375

(2) INFORMATION FOR SEQ ID NO:888:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 907 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..907
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499141

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:888:

ctatctttgt	cgccgccaaa	cctctctcag	attcttcttc	ttcctcgcag	atcgattttt	60
ttttgaagct	aaatctcaaa	aatggagaac	gacgcaggtc	aggtcacaga	gctctacatt	120
tttgagattt	agcttcaaaa	acaaatccca	aagcttcaga	ggaagaagaa	gaagagagtg	180
agaaacaatg	gcgtcgacga	ctctctcaat	cgcaacaaca	atccgttcc	cttctcctct	240
cacttccgct	tccactcatc	acttcctttc	caaaccaccc	gcaatcgaat	tcccatattcg	300
tctcagctct	tcttctagcc	accgtgcaat	caacctccgt	cctatctccg	ccgtcgaagc	360
tccggagaaa	atcgagaaga	tcggatccga	aatctcatcc	ctaaccctcg	aagaagctcg	420
tatcctcgtc	gactatctcc	aagacaaatt	cgggtgtctcc	ccactctctt	tagcccccg	480
agcagcggcg	gttgctgctc	cagccgacgg	tggcgcgggc	gctgtagtgg	aggagcaaac	540
agagttcgat	gtggttatca	atgaagttcc	cagcagttcc	cgtattgcag	tgattaaagc	600
tgtagggct	ttaactagct	tggcgttgaa	ggaagctaag	gagctaatac	aaggattacc	660
aaagaagttt	aaagaagata	tcactaaaga	tgaagctgaa	gaagctaaga	agactcttga	720
agaagctggt	gctaaagtct	ccattgctta	agtttcttca	acaatcggaa	aaaaaaaaat	780

gtgatctttt cggaatttat gagtcttttt gttgttttagt atagtttgtg tttgagttgt 840
tgattcagct tttgagaaat tgttgactt tgaatcaatt tggtttcgta ttacagtttt 900
agtcttc

(2) INFORMATION FOR SEQ ID NO:889:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 187 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..187

(D) OTHER INFORMATION: / Ceres Seq. ID 1499142

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:889:

Met Ala Ser Thr Thr Leu Ser Ile Ala Thr Thr Ile Arg Ser Ser Ser
1 5 10 15
Pro Leu Thr Ser Ala Ser Thr His His Phe Leu Ser Lys Pro Thr Ala
20 25 30
Ile Glu Phe Pro Phe Arg Leu Ser Ser Ser Ser His Arg Ala Ile
35 40 45
Asn Leu Arg Pro Ile Ser Ala Val Glu Ala Pro Glu Lys Ile Glu Lys
50 55 60
Ile Gly Ser Glu Ile Ser Ser Leu Thr Leu Glu Glu Ala Arg Ile Leu
65 70 75 80
Val Asp Tyr Leu Gln Asp Lys Phe Gly Val Ser Pro Leu Ser Leu Ala
85 90 95
Pro Ala Ala Ala Val Ala Ala Pro Ala Asp Gly Gly Ala Ala Ala
100 105 110
Val Val Glu Glu Gln Thr Glu Phe Asp Val Val Ile Asn Glu Val Pro
115 120 125
Ser Ser Ser Arg Ile Ala Val Ile Lys Ala Val Arg Ala Leu Thr Ser
130 135 140
Leu Ala Leu Lys Glu Ala Lys Glu Leu Ile Glu Gly Leu Pro Lys Lys
145 150 155 160
Phe Lys Glu Asp Ile Thr Lys Asp Glu Ala Glu Glu Ala Lys Lys Thr
165 170 175
Leu Glu Glu Ala Gly Ala Lys Val Ser Ile Ala
180 185

(2) INFORMATION FOR SEQ ID NO:890:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 674 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..674

(D) OTHER INFORMATION: / Ceres Seq. ID 1499147

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:890:

acataactcc aatgtcccag ttctgcaaac gcttagcctc aaaaggtctt aagctcactc 60
tggtcctcgt ctccgacaaa ccctctcctc catacaaaac agagcacgac tcaatcactg 120
tcttccccat ctccaacggc ttccaagaac gcgaggaacc attacaagac ctcgatgatt 180
acatggaaaag agtagaaacc agcatcaaaa acaccttacc gaagttggtt gaagacatga 240
aactgtcggg aaatccacct agggctatcg tgtacgactc caccatgcca tggcttcttg 300
atgtagctca tagttatgga ttgagcgggt ccggtgtttt cacgcaacct tggcttgatca 360
cagctattta ctaccatggt ttcaagggtt cgttctctgt accatctaca aagtacggtc 420
actcgacatt agcatctttc ccttcgttcc cgatgctgac tgcaaatgat ttgccgtctt 480
tcctctgcga atcgctcctca taccggaata tactgaggat tgtggtggat cagctctcaa 540
acattgatcg agtcgacata gtgtgtgcaa cactttcgat aaattggagg aaaagtgttg 600

aaatgggtca aagcttgtgg ccagtctgaa tatkgaccaa cggttccatc gatgtattag 660
acaacgactg tctg

(2) INFORMATION FOR SEQ ID NO:891:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 208 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..208
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499148

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:891:

Ile	Thr	Pro	Met	Ser	Gln	Phe	Cys	Lys	Arg	Leu	Ala	Ser	Lys	Gly	Leu	
1				5					10					15		
Lys	Leu	Thr	Leu	Val	Leu	Val	Ser	Asp	Lys	Pro	Ser	Pro	Pro	Tyr	Lys	
			20					25					30			
Thr	Glu	His	Asp	Ser	Ile	Thr	Val	Phe	Pro	Ile	Ser	Asn	Gly	Phe	Gln	
		35					40					45				
Glu	Arg	Glu	Glu	Pro	Leu	Gln	Asp	Leu	Asp	Asp	Tyr	Met	Glu	Arg	Val	
	50					55					60					
Glu	Thr	Ser	Ile	Lys	Asn	Thr	Leu	Pro	Lys	Leu	Val	Glu	Asp	Met	Lys	
65					70					75				80		
Leu	Ser	Gly	Asn	Pro	Arg	Ala	Ile	Val	Tyr	Asp	Ser	Thr	Met	Pro		
			85					90				95				
Trp	Leu	Leu	Asp	Val	Ala	His	Ser	Tyr	Gly	Leu	Ser	Gly	Ala	Val	Phe	
			100					105					110			
Phe	Thr	Gln	Pro	Trp	Leu	Val	Thr	Ala	Ile	Tyr	Tyr	His	Val	Phe	Lys	
		115					120					125				
Gly	Ser	Phe	Ser	Val	Pro	Ser	Thr	Lys	Tyr	Gly	His	Ser	Thr	Leu	Ala	
	130					135					140					
Ser	Phe	Pro	Ser	Phe	Pro	Met	Leu	Thr	Ala	Asn	Asp	Leu	Pro	Ser	Phe	
145					150					155					160	
Leu	Cys	Glu	Ser	Ser	Ser	Tyr	Pro	Asn	Ile	Leu	Arg	Ile	Val	Val	Asp	
				165				170					175			
Gln	Leu	Ser	Asn	Ile	Asp	Arg	Val	Asp	Ile	Val	Cys	Ala	Thr	Leu	Ser	
			180					185					190			
Ile	Asn	Trp	Arg	Lys	Ser	Val	Glu	Met	Gly	Gln	Ser	Leu	Trp	Pro	Val	
		195					200					205				

(2) INFORMATION FOR SEQ ID NO:892:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 205 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..205
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499149

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:892:

Met	Ser	Gln	Phe	Cys	Lys	Arg	Leu	Ala	Ser	Lys	Gly	Leu	Lys	Leu	Thr	
1				5					10					15		
Leu	Val	Leu	Val	Ser	Asp	Lys	Pro	Ser	Pro	Pro	Tyr	Lys	Thr	Glu	His	
			20					25					30			
Asp	Ser	Ile	Thr	Val	Phe	Pro	Ile	Ser	Asn	Gly	Phe	Gln	Glu	Arg	Glu	
		35					40					45				
Glu	Pro	Leu	Gln	Asp	Leu	Asp	Asp	Tyr	Met	Glu	Arg	Val	Glu	Thr	Ser	

50		55		60											
Ile	Lys	Asn	Thr	Leu	Pro	Lys	Leu	Val	Glu	Asp	Met	Lys	Leu	Ser	Gly
65					70					75					80
Asn	Pro	Pro	Arg	Ala	Ile	Val	Tyr	Asp	Ser	Thr	Met	Pro	Trp	Leu	Leu
				85						90					95
Asp	Val	Ala	His	Ser	Tyr	Gly	Leu	Ser	Gly	Ala	Val	Phe	Phe	Thr	Gln
				100						105				110	
Pro	Trp	Leu	Val	Thr	Ala	Ile	Tyr	Tyr	His	Val	Phe	Lys	Gly	Ser	Phe
				115						120				125	
Ser	Val	Pro	Ser	Thr	Lys	Tyr	Gly	His	Ser	Thr	Leu	Ala	Ser	Phe	Pro
				130						135				140	
Ser	Phe	Pro	Met	Leu	Thr	Ala	Asn	Asp	Leu	Pro	Ser	Phe	Leu	Cys	Glu
145						150					155				160
Ser	Ser	Ser	Tyr	Pro	Asn	Ile	Leu	Arg	Ile	Val	Val	Asp	Gln	Leu	Ser
				165							170				175
Asn	Ile	Asp	Arg	Val	Asp	Ile	Val	Cys	Ala	Thr	Leu	Ser	Ile	Asn	Trp
				180						185				190	
Arg	Lys	Ser	Val	Glu	Met	Gly	Gln	Ser	Leu	Trp	Pro	Val			
				195						200				205	

(2) INFORMATION FOR SEQ ID NO:893:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 148 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..148
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499150

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:893:

Met	Glu	Arg	Val	Glu	Thr	Ser	Ile	Lys	Asn	Thr	Leu	Pro	Lys	Leu	Val
1				5				10						15	
Glu	Asp	Met	Lys	Leu	Ser	Gly	Asn	Pro	Pro	Arg	Ala	Ile	Val	Tyr	Asp
				20				25					30		
Ser	Thr	Met	Pro	Trp	Leu	Leu	Asp	Val	Ala	His	Ser	Tyr	Gly	Leu	Ser
				35				40					45		
Gly	Ala	Val	Phe	Phe	Thr	Gln	Pro	Trp	Leu	Val	Thr	Ala	Ile	Tyr	Tyr
				50				55					60		
His	Val	Phe	Lys	Gly	Ser	Phe	Ser	Val	Pro	Ser	Thr	Lys	Tyr	Gly	His
65						70					75				80
Ser	Thr	Leu	Ala	Ser	Phe	Pro	Ser	Phe	Pro	Met	Leu	Thr	Ala	Asn	Asp
				85						90				95	
Leu	Pro	Ser	Phe	Leu	Cys	Glu	Ser	Ser	Ser	Tyr	Pro	Asn	Ile	Leu	Arg
				100						105				110	
Ile	Val	Val	Asp	Gln	Leu	Ser	Asn	Ile	Asp	Arg	Val	Asp	Ile	Val	Cys
				115						120				125	
Ala	Thr	Leu	Ser	Ile	Asn	Trp	Arg	Lys	Ser	Val	Glu	Met	Gly	Gln	Ser
				130						135				140	
Leu	Trp	Pro	Val												
145															

(2) INFORMATION FOR SEQ ID NO:894:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1689 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1689

(D) OTHER INFORMATION: / Ceres Seq. ID 1499159

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:894:

```
accgactctc tctctctctc tctccgtaac aaaaaaatca ccaatggcaa aacaatatct 60
ctttgtactc ctctcaatct cctatctctt atcactggag ctacacggcg ccaccgcagc 120
ctcacagacc ggagcttcca aaaaagccat aaacttcatc caatcttctt aaaaaaccac 180
cacataccct gccttatgtg tccactcact ctccgtctac gcaaacgaca tccaaacaag 240
ccctaaacgt ttagctgaga ccgctatagc cgtgacacta agccgagccc aatccacgaa 300
gctcttcgtc tcgctgtctaa cagctatgaa gggtcttaag aagcgcgagg tcgaagccat 360
caaagattgc gtcgaggaga tgaacgatac cggtgaccgt ttgaccaa atgtttcaaga 420
actgaagttg tgtgggagtg tcaaacagaa gaaagagtcg agttctgaag agtcgggagc 480
ggaggaagag tgaacagaa atgagatttt acattgataa acaaaacaaa aaatacaata 540
cttttgcctt aatcttgacg gaaacttttt tttttgctgc ggaacatttc ctttatttta 600
atataatggt atgtgaaaat gaattcatct aaagacaaaac tgaaaaacat gaaacaagac 660
tctctttttg tagcagatag agagagacac agagagaaaa agagatggca aacgaaacgg 720
ctagtaaagt agcgggttac ttatctaacc aagactcaag acaccaaaac agacatgttt 780
gcatctaaga tatgcttatt tgttgacaga ttaataatac tcagggtagt ggcactggtg 840
gaacttggcc gttgcttcct gtgccagctc caatggctcg gggtggcgct tcaaattcgg 900
ggtttgggac aagcgtatca tgcaccacag ggagttgggt gtgaggtccg gccccttctc 960
caccattata tgatgggatt cccccaccag taagtggagc tccggtgaca ggattgtaag 1020
ggtagaacgg cttcttgcat ttgggaggaa gcaagaacct tccaacaccg ggaatgagaa 1080
tagttggttt gggctcaatg gttacaagaa agtcagggtg tttgacatca gtggtcttag 1140
gggacttggg aacgtgacgt agtccactca cttgctctac agatccaagc actaggctta 1200
aaaccacgac aatgactgcg gaggtgataa gtgaagaagc cattaatttt attttatttt 1260
gtttagagag agaaagctcg tgtgtttgtt tgaccaaadc tgttcaagaa ctgaagttgt 1320
gtgggagtgc caaagatcaa gaccagtttg cgtaccacat tagtaatgct cagacttoga 1380
ctagtgcggc tttgactgac gagaacactt gctccgatgg gttctcgggt cgggttatgg 1440
atgggaggat caagaactcg gttcgggcta gaatcatgaa cgtgggacat gaaaccagca 1500
acgctttgtc cttgattaat gcctttgcta aaacttacta attttaaact atattttgtc 1560
ctgtaaaata tatatataga taaatgtaat gtcttgctaa gagtttgatg tgatatattt 1620
ttttcgattt tggtagtttc tttttgtttt gtaacgtggg ttataatagt ataatgtgta 1680
ttttgagct
```

(2) INFORMATION FOR SEQ ID NO:895:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 81 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..81

(D) OTHER INFORMATION: / Ceres Seq. ID 1499160

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:895:

```
Thr Asp Ser Leu Ser Leu Ser Leu Arg Asn Lys Lys Ile Thr Asn Gly
1          5          10          15
Lys Thr Ile Ser Leu Cys Thr Pro Leu Asn Leu Leu Ser Leu Ile Thr
20          25          30
Gly Ala His Gly Gly His Arg Ser Leu Thr Asp Arg Ser Phe Gln Lys
35          40          45
Ser His Lys Leu His Pro Ile Phe Leu Lys Asn His His Ile Pro Cys
50          55          60
Leu Met Cys Pro Leu Thr Leu Arg Leu Arg Lys Arg His Pro Asn Lys
65          70          75          80
Pro
```

(2) INFORMATION FOR SEQ ID NO:896:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 72 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..72
 (D) OTHER INFORMATION: / Ceres Seq. ID 1499161

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:896:

```
Met Phe Ala Ser Lys Ile Cys Leu Phe Val Asp Arg Leu Ile Ile Leu
1           5           10           15
Arg Val Val Ala Leu Val Glu Leu Gly Arg Cys Phe Leu Cys Gln Leu
          20           25           30
Gln Trp Ser Gly Leu Ala Leu Gln Ile Arg Gly Leu Gly Gln Ala Tyr
          35           40           45
His Arg His Gln Gly Val Gly Cys Glu Val Arg Pro Leu Val His His
          50           55           60
Tyr Met Met Gly Phe Pro His Gln
65           70
```

(2) INFORMATION FOR SEQ ID NO:897:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 109 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..109
(D) OTHER INFORMATION: / Ceres Seq. ID 1499162

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:897:

```
Met Thr Ala Glu Val Ile Ser Glu Glu Ala Ile Asn Phe Ile Leu Phe
1           5           10           15
Cys Cys Arg Gly Glu Ser Ser Cys Val Cys Leu Thr Lys Ser Val Gln
          20           25           30
Glu Leu Lys Leu Cys Gly Ser Ala Lys Asp Gln Asp Gln Phe Ala Tyr
          35           40           45
His Ile Ser Asn Ala Gln Thr Trp Thr Ser Ala Ala Leu Thr Asp Glu
          50           55           60
Asn Thr Cys Ser Asp Gly Phe Ser Gly Arg Val Met Asp Gly Arg Ile
65           70           75           80
Lys Asn Ser Val Arg Ala Arg Ile Met Asn Val Gly His Glu Thr Ser
          85           90           95
Asn Ala Leu Ser Leu Ile Asn Ala Phe Ala Lys Thr Tyr
          100          105
```

(2) INFORMATION FOR SEQ ID NO:898:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1367 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
(B) LOCATION: 1..1367
(D) OTHER INFORMATION: / Ceres Seq. ID 1499163

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:898:

```
gattttcact ttcaaaattc gttccgcttt ttcttttttc ggagaaagat tcaatctttc      60
tgaatcatgt actgaaatat catcattcaa acgaacagtg ttctccattt tgtcgggaat      120
cagagtttct gcttctctgt aaaaccaaag ctttctcttt tataattttc taatggcgtc      180
aagagaagta tcaacgatga taagaaaagg gtttatctct gatcattctc tctctttctc      240
tcctttaaga accacgtctg tctccaaacc cttgtccccc atagcctctc ctctttctcc      300
gtacgattcc actagcctct ggcaagaagc tgaatttggt gggcatagat gggtagagag      360
tgaccatgga tgtgcacaag aggccttttg agagagaatg gagtctctca ttctaaaaat      420
```

ggtggagata	agtgagtgcg	atgtgtacgt	agagactgtg	gtgttgatgt	attgagatga	480
tcttaacaac	aagttagttg	gtgaaactgt	catcaaaatc	ttggctttcc	ttaaggtttc	540
ttcagctata	atgcttgacg	agggaataaa	gtattaccta	ctatggccgg	gtcagaagga	600
gctagcaatc	cccattccaa	gattccagct	atgtacagac	acaaaatatg	caagatcact	660
gcaagaaatc	tatctttttg	gtaaaggaag	gatcttggtg	aatagggaga	ctcggttttc	720
ggtgaattga	tacagtgcact	actctacttt	gcaactgcaa	actaataatg	aaacagagag	780
aactcaacat	ggctctattc	acttccgtgc	tccttccaaa	atcttctggc	gtaccgttcg	840
cggatatgatt	ccacacaaga	cgaagcgtgg	agctgctgca	ctagcacgtt	tgaagggtata	900
tgaagggtgtt	cctactccat	atgacaagat	caagaggatg	gtcatccctg	atgctctcaa	960
ggtgttgagg	cttcaagctg	gtcacaaata	ctgtctggtg	ggccgtcttt	cttctgaagt	1020
tgggtggaac	cattacgaca	ccatcaagga	gctggagaca	aagaggaagg	agagagccca	1080
cgtggtttac	gagcgaaaga	agcaacttaa	caaacttaga	gttaaggccg	agaagggtgc	1140
tgaagagaag	ctcggagcac	agctcgatat	tcttgcgcca	gttaagtact	gagcttgtea	1200
gtagtagttt	tttttttttt	ggtaaggagc	ttgtcagtag	tagtttgtct	ttgcatgttt	1260
tgagccaacc	caataccttt	ttacttttta	tcttttactt	aggtcttgta	tcgaaatttg	1320
tactcctaac	atttttattct	tgagttttat	ttatttatatt	gcgtggc		

(2) INFORMATION FOR SEQ ID NO:899:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 100 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..100

(D) OTHER INFORMATION: / Ceres Seq. ID 1499164

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:899:

Met	Ala	Ser	Arg	Glu	Val	Ser	Thr	Met	Ile	Arg	Lys	Gly	Phe	Ile	Ser
1				5				10						15	
Asp	His	Ser	Leu	Ser	Phe	Ser	Pro	Leu	Arg	Thr	Thr	Ser	Val	Ser	Lys
			20					25					30		
Pro	Leu	Ser	Pro	Ile	Ala	Ser	Pro	Pro	Ser	Pro	Tyr	Asp	Ser	Thr	Ser
			35					40				45			
Leu	Trp	Gln	Glu	Ala	Glu	Phe	Gly	Gly	His	Arg	Trp	Val	Gln	Ser	Asp
	50					55					60				
His	Gly	Cys	Ala	Gln	Glu	Ala	Phe	Glu	Glu	Arg	Met	Glu	Ser	Leu	Ile
65				70				75						80	
Leu	Lys	Met	Val	Glu	Ile	Ser	Glu	Cys	Asp	Val	Tyr	Val	Glu	Thr	Val
			85					90						95	
Val	Leu	Met	Tyr												
			100												

(2) INFORMATION FOR SEQ ID NO:900:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 92 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..92

(D) OTHER INFORMATION: / Ceres Seq. ID 1499165

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:900:

Met	Ile	Arg	Lys	Gly	Phe	Ile	Ser	Asp	His	Ser	Leu	Ser	Phe	Ser	Pro
1				5				10						15	
Leu	Arg	Thr	Thr	Ser	Val	Ser	Lys	Pro	Leu	Ser	Pro	Ile	Ala	Ser	Pro
			20					25					30		
Pro	Ser	Pro	Tyr	Asp	Ser	Thr	Ser	Leu	Trp	Gln	Glu	Ala	Glu	Phe	Gly
			35					40				45			
Gly	His	Arg	Trp	Val	Gln	Ser	Asp	His	Gly	Cys	Ala	Gln	Glu	Ala	Phe

50 55 60
Glu Glu Arg Met Glu Ser Leu Ile Leu Lys Met Val Glu Ile Ser Glu
65 70 75 80
Cys Asp Val Tyr Val Glu Thr Val Val Leu Met Tyr
85 90

(2) INFORMATION FOR SEQ ID NO:901:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 115 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..115

(D) OTHER INFORMATION: / Ceres Seq. ID 1499166

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:901:

Met Ile Pro His Lys Thr Lys Arg Gly Ala Ala Leu Ala Arg Leu
1 5 10 15
Lys Val Tyr Glu Gly Val Pro Thr Pro Tyr Asp Lys Ile Lys Arg Met
20 25 30
Val Ile Pro Asp Ala Leu Lys Val Leu Arg Leu Gln Ala Gly His Lys
35 40 45
Tyr Cys Leu Leu Gly Arg Leu Ser Ser Glu Val Gly Trp Asn His Tyr
50 55 60
Asp Thr Ile Lys Glu Leu Glu Thr Lys Arg Lys Glu Arg Ala His Val
65 70 75 80
Val Tyr Glu Arg Lys Lys Gln Leu Asn Lys Leu Arg Val Lys Ala Glu
85 90 95
Lys Val Ala Glu Lys Leu Gly Ala Gln Leu Asp Ile Leu Ala Pro
100 105 110
Val Lys Tyr
115

(2) INFORMATION FOR SEQ ID NO:902:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1368 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1368

(D) OTHER INFORMATION: / Ceres Seq. ID 1499185

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:902:

aactgataaa gtgataacgg agttgggttg aacgtgaaac gcttataaaa ataaaccggt 60
ttaatttcac cggtttacct tccgccgtag atatcagccg caatgtacat tctcgacacc 120
ggagctcgat tctccgccgt cagattctca ccggtattca atcctcctcc aacatctctc 180
cgtagacgat acttcacgtg aagagctaatt cttccattcc caaagcatca agctaagtat 240
cataaagagc ttgaggtcgc cattgatgct gttgatcgag cttgtcgtct ctgtgttgat 300
gtcaaaagat ctcttttttc ttctaaagag aagattgttg agaagaatga tcaaactcca 360
gttacaattg cagatttttg agttcaagct ttagtcagct tggagctttc gaaattgttt 420
ccttcaatac cattagtggc tgaggaagac tctcattttg tgcgtgctaa taaccttgta 480
agctctgttg taagtgaagt caaatcaaaa gcaagcattg gagacaatca cttgtctgat 540
gctgatgtac ttgaagcaat tgatagaggt ggcaaagatg cttacacgtt ttgcaacaaa 600
ccagctactt attgggtttt ggaatccaatt gatggcacca ggggatttct taaaggagat 660
gaggctttat atgtggtagg attggccctt gttgtagata atgaaattgt gctaggagtc 720
atgggttgtc caaactggcc aggagattct tcagatggat ctactggaac cctaagtctc 780
tcgcatatag gctgtggaac gtggaccaag aagttacaaa atgtctctgg caatgtagcc 840
ggtgattgga taagggtgtt cgttgatgct tgtgttttaa tgaacaaagc aagattttgt 900
atacaagaaa gccaaacctg ggaatcactt cctctctctg gtttcttoga cgcaagtact 960

gtttcagagg acttaaaaca taaagagatt cttcttttgc ccacatgttg tggaagtttg 1020
tgcaagtatc tgatggtagc ttctggcaga gcatcagttt ttctttctccg agccaaaact 1080
cagagaacaa taaagtcgtg ggatcatgct gttgggatca tatgtgtaca tgaagctgga 1140
ggaaaggtaa cagattggga aggagatgaa ataaatttgg aggaagatca atcagaaagg 1200
aggctcattt ttccggcggg cgggtgttga gtaagcaacg gaagtttaca taatcagatt 1260
cttgagatga tctcttctgc ttcaccaact ctttgattta tgacactact actctctata 1320
cacttgtaa tgtttaccgt tactatttat ttatcataat ctttttct

(2) INFORMATION FOR SEQ ID NO:903:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 397 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..397

(D) OTHER INFORMATION: / Ceres Seq. ID 1499186

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:903:

Met Tyr Ile Leu Asp Thr Gly Ala Arg Phe Ser Ala Val Arg Phe Ser
1 5 10 15
Pro Val Phe Asn Pro Pro Pro Thr Ser Leu Arg Arg Arg Tyr Phe Ile
20 25 30
Val Arg Ala Asn Leu Pro Phe Pro Lys His Gln Ala Lys Tyr His Lys
35 40 45
Glu Leu Glu Val Ala Ile Asp Ala Val Asp Arg Ala Cys Arg Leu Cys
50 55 60
Val Asp Val Lys Arg Ser Leu Phe Ser Ser Lys Glu Lys Ile Val Glu
65 70 75 80
Lys Asn Asp Gln Thr Pro Val Thr Ile Ala Asp Phe Gly Val Gln Ala
85 90 95
Leu Val Ser Leu Glu Leu Ser Lys Leu Phe Pro Ser Ile Pro Leu Val
100 105 110
Ala Glu Glu Asp Ser His Phe Val Arg Ala Asn Asn Leu Val Ser Ser
115 120 125
Val Val Ser Glu Val Lys Ser Lys Ala Ser Ile Gly Asp Asn His Leu
130 135 140
Ser Asp Ala Asp Val Leu Glu Ala Ile Asp Arg Gly Gly Lys Asp Ala
145 150 155 160
Tyr Thr Phe Cys Asn Lys Pro Ala Thr Tyr Trp Val Leu Asp Pro Ile
165 170 175
Asp Gly Thr Arg Gly Phe Leu Lys Gly Asp Glu Ala Leu Tyr Val Val
180 185 190
Gly Leu Ala Leu Val Val Asp Asn Glu Ile Val Leu Gly Val Met Gly
195 200 205
Cys Pro Asn Trp Pro Gly Asp Ser Ser Asp Gly Ser Thr Gly Thr Leu
210 215 220
Met Leu Ser His Ile Gly Cys Gly Thr Trp Thr Lys Lys Leu Gln Asn
225 230 235 240
Val Ser Gly Asn Val Ala Gly Asp Trp Ile Arg Cys Phe Val Asp Ala
245 250 255
Cys Val Leu Met Asn Lys Ala Arg Phe Cys Ile Gln Glu Ser Gln Thr
260 265 270
Trp Glu Ser Leu Pro Leu Ser Gly Phe Phe Asp Ala Ser Thr Val Ser
275 280 285
Glu Asp Leu Lys His Lys Glu Ile Leu Leu Leu Pro Thr Cys Cys Gly
290 295 300
Ser Leu Cys Lys Tyr Leu Met Val Ala Ser Gly Arg Ala Ser Val Phe
305 310 315 320
Leu Leu Arg Ala Lys Thr Gln Arg Thr Ile Lys Ser Trp Asp His Ala
325 330 335

Val Gly Ile Ile Cys Val His Glu Ala Gly Gly Lys Val Thr Asp Trp
340 345 350
Glu Gly Asp Glu Ile Asn Leu Glu Glu Asp Gln Ser Glu Arg Arg Leu
355 360 365
Ile Phe Pro Ala Gly Gly Val Val Ser Asn Gly Ser Leu His Asn
370 375 380
Gln Ile Leu Glu Met Ile Ser Ser Ala Ser Pro Thr Leu
385 390 395

(2) INFORMATION FOR SEQ ID NO:904:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1063 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1063
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499190

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:904:

ctctttcctt	ttctcacgcc	gagatttctg	cgactgctct	agtcttacga	ccttataaga	60
aacgacgcta	ttttcactct	gcttgagctc	ttcatcgtgt	cacacagcac	gatcttggac	120
gtcgttttaa	gcgcaaaaca	aaggaaaaag	actgacgttt	atacatacta	aataccgggt	180
tggagttttg	ccttttggac	tcagaaaact	caaaagagag	agagagagag	agacatttct	240
gtatcttatc	gggttttgtg	ttgtcagaaa	gaagctcaag	gacaaaaaaa	aaagcaatta	300
tttttagggg	tcaaaagaag	caaaatttgg	aactttcaga	agttgtgggt	gggtggcttct	360
tgaacaataa	agctttttct	tagactcttc	ttccaatttg	tgactctacc	tatctctctc	420
tccaggtatg	gaattctctg	gagacgcttg	aatgatgatg	gagaacaagc	ggaatgtctg	480
ctctctcgga	gaaagcagca	tcaaacgccca	caagtctgat	ctctctttca	attccaagga	540
gaggaaggac	aagggttgag	aacgtatttc	agctcttcaa	caaatagttt	ccccttatgg	600
aaagaccgac	actgcatcag	ttcttctaga	cgcgatgcat	tacatagagt	ttcttcacga	660
acaagtgaag	gtgctaagtg	ctccgtatct	gcaaacgata	cctgatgcta	cgcaggagga	720
gctggagcag	tacagcctga	gaaacagagg	attatgtctt	gttccaatgg	agaatacagt	780
tggagttgct	caaagcaacg	gcgctgatat	atgggcgccc	gtgaagactc	ctctatcacc	840
agctttcagt	gtcacatctc	aatcaccctt	tagatgacca	attcgactaa	tcacctacta	900
cgatctttgt	gttaagccta	aaaaagaatg	accaattggt	atttttctga	tgatgcctct	960
gtaacatata	tagacagaga	gcacatgatg	ttggtttaga	actgctcatg	gttggcaatg	1020
attgttatta	ttatttgact	gcttaatgca	tccccttact	ttg		

(2) INFORMATION FOR SEQ ID NO:905:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 149 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..149
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499191

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:905:

Met	Glu	Phe	Ser	Gly	Asp	Ala	Gly	Met	Met	Met	Glu	Asn	Lys	Arg	Asn
1				5				10						15	
Val	Cys	Ser	Leu	Gly	Glu	Ser	Ser	Ile	Lys	Arg	His	Lys	Ser	Asp	Leu
			20					25						30	
Ser	Phe	Asn	Ser	Lys	Glu	Arg	Lys	Asp	Lys	Val	Gly	Glu	Arg	Ile	Ser
		35					40					45			
Ala	Leu	Gln	Gln	Ile	Val	Ser	Pro	Tyr	Gly	Lys	Thr	Asp	Thr	Ala	Ser
		50				55					60				
Val	Leu	Leu	Asp	Ala	Met	His	Tyr	Ile	Glu	Phe	Leu	His	Glu	Gln	Val
65					70					75				80	
Lys	Val	Leu	Ser	Ala	Pro	Tyr	Leu	Gln	Thr	Ile	Pro	Asp	Ala	Thr	Gln

85 90 95
Glu Glu Leu Glu Gln Tyr Ser Leu Arg Asn Arg Gly Leu Cys Leu Val
100 105 110
Pro Met Glu Asn Thr Val Gly Val Ala Gln Ser Asn Gly Ala Asp Ile
115 120 125
Trp Ala Pro Val Lys Thr Pro Leu Ser Pro Ala Phe Ser Val Thr Ser
130 135 140
Gln Ser Pro Phe Arg
145

(2) INFORMATION FOR SEQ ID NO:906:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 141 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..141
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499192

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:906:

Met Met Met Glu Asn Lys Arg Asn Val Cys Ser Leu Gly Glu Ser Ser
1 5 10 15
Ile Lys Arg His Lys Ser Asp Leu Ser Phe Asn Ser Lys Glu Arg Lys
20 25 30
Asp Lys Val Gly Glu Arg Ile Ser Ala Leu Gln Gln Ile Val Ser Pro
35 40 45
Tyr Gly Lys Thr Asp Thr Ala Ser Val Leu Leu Asp Ala Met His Tyr
50 55 60
Ile Glu Phe Leu His Glu Gln Val Lys Val Leu Ser Ala Pro Tyr Leu
65 70 75 80
Gln Thr Ile Pro Asp Ala Thr Gln Glu Glu Leu Glu Gln Tyr Ser Leu
85 90 95
Arg Asn Arg Gly Leu Cys Leu Val Pro Met Glu Asn Thr Val Gly Val
100 105 110
Ala Gln Ser Asn Gly Ala Asp Ile Trp Ala Pro Val Lys Thr Pro Leu
115 120 125
Ser Pro Ala Phe Ser Val Thr Ser Gln Ser Pro Phe Arg
130 135 140

(2) INFORMATION FOR SEQ ID NO:907:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 140 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..140
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499193

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:907:

Met Met Glu Asn Lys Arg Asn Val Cys Ser Leu Gly Glu Ser Ser Ile
1 5 10 15
Lys Arg His Lys Ser Asp Leu Ser Phe Asn Ser Lys Glu Arg Lys Asp
20 25 30
Lys Val Gly Glu Arg Ile Ser Ala Leu Gln Gln Ile Val Ser Pro Tyr
35 40 45
Gly Lys Thr Asp Thr Ala Ser Val Leu Leu Asp Ala Met His Tyr Ile
50 55 60
Glu Phe Leu His Glu Gln Val Lys Val Leu Ser Ala Pro Tyr Leu Gln
65 70 75 80

Thr Ile Pro Asp Ala Thr Gln Glu Glu Leu Glu Gln Tyr Ser Leu Arg
85 90 95
Asn Arg Gly Leu Cys Leu Val Pro Met Glu Asn Thr Val Gly Val Ala
100 105 110
Gln Ser Asn Gly Ala Asp Ile Trp Ala Pro Val Lys Thr Pro Leu Ser
115 120 125
Pro Ala Phe Ser Val Thr Ser Gln Ser Pro Phe Arg
130 135 140

(2) INFORMATION FOR SEQ ID NO:908:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1819 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1819
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499194

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:908:

gtcttttgggt	gggtcttcgt	caaagctctc	tcctttacgg	tccttttctc	cagcgcgatga	60
aataataaag	gacacctgta	tttattaaaa	tcactacatt	ttccgtaaca	aaaaaaatca	120
aactttggtt	tctcaatgga	cggtgcggga	gaatcacgac	tcgggtggtga	tggtgggtggt	180
gatggttctg	ttggagttca	gatccgacaa	acacggatgc	taccggattt	tctccagagc	240
gtgaatctca	agtatgtgaa	attagggttac	aattacttaa	tctcaaactct	cttgactctc	300
tgttttattcc	ctctcgccgt	tgttatctcc	gtcgaagcct	ctcagatgaa	cccagatgat	360
ctcaaacagc	tctggatcca	tctacaatac	aatctggtta	gtatcatcat	ctgttcagcg	420
attctagtct	tcgggttaac	ggtttatggt	acgaccgcac	ctagaccggt	ttacttggtt	480
gatttctctt	gttatctccc	acctgatcat	ctcaaagctc	cttacgctcg	gttcatggaa	540
cattctagac	tcaccggaga	tttcgatgac	tctgctctcg	agtttcaacg	caagatcctt	600
gagcgttctg	gtttaggagg	agacacttgt	ccctgaagct	atgcattatg	ttccaccgag	660
aatttcaatg	gctgctgcta	gagaagaagc	tgaacaagtc	atgtttggtg	ctttagataa	720
ccttttcgct	aacactaatg	tgaaaccaaa	ggatattgga	atccttggtg	tgaattgtag	780
tctctttaat	ccaactcctt	cgttatctgc	aatgattgtg	aacaagtata	agcttagagg	840
taacattaga	agctacaatc	taggcgggat	gggttgacgc	gcgggagtta	tcgctgtgga	900
tcttgctaaa	gacatgttgt	tggtacatag	gaacacttat	gcggttggtg	tttctactga	960
gaacattact	cagaattggt	attttggtta	caagaaatcg	atgttgatac	cgaactgctt	1020
gtttcgagtt	ggtggctctg	cggttttgct	atcgaacaag	tcgagggaca	agagacggtc	1080
taagtacagg	cttgtagatg	tagtcaggac	tcaccgtgga	gcagatgata	aagctttccg	1140
ttgtgtttat	caagagcagg	atgatacagg	gagaaccggg	gtttcggtgt	cgaaagatct	1200
aatggcgatt	gcaggggaaa	ctctcaaaaac	caatatcact	acattgggtc	ctcttgttct	1260
accgataagt	gagcagattc	tcttctttat	gactctagtt	gtgaagaagc	tctttaacgg	1320
taaagtgaag	cgtatatcc	cggatttcaa	acttgctttc	gagcatttct	gtatccatgc	1380
tggttgaaga	gctgtgatcg	atgagttaga	gaagaatctg	cagctttcac	cagttcatgt	1440
cgaggcttcg	aggatgactc	ttcatcgatt	tggttaacaca	tcttcgagct	ccatttggtta	1500
tgaattggct	tacattgaag	cgaagggaag	gatgcgaaga	ggtaatcgtg	tttggaat	1560
cgcgttcgga	agtggattta	aatgtaatag	cgcgatttgg	gaagcattaa	ggcatgtgaa	1620
accttcgaac	aacagtcctt	gtgaagattg	tattgacaag	tatccggtaa	ctttaagtta	1680
ttagcttcgt	ttgagggaact	gttattgtgt	aacttcgaga	ctaattccatg	gttggtttttt	1740
ttcttagaga	agaaaccctt	agatttgatc	tctgacaatg	tcaatgtggtt	tggtgtttat	1800
gtgttttggga	gagtttgtg					

(2) INFORMATION FOR SEQ ID NO:909:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 347 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..347

(D) OTHER INFORMATION: / Ceres Seq. ID 1499195

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:909:

Met	His	Tyr	Val	Pro	Arg	Ile	Ser	Met	Ala	Ala	Ala	Arg	Glu	Glu	
1			5				10						15		
Ala	Glu	Gln	Val	Met	Phe	Gly	Ala	Leu	Asp	Asn	Leu	Phe	Ala	Asn	Thr
			20				25					30			
Asn	Val	Lys	Pro	Lys	Asp	Ile	Gly	Ile	Leu	Val	Val	Asn	Cys	Ser	Leu
		35				40					45				
Phe	Asn	Pro	Thr	Pro	Ser	Leu	Ser	Ala	Met	Ile	Val	Asn	Lys	Tyr	Lys
	50				55					60					
Leu	Arg	Gly	Asn	Ile	Arg	Ser	Tyr	Asn	Leu	Gly	Gly	Met	Gly	Cys	Ser
65				70					75					80	
Ala	Gly	Val	Ile	Ala	Val	Asp	Leu	Ala	Lys	Asp	Met	Leu	Leu	Val	His
			85				90							95	
Arg	Asn	Thr	Tyr	Ala	Val	Val	Val	Ser	Thr	Glu	Asn	Ile	Thr	Gln	Asn
		100					105					110			
Trp	Tyr	Phe	Gly	Asn	Lys	Lys	Ser	Met	Leu	Ile	Pro	Asn	Cys	Leu	Phe
		115				120						125			
Arg	Val	Gly	Gly	Ser	Ala	Val	Leu	Leu	Ser	Asn	Lys	Ser	Arg	Asp	Lys
	130				135						140				
Arg	Arg	Ser	Lys	Tyr	Arg	Leu	Val	His	Val	Val	Arg	Thr	His	Arg	Gly
145				150						155					160
Ala	Asp	Asp	Lys	Ala	Phe	Arg	Cys	Val	Tyr	Gln	Glu	Gln	Asp	Asp	Thr
			165				170							175	
Gly	Arg	Thr	Gly	Val	Ser	Leu	Ser	Lys	Asp	Leu	Met	Ala	Ile	Ala	Gly
		180					185						190		
Glu	Thr	Leu	Lys	Thr	Asn	Ile	Thr	Leu	Gly	Pro	Leu	Val	Leu	Pro	
	195				200						205				
Ile	Ser	Glu	Gln	Ile	Leu	Phe	Phe	Met	Thr	Leu	Val	Val	Lys	Lys	Leu
	210				215						220				
Phe	Asn	Gly	Lys	Val	Lys	Pro	Tyr	Ile	Pro	Asp	Phe	Lys	Leu	Ala	Phe
225				230						235					240
Glu	His	Phe	Cys	Ile	His	Ala	Gly	Gly	Arg	Ala	Val	Ile	Asp	Glu	Leu
			245						250					255	
Glu	Lys	Asn	Leu	Gln	Leu	Ser	Pro	Val	His	Val	Glu	Ala	Ser	Arg	Met
		260					265						270		
Thr	Leu	His	Arg	Phe	Gly	Asn	Thr	Ser	Ser	Ser	Ser	Ile	Trp	Tyr	Glu
	275					280						285			
Leu	Ala	Tyr	Ile	Glu	Ala	Lys	Gly	Arg	Met	Arg	Arg	Gly	Asn	Arg	Val
	290				295						300				
Trp	Gln	Ile	Ala	Phe	Gly	Ser	Gly	Phe	Lys	Cys	Asn	Ser	Ala	Ile	Trp
305				310						315					320
Glu	Ala	Leu	Arg	His	Val	Lys	Pro	Ser	Asn	Asn	Ser	Pro	Cys	Glu	Asp
			325						330					335	
Cys	Ile	Asp	Lys	Tyr	Pro	Val	Thr	Leu	Ser	Tyr					
		340					345								

(2) INFORMATION FOR SEQ ID NO:910:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 338 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..338

(D) OTHER INFORMATION: / Ceres Seq. ID 1499196

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:910:

Met	Ala	Ala	Ala	Arg	Glu	Glu	Ala	Glu	Gln	Val	Met	Phe	Gly	Ala	Leu
1			5					10						15	
Asp	Asn	Leu	Phe	Ala	Asn	Thr	Asn	Val	Lys	Pro	Lys	Asp	Ile	Gly	Ile

Met	Phe	Gly	Ala	Leu	Asp	Asn	Leu	Phe	Ala	Asn	Thr	Asn	Val	Lys	Pro
1				5					10					15	
Lys	Asp	Ile	Gly	Ile	Leu	Val	Val	Asn	Cys	Ser	Leu	Phe	Asn	Pro	Thr
			20					25					30		
Pro	Ser	Leu	Ser	Ala	Met	Ile	Val	Asn	Lys	Tyr	Lys	Leu	Arg	Gly	Asn
		35					40					45			
Ile	Arg	Ser	Tyr	Asn	Leu	Gly	Gly	Met	Gly	Cys	Ser	Ala	Gly	Val	Ile
	50					55				60					

Ala Val Asp Leu Ala Lys Asp Met Leu Leu Val His Arg Asn Thr Tyr
65 70 75 80
Ala Val Val Val Ser Thr Glu Asn Ile Thr Gln Asn Trp Tyr Phe Gly
85 90 95
Asn Lys Lys Ser Met Leu Ile Pro Asn Cys Leu Phe Arg Val Gly Gly
100 105 110
Ser Ala Val Leu Leu Ser Asn Lys Ser Arg Asp Lys Arg Arg Ser Lys
115 120 125
Tyr Arg Leu Val His Val Val Arg Thr His Arg Gly Ala Asp Asp Lys
130 135 140
Ala Phe Arg Cys Val Tyr Gln Glu Gln Asp Asp Thr Gly Arg Thr Gly
145 150 155 160
Val Ser Leu Ser Lys Asp Leu Met Ala Ile Ala Gly Glu Thr Leu Lys
165 170 175
Thr Asn Ile Thr Thr Leu Gly Pro Leu Val Leu Pro Ile Ser Glu Gln
180 185 190
Ile Leu Phe Phe Met Thr Leu Val Val Lys Lys Leu Phe Asn Gly Lys
195 200 205
Val Lys Pro Tyr Ile Pro Asp Phe Lys Leu Ala Phe Glu His Phe Cys
210 215 220
Ile His Ala Gly Gly Arg Ala Val Ile Asp Glu Leu Glu Lys Asn Leu
225 230 235 240
Gln Leu Ser Pro Val His Val Glu Ala Ser Arg Met Thr Leu His Arg
245 250 255
Phe Gly Asn Thr Ser Ser Ser Ser Ile Trp Tyr Glu Leu Ala Tyr Ile
260 265 270
Glu Ala Lys Gly Arg Met Arg Arg Gly Asn Arg Val Trp Gln Ile Ala
275 280 285
Phe Gly Ser Gly Phe Lys Cys Asn Ser Ala Ile Trp Glu Ala Leu Arg
290 295 300
His Val Lys Pro Ser Asn Asn Ser Pro Cys Glu Asp Cys Ile Asp Lys
305 310 315 320
Tyr Pro Val Thr Leu Ser Tyr
325

(2) INFORMATION FOR SEQ ID NO:912:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 976 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..976
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499198

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:912:

acgtctgacg	gaagtcggtt	cacttccacc	tgtgccgtgg	ggatgttctg	tcgtcacagt	60
cggatcaagag	atgtatgtaa	ttggtggact	cctagacata	agacgtttac	aggtaatgac	120
tctcatcgat	tgcagaactc	acaaatttcg	ctcgcttcg	agtatgaaaa	gaggtcgttg	180
caaagcagcc	gccggagttg	tcgacggaaa	gatttacgta	atcgagggtt	tcaggatgag	240
aaaaccggat	gctgaatgga	ttgaagtgtt	tgatctaaag	acacagattt	gggaatcttt	300
gcctggtccg	taccctaaaa	ctagttcgtg	ttgcgagttg	gacgcttatg	tggtgatgga	360
agagaagtta	tacatgttgg	gttctaaatt	ttgtttgggt	tacgaaccaa	aaagaaacgg	420
tgaatgggac	gcattccgtc	gagcaacccc	attaaaagat	ttgtgggaca	agacttggtg	480
tgtggtagat	gatagtgtgt	atacgactga	tcctcggcgt	actcttggac	atccaatagt	540
cgtgtatcat	ccaaaggaca	agacttggag	acctgtgaaa	ggtgaatcct	tggggagttt	600
gcctagttat	ttcttttcta	agtctgaaaa	tggcgaattt	tggtggaaa	ttggtgattt	660
tgggcagaaa	caagagctat	gttactgggt	attgcattgg	agaaaaagtt	atttggtgcg	720
taatgatcga	gttggaaaaa	cgtgaaggag	gtgagatttg	ggggaagggt	gaatcactcg	780
actgtgtgtt	tggatacata	gacattgtgt	cggttgggct	ttgtcgatct	ctgaccattt	840
gatgatacat	gggatggtat	cttgcaggta	cgttgatgtg	aatgagtatg	acttttttgt	900

tggtcatgcc ttttcttttag cctcaagact tacttgtctt tttcatgac tttattactc 960
accttaacct ttgtgc

(2) INFORMATION FOR SEQ ID NO:913:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 229 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..229

(D) OTHER INFORMATION: / Ceres Seq. ID 1499199

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:913:

Arg Leu Thr Glu Val Gly Ser Leu Pro Pro Val Pro Trp Gly Cys Ser
1 5 10 15
Val Val Thr Val Gly Gln Glu Met Tyr Val Ile Gly Gly Leu Leu Asp
20 25 30
Ile Arg Arg Leu Gln Val Met Thr Leu Ile Asp Cys Arg Thr His Lys
35 40 45
Phe Arg Ser Leu Pro Ser Met Lys Arg Gly Arg Cys Lys Ala Ala Ala
50 55 60
Gly Val Val Asp Gly Lys Ile Tyr Val Ile Gly Gly Phe Arg Met Arg
65 70 75 80
Lys Pro Asp Ala Glu Trp Ile Glu Val Phe Asp Leu Lys Thr Gln Ile
85 90 95
Trp Glu Ser Leu Pro Gly Pro Tyr Pro Lys Thr Ser Ser Cys Cys Glu
100 105 110
Leu Asp Ala Tyr Val Val Met Glu Glu Lys Leu Tyr Met Leu Gly Ser
115 120 125
Lys Phe Cys Leu Val Tyr Glu Pro Lys Arg Asn Gly Glu Trp Asp Ala
130 135 140
Ser Val Gly Ala Thr Pro Leu Lys Asp Leu Trp Asp Lys Thr Cys Cys
145 150 155 160
Val Val Asp Asp Met Leu Tyr Thr Thr Asp Pro Arg Arg Thr Leu Gly
165 170 175
His Pro Ile Val Val Tyr His Pro Lys Asp Lys Thr Trp Arg Pro Val
180 185 190
Lys Gly Glu Ser Leu Gly Ser Leu Pro Ser Tyr Phe Phe Ser Lys Ser
195 200 205
Glu Asn Gly Glu Phe Trp Trp Lys Val Gly Asp Phe Gly Gln Lys Gln
210 215 220
Glu Leu Cys Tyr Trp
225

(2) INFORMATION FOR SEQ ID NO:914:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 206 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..206

(D) OTHER INFORMATION: / Ceres Seq. ID 1499200

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:914:

Met Tyr Val Ile Gly Gly Leu Leu Asp Ile Arg Arg Leu Gln Val Met
1 5 10 15
Thr Leu Ile Asp Cys Arg Thr His Lys Phe Arg Ser Leu Pro Ser Met
20 25 30
Lys Arg Gly Arg Cys Lys Ala Ala Ala Gly Val Val Asp Gly Lys Ile

	35		40		45														
Tyr	Val	Ile	Gly	Gly	Phe	Arg	Met	Arg	Lys	Pro	Asp	Ala	Glu	Trp	Ile				
	50					55					60								
Glu	Val	Phe	Asp	Leu	Lys	Thr	Gln	Ile	Trp	Glu	Ser	Leu	Pro	Gly	Pro				
65					70					75					80				
Tyr	Pro	Lys	Thr	Ser	Ser	Cys	Cys	Glu	Leu	Asp	Ala	Tyr	Val	Val	Met				
				85					90					95					
Glu	Glu	Lys	Leu	Tyr	Met	Leu	Gly	Ser	Lys	Phe	Cys	Leu	Val	Tyr	Glu				
			100					105					110						
Pro	Lys	Arg	Asn	Gly	Glu	Trp	Asp	Ala	Ser	Val	Gly	Ala	Thr	Pro	Leu				
		115					120					125							
Lys	Asp	Leu	Trp	Asp	Lys	Thr	Cys	Cys	Val	Val	Asp	Asp	Met	Leu	Tyr				
	130					135					140								
Thr	Thr	Asp	Pro	Arg	Arg	Thr	Leu	Gly	His	Pro	Ile	Val	Val	Tyr	His				
145					150					155					160				
Pro	Lys	Asp	Lys	Thr	Trp	Arg	Pro	Val	Lys	Gly	Glu	Ser	Leu	Gly	Ser				
			165						170					175					
Leu	Pro	Ser	Tyr	Phe	Phe	Ser	Lys	Ser	Glu	Asn	Gly	Glu	Phe	Trp	Trp				
			180					185					190						
Lys	Val	Gly	Asp	Phe	Gly	Gln	Lys	Gln	Glu	Leu	Cys	Tyr	Trp						
	195					200						205							

(2) INFORMATION FOR SEQ ID NO:915:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 191 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..191

(D) OTHER INFORMATION: / Ceres Seq. ID 1499201

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:915:

Met	Thr	Leu	Ile	Asp	Cys	Arg	Thr	His	Lys	Phe	Arg	Ser	Leu	Pro	Ser				
1				5					10					15					
Met	Lys	Arg	Gly	Arg	Cys	Lys	Ala	Ala	Ala	Gly	Val	Val	Asp	Gly	Lys				
		20					25						30						
Ile	Tyr	Val	Ile	Gly	Gly	Phe	Arg	Met	Arg	Lys	Pro	Asp	Ala	Glu	Trp				
	35					40					45								
Ile	Glu	Val	Phe	Asp	Leu	Lys	Thr	Gln	Ile	Trp	Glu	Ser	Leu	Pro	Gly				
	50				55					60									
Pro	Tyr	Pro	Lys	Thr	Ser	Ser	Cys	Cys	Glu	Leu	Asp	Ala	Tyr	Val	Val				
65				70					75					80					
Met	Glu	Glu	Lys	Leu	Tyr	Met	Leu	Gly	Ser	Lys	Phe	Cys	Leu	Val	Tyr				
			85					90					95						
Glu	Pro	Lys	Arg	Asn	Gly	Glu	Trp	Asp	Ala	Ser	Val	Gly	Ala	Thr	Pro				
		100					105						110						
Leu	Lys	Asp	Leu	Trp	Asp	Lys	Thr	Cys	Cys	Val	Val	Asp	Asp	Met	Leu				
	115					120						125							
Tyr	Thr	Thr	Asp	Pro	Arg	Arg	Thr	Leu	Gly	His	Pro	Ile	Val	Val	Tyr				
	130				135					140									
His	Pro	Lys	Asp	Lys	Thr	Trp	Arg	Pro	Val	Lys	Gly	Glu	Ser	Leu	Gly				
145				150					155					160					
Ser	Leu	Pro	Ser	Tyr	Phe	Phe	Ser	Lys	Ser	Glu	Asn	Gly	Glu	Phe	Trp				
			165					170					175						
Trp	Lys	Val	Gly	Asp	Phe	Gly	Gln	Lys	Gln	Glu	Leu	Cys	Tyr	Trp					
	180					185						190							

(2) INFORMATION FOR SEQ ID NO:916:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1255 base pairs

(B) TYPE: nucleic acid

- (C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
(A) NAME/KEY: -
(B) LOCATION: 1..1255
(D) OTHER INFORMATION: / Ceres Seq. ID 1499206

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:916:

atcatcgaaa	atggcggaaa	gaggaggaga	aagcggcgca	gggcgggtgac	cggtggtgact	60
tccgacgtgg	attcggcggt	ggacgtggag	gtggccgtgg	ccgtgatcgt	ggtccaagag	120
gccgtggacg	acgtggaggc	cgtgcttcgg	aagaaacgaa	atggggtcca	gtgaccaaac	180
taggtcgtct	agtggctgac	aataaaataa	cgaagctaga	gcagatctat	ctccattctc	240
tcccagtaaa	ggagtaccaa	atcatagatc	atctggttgg	acctacgttg	aaagacgagg	300
ttatgaagat	catgcctggt	cagaaacaaa	ccagagctgg	tcaaagaact	agattcaagg	360
cctttgttgt	tgttggtgat	ggtaatggtc	atggttggtt	gggtgtcaag	cgttctaagg	420
aagttgcaac	tgccattaga	ggagctatta	ttcttgctaa	gctttctggt	gttccggtga	480
ggagaggtta	ttgggggaat	aagattggga	agccacacac	tgtgccttgt	aaggttactg	540
gtaaagtgtg	ttctgttact	gtgagaatgg	ttcctgctcc	gagaggttct	ggtattgttg	600
ctgctagggt	tcctaagaag	gttcttcagt	tcgctggtat	tgatgatgtt	ttcacttctt	660
ctagaggatc	taccaaaaca	ctcggaaact	ttgttaaggc	gacattcgat	tgcttacaga	720
agacatatgg	gttccttaca	ccagagttct	ggaaagagac	tagattctcc	agatcgccct	780
accaagagca	caactgatttc	ctgtcgacta	aggctcttca	ggccgccaaa	gttgtcaccg	840
agggtgaaga	acaagcttaa	gaccttcatt	agatgagctt	ggttttatag	gttctggttg	900
tggcaaatat	ctttatcttt	tctggctcat	tttcttggtt	gtcttatcag	tttttgatat	960
tggagattta	attacaagga	taatcatatt	tagttatggt	tgggttttag	tacgaatttt	1020
ataatgagtg	tgccataatt	tacctaaaaa	agaaaaaaag	agaaaaaaag	agtgttgtat	1080
gtacgtgtgt	ttgacttgga	taattagtga	cattttaagc	aaatgtgtat	ttggaaaagt	1140
gatgtcaatg	aatatgaat	atgggtcgaa	taaagaagcg	aagatctgta	gactgtgtgt	1200
tctctgcata	tggtgttgta	ttcccgatca	tattgttgta	tggtttataat	ttatt	

(2) INFORMATION FOR SEQ ID NO:917:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 285 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..285
(D) OTHER INFORMATION: / Ceres Seq. ID 1499207

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:917:

His	Arg	Lys	Trp	Arg	Lys	Glu	Glu	Glu	Lys	Ala	Ala	Gln	Gly	Gly	Asp	
1			5					10					15			
Arg	Gly	Asp	Phe	Gly	Arg	Gly	Phe	Gly	Gly	Gly	Arg	Gly	Gly	Gly	Arg	
		20						25					30			
Gly	Arg	Asp	Arg	Gly	Pro	Arg	Gly	Arg	Gly	Arg	Arg	Gly	Gly	Arg	Ala	
		35						40					45			
Ser	Glu	Glu	Thr	Lys	Trp	Val	Pro	Val	Thr	Lys	Leu	Gly	Arg	Leu	Val	
	50					55				60						
Ala	Asp	Asn	Lys	Ile	Thr	Lys	Leu	Glu	Gln	Ile	Tyr	Leu	His	Ser	Leu	
65					70					75				80		
Pro	Val	Lys	Glu	Tyr	Gln	Ile	Ile	Asp	His	Leu	Val	Gly	Pro	Thr	Leu	
			85					90						95		
Lys	Asp	Glu	Val	Met	Lys	Ile	Met	Pro	Val	Gln	Lys	Gln	Thr	Arg	Ala	
		100						105					110			
Gly	Gln	Arg	Thr	Arg	Phe	Lys	Ala	Phe	Val	Val	Val	Gly	Asp	Gly	Asn	
	115						120					125				
Gly	His	Val	Gly	Leu	Gly	Val	Lys	Arg	Ser	Lys	Glu	Val	Ala	Thr	Ala	
	130						135				140					
Ile	Arg	Gly	Ala	Ile	Ile	Leu	Ala	Lys	Leu	Ser	Val	Val	Pro	Val	Arg	
145					150					155					160	

Arg Gly Tyr Trp Gly Asn Lys Ile Gly Lys Pro His Thr Val Pro Cys
165 170 175
Lys Val Thr Gly Lys Cys Gly Ser Val Thr Val Arg Met Val Pro Ala
180 185 190
Pro Arg Gly Ser Gly Ile Val Ala Ala Arg Val Pro Lys Lys Val Leu
195 200 205
Gln Phe Ala Gly Ile Asp Asp Val Phe Thr Ser Ser Arg Gly Ser Thr
210 215 220
Lys Thr Leu Gly Asn Phe Val Lys Ala Thr Phe Asp Cys Leu Gln Lys
225 230 235 240
Thr Tyr Gly Phe Leu Thr Pro Glu Phe Trp Lys Glu Thr Arg Phe Ser
245 250 255
Arg Ser Pro Tyr Gln Glu His Thr Asp Phe Leu Ser Thr Lys Ala Leu
260 265 270
Gln Ala Ala Lys Val Val Thr Glu Gly Glu Glu Gln Ala
275 280 285

(2) INFORMATION FOR SEQ ID NO:918:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 185 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..185

(D) OTHER INFORMATION: / Ceres Seq. ID 1499208

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:918:

Met Lys Ile Met Pro Val Gln Lys Gln Thr Arg Ala Gly Gln Arg Thr
1 5 10 15
Arg Phe Lys Ala Phe Val Val Val Gly Asp Gly Asn Gly His Val Gly
20 25 30
Leu Gly Val Lys Arg Ser Lys Glu Val Ala Thr Ala Ile Arg Gly Ala
35 40 45
Ile Ile Leu Ala Lys Leu Ser Val Val Pro Val Arg Arg Gly Tyr Trp
50 55 60
Gly Asn Lys Ile Gly Lys Pro His Thr Val Pro Cys Lys Val Thr Gly
65 70 75 80
Lys Cys Gly Ser Val Thr Val Arg Met Val Pro Ala Pro Arg Gly Ser
85 90 95
Gly Ile Val Ala Arg Val Pro Lys Lys Val Leu Gln Phe Ala Gly
100 105 110
Ile Asp Asp Val Phe Thr Ser Ser Arg Gly Ser Thr Lys Thr Leu Gly
115 120 125
Asn Phe Val Lys Ala Thr Phe Asp Cys Leu Gln Lys Thr Tyr Gly Phe
130 135 140
Leu Thr Pro Glu Phe Trp Lys Glu Thr Arg Phe Ser Arg Ser Pro Tyr
145 150 155 160
Gln Glu His Thr Asp Phe Leu Ser Thr Lys Ala Leu Gln Ala Ala Lys
165 170 175
Val Val Thr Glu Gly Glu Glu Gln Ala
180 185

(2) INFORMATION FOR SEQ ID NO:919:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 182 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..182

(D) OTHER INFORMATION: / Ceres Seq. ID 1499209

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:919:

Met Pro Val Gln Lys Gln Thr Arg Ala Gly Gln Arg Thr Arg Phe Lys
1 5 10 15
Ala Phe Val Val Val Gly Asp Gly Asn Gly His Val Gly Leu Gly Val
20 25 30
Lys Arg Ser Lys Glu Val Ala Thr Ala Ile Arg Gly Ala Ile Ile Leu
35 40 45
Ala Lys Leu Ser Val Val Pro Val Arg Arg Gly Tyr Trp Gly Asn Lys
50 55 60
Ile Gly Lys Pro His Thr Val Pro Cys Lys Val Thr Gly Lys Cys Gly
65 70 75 80
Ser Val Thr Val Arg Met Val Pro Ala Pro Arg Gly Ser Gly Ile Val
85 90 95
Ala Ala Arg Val Pro Lys Lys Val Leu Gln Phe Ala Gly Ile Asp Asp
100 105 110
Val Phe Thr Ser Ser Arg Gly Ser Thr Lys Thr Leu Gly Asn Phe Val
115 120 125
Lys Ala Thr Phe Asp Cys Leu Gln Lys Thr Tyr Gly Phe Leu Thr Pro
130 135 140
Glu Phe Trp Lys Glu Thr Arg Phe Ser Arg Ser Pro Tyr Gln Glu His
145 150 155 160
Thr Asp Phe Leu Ser Thr Lys Ala Leu Gln Ala Ala Lys Val Val Thr
165 170 175
Glu Gly Glu Glu Gln Ala
180

(2) INFORMATION FOR SEQ ID NO:920:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1170 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1170

(D) OTHER INFORMATION: / Ceres Seq. ID 1499210

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:920:

aagtgttagc tgctgccgct gttgtttctc ctccatttct ctatctttct ctctcgctgc 60
ttctcgaatc ttctgtatca tcttcttctt cttcaagtga aaaatggccg atggtgagga 120
tattcagcca cttgtctgtg acaatggaac ttggaatggg aaggctgggt ttgtctggta 180
tgatgccccg agagcagtggt tcccaagtat tgttggtcgt acaaccggta ttgtgctcga 240
ttctgggtgat ggtgtgtctc aactgtgcc aatctacgar gggtagctc ttctcatgc 300
tattcttctg cttgatcttg cgggtcggga tctcacagac tcatcatga agattctcac 360
tgagagaggt tacatgttca ccactaccgc agaacgggaa attgtccgtg acataaagga 420
gaaacttgck tatgtcgctc ttgactacga gcaagagcta gagacagcca agagcagttc 480
ttcagtgag aargaactac gagcttccctg atggacaagt cataaccatc ggagctgaga 540
gatyccggtt tcttgagggt ctgttccagc catcgctcat cggaatggaa gctcctggaa 600
tccatgaaac aacttacaac tccatcatga aatgtgatgt cgatatcagg aaggwtctct 660
atggaaacat cgttctcagt ggtggttcca ccatgttccc aggaattgct gaccgtatga 720
gcaaagagat caccgctctt gcacctagca gcatgaagat caaggtgggt gcaccgccag 780
agagaaaata cagtgtctgg atcggaggat caatccttgc atccctcagc acctccaac 840
agatgtggat ttcaaagagt gagtacgatg agtcaggctc atcgattgtt cacaggaaat 900
gtttctaagt gtgtcttgtc ttatcttggt cgtggtgggt agtttggtac aaaaaaatct 960
atcttcctta gttgagatgg gaattgaact atctgttggt atgtggattt tattttcttt 1020
tttctcttta gaaccttatg gttgtgtcaa gaagtcttgt gtactttagt tttatatctc 1080
tgttttatct cttctatctt ctttaggatg cttgtgatga tgctgttttt ttttgtccct 1140
aagcaaaaaa atatcatatt atatttgcc

(2) INFORMATION FOR SEQ ID NO:921:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 135 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..135
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1499211
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:921:

Met Ala Asp Gly Glu Asp Ile Gln Pro Leu Val Cys Asp Asn Gly Thr
1 5 10 15
Gly Met Val Lys Ala Gly Phe Ala Gly Asp Asp Ala Pro Arg Ala Val
20 25 30
Phe Pro Ser Ile Val Gly Arg Thr Thr Gly Ile Val Leu Asp Ser Gly
35 40 45
Asp Gly Val Ser His Thr Val Pro Ile Tyr Xaa Gly Tyr Ala Leu Pro
50 55 60
His Ala Ile Leu Arg Leu Asp Leu Ala Gly Arg Asp Leu Thr Asp Ser
65 70 75 80
Leu Met Lys Ile Leu Thr Glu Arg Gly Tyr Met Phe Thr Thr Thr Ala
85 90 95
Glu Arg Glu Ile Val Arg Asp Ile Lys Glu Lys Leu Xaa Tyr Val Ala
100 105 110
Leu Asp Tyr Glu Gln Glu Leu Glu Thr Ala Lys Ser Ser Ser Val
115 120 125
Glu Xaa Glu Leu Arg Ala Ser
130 135

(2) INFORMATION FOR SEQ ID NO:922:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 118 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..118
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1499212
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:922:

Met Val Lys Ala Gly Phe Ala Gly Asp Asp Ala Pro Arg Ala Val Phe
1 5 10 15
Pro Ser Ile Val Gly Arg Thr Thr Gly Ile Val Leu Asp Ser Gly Asp
20 25 30
Gly Val Ser His Thr Val Pro Ile Tyr Xaa Gly Tyr Ala Leu Pro His
35 40 45
Ala Ile Leu Arg Leu Asp Leu Ala Gly Arg Asp Leu Thr Asp Ser Leu
50 55 60
Met Lys Ile Leu Thr Glu Arg Gly Tyr Met Phe Thr Thr Thr Ala Glu
65 70 75 80
Arg Glu Ile Val Arg Asp Ile Lys Glu Lys Leu Xaa Tyr Val Ala Leu
85 90 95
Asp Tyr Glu Gln Glu Leu Glu Thr Ala Lys Ser Ser Ser Ser Val Glu
100 105 110
Xaa Glu Leu Arg Ala Ser
115

(2) INFORMATION FOR SEQ ID NO:923:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 107 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:

- (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..107
 (D) OTHER INFORMATION: / Ceres Seq. ID 1499213

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:923:

```
Met Glu Ala Pro Gly Ile His Glu Thr Thr Tyr Asn Ser Ile Met Lys
1          5          10          15
Cys Asp Val Asp Ile Arg Lys Xaa Leu Tyr Gly Asn Ile Val Leu Ser
          20          25          30
Gly Gly Ser Thr Met Phe Pro Gly Ile Ala Asp Arg Met Ser Lys Glu
          35          40          45
Ile Thr Ala Leu Ala Pro Ser Ser Met Lys Ile Lys Val Val Ala Pro
          50          55          60
Pro Glu Arg Lys Tyr Ser Val Trp Ile Gly Gly Ser Ile Leu Ala Ser
65          70          75          80
Leu Ser Thr Phe Gln Met Trp Ile Ser Lys Ser Glu Tyr Asp Glu
          85          90          95
Ser Gly Pro Ser Ile Val His Arg Lys Cys Phe
          100          105
```

(2) INFORMATION FOR SEQ ID NO:924:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1107 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
 (A) NAME/KEY: -
 (B) LOCATION: 1..1107
 (D) OTHER INFORMATION: / Ceres Seq. ID 1499214

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:924:

```
aaatttcggt gtmcagagaa gaagcaaaag agagaaacat ccgaccgga atctgacctg      60
aaaaccgga agaatcgaaa aatggggaaa gatggtctga gcgacgatca ggtctcgctg      120
atgaaggaag ctttcagtct cttcgacacc gatggcgacg gcaaaatcgc accgtcagag      180
ctcgggatcc tcatgcgac tctcggcgga aaccgaccc aagcccagct gaaatccata      240
atcgcatccg agaatctctc ttcaccgttt gatttcaaca gattcctcga tctcatggcg      300
aaacatctga agacggaacc ttctgatcgc cagctccgtg acgcattcaa agtgctcgat      360
aaggaaggtg ccgggttcgt tgctgtggcg gatctgaggc atattctgac cagtatcgga      420
gagaagctgg agcctaata gttcgatgag tggatcaagg aggtggatgt tggatccgat      480
ggaagatccc ggtacttctg aatgtatgtc cgcaattgcc ggctcctacg gctacatagc      540
tccagagtac gcgtatacat tgaaggtaga tgagaagagc gatgtgtata gtttcgggtg      600
tgttcttcta gaactcatca ccgggaaaaa acccgctcga gaatttggcg acggcggttg      660
tattgttcaa tgggtgagaa gcatgacgga ttcaaataaa gattgtgtgc tcaaagtaat      720
cgatcttaga ctctcttcag ttccagttca cgaggtaaca cacgtcttct acgttgcggt      780
gctctgtggt gaagaacaag cgggtggagag gccgacgatg cgtgaagtcg ttcagattct      840
cactgagatc caaaaaattc ctctttcgaa gcagcaagcg gcggaatcag acgtgactga      900
gaaagctccg gcgattaatg aatcgtcgcc ggattcagga agtccaccgg atcttttaag      960
taattagact ttccggcgat tgggtttggt cattgagggg caaatttgtc tttctaattt      1020
tcttgtcacc gacgtctcgg tagtgaggtt aattacttaa ttagcccgtt gttgtctggt      1080
tccggttaag gcaacaatta gtggttt
```

(2) INFORMATION FOR SEQ ID NO:925:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 166 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide

(B) LOCATION: 1..166

(D) OTHER INFORMATION: / Ceres Seq. ID 1499215

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:925:

Lys	Phe	Arg	Cys	Xaa	Glu	Lys	Lys	Gln	Lys	Arg	Glu	Thr	Ser	Asp	Pro
1			5					10						15	
Glu	Ser	Asp	Leu	Lys	Thr	Arg	Lys	Asn	Arg	Lys	Met	Gly	Lys	Asp	Gly
			20					25					30		
Leu	Ser	Asp	Asp	Gln	Val	Ser	Ser	Met	Lys	Glu	Ala	Phe	Met	Leu	Phe
			35					40					45		
Asp	Thr	Asp	Gly	Asp	Gly	Lys	Ile	Ala	Pro	Ser	Glu	Leu	Gly	Ile	Leu
			50				55				60				
Met	Arg	Ser	Leu	Gly	Gly	Asn	Pro	Thr	Gln	Ala	Gln	Leu	Lys	Ser	Ile
65						70					75				80
Ile	Ala	Ser	Glu	Asn	Leu	Ser	Ser	Pro	Phe	Asp	Phe	Asn	Arg	Phe	Leu
				85					90					95	
Asp	Leu	Met	Ala	Lys	His	Leu	Lys	Thr	Glu	Pro	Phe	Asp	Arg	Gln	Leu
			100					105					110		
Arg	Asp	Ala	Phe	Lys	Val	Leu	Asp	Lys	Glu	Gly	Thr	Gly	Phe	Val	Ala
			115					120					125		
Val	Ala	Asp	Leu	Arg	His	Ile	Leu	Thr	Ser	Ile	Gly	Glu	Lys	Leu	Glu
			130				135					140			
Pro	Asn	Glu	Phe	Asp	Glu	Trp	Ile	Lys	Glu	Val	Asp	Val	Gly	Ser	Asp
145					150					155					160
Gly	Lys	Ile	Arg	Tyr	Phe										
					165										

(2) INFORMATION FOR SEQ ID NO:926:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 176 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..176

(D) OTHER INFORMATION: / Ceres Seq. ID 1499216

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:926:

Met	Ser	Ser	Met	Ser	Gly	Ser	Arg	Arg	Trp	Met	Leu	Asp	Pro	Met	Glu
1			5						10					15	
Arg	Ser	Gly	Thr	Ser	Glu	Cys	Met	Ser	Ala	Ile	Ala	Gly	Ser	Tyr	Gly
			20					25					30		
Tyr	Ile	Ala	Pro	Glu	Tyr	Ala	Tyr	Thr	Leu	Lys	Val	Asp	Glu	Lys	Ser
			35					40					45		
Asp	Val	Tyr	Ser	Phe	Gly	Val	Val	Leu	Leu	Glu	Leu	Ile	Thr	Gly	Lys
			50				55					60			
Lys	Pro	Val	Gly	Glu	Phe	Gly	Asp	Gly	Val	Asp	Ile	Val	Gln	Trp	Val
65					70					75					80
Arg	Ser	Met	Thr	Asp	Ser	Asn	Lys	Asp	Cys	Val	Leu	Lys	Val	Ile	Asp
				85					90					95	
Leu	Arg	Leu	Ser	Ser	Val	Pro	Val	His	Glu	Val	Thr	His	Val	Phe	Tyr
			100					105					110		
Val	Ala	Leu	Leu	Cys	Val	Glu	Glu	Gln	Ala	Val	Glu	Arg	Pro	Thr	Met
			115					120					125		
Arg	Glu	Val	Val	Gln	Ile	Leu	Thr	Glu	Ile	Pro	Lys	Ile	Pro	Leu	Ser
			130				135					140			
Lys	Gln	Gln	Ala	Ala	Glu	Ser	Asp	Val	Thr	Glu	Lys	Ala	Pro	Ala	Ile
145					150					155					160
Asn	Glu	Ser	Ser	Pro	Asp	Ser	Gly	Ser	Pro	Pro	Asp	Leu	Leu	Ser	Asn
				165					170						175

(2) INFORMATION FOR SEQ ID NO:927:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 173 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..173
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499217

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:927:

Met Ser Gly Ser Arg Arg Trp Met Leu Asp Pro Met Glu Arg Ser Gly
1 5 10 15
Thr Ser Glu Cys Met Ser Ala Ile Ala Gly Ser Tyr Gly Tyr Ile Ala
20 25 30
Pro Glu Tyr Ala Tyr Thr Leu Lys Val Asp Glu Lys Ser Asp Val Tyr
35 40 45
Ser Phe Gly Val Val Leu Leu Glu Leu Ile Thr Gly Lys Lys Pro Val
50 55 60
Gly Glu Phe Gly Asp Gly Val Asp Ile Val Gln Trp Val Arg Ser Met
65 70 75 80
Thr Asp Ser Asn Lys Asp Cys Val Leu Lys Val Ile Asp Leu Arg Leu
85 90 95
Ser Ser Val Pro Val His Glu Val Thr His Val Phe Tyr Val Ala Leu
100 105 110
Leu Cys Val Glu Glu Gln Ala Val Glu Arg Pro Thr Met Arg Glu Val
115 120 125
Val Gln Ile Leu Thr Glu Ile Pro Lys Ile Pro Leu Ser Lys Gln Gln
130 135 140
Ala Ala Glu Ser Asp Val Thr Glu Lys Ala Pro Ala Ile Asn Glu Ser
145 150 155 160
Ser Pro Asp Ser Gly Ser Pro Pro Asp Leu Ser Asn
165 170

(2) INFORMATION FOR SEQ ID NO:928:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1663 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1663
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499218

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:928:

aagcaaaaat gctacaaatt aaaaagtgtc tccaacatgt gcatattcac acacaagttg 60
gtgtcaacgc tcagacaaga aaggcgtgtg ttcattgttg aatcttccca tttcctcatc 120
caaattccga cataactatc ctagccgcca tttgttctcc acattacaaa accctcagca 180
gcttcaaaaac tcttccgatc tctccctcac gctcgcaatt ctctcgctctc cattttaata 240
gtttttcttc tcggaatcac aaatcttcgg cttcttggtc cttggcgtgt gtgtgtgttg 300
ttgaatggct cttgttcagc ggattccaat ttctctccc agtattcgga attggcaaca 360
agcgaggacc aatttgactc ctatttggtg tttacattac aatactgcat cttctctctc 420
ttcacccttt acagagaagc actctgtgga gagataccaa agggatcaat ggctgtacaa 480
agcggttgaa ccaacgccac catcgactcc atctccatcg ccatttgaag atgaagtctt 540
tgtagggaa aacgacattg catcgagct gcctgagctg aagaagcttt tggcagtgtc 600
gaaagagaa agagttaaag gatgcaaagg tgggtattgt ggaccaggag atgtgtatct 660
tgtagggaca gggccaggag atcctgagct tttgactctt aaagctgtca gaggatttca 720
aagtgccgat cttttgcttt acgacaggct tgtctccaat gatgtcttgg agttgggttg 780
tcctgatgct agacttcttt atgtcggcaa aactgctggt tatcatagca gaactcagga 840
agagattcat gaactactcc taaattttgc tgaagctggt gccactgttg tcaggcttaa 900

```
aggtggagat cctctggtct ttggacgggg cggcgaagaa atggactttc tgcaacagca 960
agggattcga gttcaagtta taccagggat aactgcggcg tcggggatag cagcagagtt 1020
ggggattcca ctaacacatc gaggtgttgc aactagtgtg aggtttctca ctggtcattc 1080
aaggaaagga gggacagacc ctctgtttgt tgcagagaat gcagctgacc cggatacaac 1140
acttgctggt tatatgggtt tgggaacttt accttctctt gcacaaaaaac taatggacca 1200
tggctctccct tctgatacac cagctgttgc ggttgaacgt ggaaccactc ctctacagcg 1260
tacagttttt gctgagctta aagattttgc aactgagatt cagtcagctg gattggtgtc 1320
accaacactc atcatcatag ggaaagtcgt tgagctctca cctttatggc cacattgcac 1380
gaaagaatcc tcctgccttg tagagaccgg gtagatattt cactcttatt ttacgggcgt 1440
gtggcttcca tcgacattac ggtgaagttt taggagctat ggagctatga aggttgagac 1500
ttgagagatg taataaacia aaaggaaagc tgatagtttc ttatgacgtg tccttcaatt 1560
gttttgggac aatggtaatg gcaatgttaa tgtaataaac aagttatcaa tcagtggcac 1620
tgtgactaat ttttccacca caagatgatg tctttaaaac ttt
```

(2) INFORMATION FOR SEQ ID NO:929:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 369 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..369
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499219

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:929:

```
Met Ala Leu Val Gln Arg Ile Pro Ile Ser Ser Ser Ser Ile Arg Asn
1          5          10          15
Trp Gln Gln Ala Arg Thr Asn Leu Thr Pro Ile Cys Cys Leu His Tyr
          20          25          30
Asn Thr Ala Ser Ser Ser Ser Ser Pro Phe Thr Glu Lys His Ser Val
          35          40          45
Glu Arg Tyr Gln Arg Asp Gln Trp Leu Tyr Lys Ala Val Glu Pro Thr
          50          55          60
Pro Pro Ser Thr Pro Ser Pro Ser Pro Phe Glu Asp Glu Val Phe Val
          65          70          75          80
Arg Glu Asn Asp Ile Ala Ser Gln Leu Pro Glu Leu Lys Lys Leu Leu
          85          90          95
Ala Val Leu Lys Glu Lys Arg Val Lys Gly Cys Lys Gly Gly Asp Cys
          100          105          110
Gly Pro Gly Asp Val Tyr Leu Val Gly Thr Gly Pro Gly Asp Pro Glu
          115          120          125
Leu Leu Thr Leu Lys Ala Val Arg Val Ile Gln Ser Ala Asp Leu Leu
          130          135          140
Leu Tyr Asp Arg Leu Val Ser Asn Asp Val Leu Glu Leu Val Ala Pro
          145          150          155          160
Asp Ala Arg Leu Leu Tyr Val Gly Lys Thr Ala Gly Tyr His Ser Arg
          165          170          175
Thr Gln Glu Glu Ile His Glu Leu Leu Asn Phe Ala Glu Ala Gly
          180          185          190
Ala Thr Val Val Arg Leu Lys Gly Gly Asp Pro Leu Val Phe Gly Arg
          195          200          205
Gly Gly Glu Glu Met Asp Phe Leu Gln Gln Gln Gly Ile Arg Val Gln
          210          215          220
Val Ile Pro Gly Ile Thr Ala Ala Ser Gly Ile Ala Ala Glu Leu Gly
          225          230          235          240
Ile Pro Leu Thr His Arg Gly Val Ala Thr Ser Val Arg Phe Leu Thr
          245          250          255
Gly His Ser Arg Lys Gly Gly Thr Asp Pro Leu Phe Val Ala Glu Asn
          260          265          270
Ala Ala Asp Pro Asp Thr Thr Leu Val Val Tyr Met Gly Leu Gly Thr
          275          280          285
```


Leu Pro Ser Leu Ala Gln Lys Leu Met Asp His Gly Leu Pro Ser Asp
290 295 300
Thr Pro Ala Val Ala Val Glu Arg Gly Thr Thr Pro Leu Gln Arg Thr
305 310 315 320
Val Phe Ala Glu Leu Lys Asp Phe Ala Thr Glu Ile Gln Ser Ala Gly
325 330 335
Leu Val Ser Pro Thr Leu Ile Ile Ile Gly Lys Val Val Glu Leu Ser
340 345 350
Pro Leu Trp Pro His Cys Thr Lys Glu Ser Ser Cys Leu Val Glu Thr
355 360 365
Arg

(2) INFORMATION FOR SEQ ID NO:930:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1526 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1526
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499220

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:930:

```
aaaacacgag ttctaattgtt gctgttgatt taagtaaact tcagaaactt agaagtaaag      60
gagtcagagg tagaggaggt gtaaggaaaa ctgacagtat aggtaataag agttccaagg      120
tagcggaacc agccaaaaag gcgacaaaga aaaacagggt ttgggatgat gcggctccca      180
aacaatcgaa attggacttc acggattcca tcgatgaaaa tgggaacaat gatcatgtag      240
atattgtggc tgctgaccaa ggagaaagta tgatggacaa ggaagagggt ttcagcagt      300
atagtgaag tgaagatgat gacgaaccag gaagtgatga gaagcctgct caggctaaga      360
aaaagggatg gttttcttct gttttccaga gtattactgg gaaagcgaat cttgaaagga      420
cagaccttgg accggcggtg aaagctctga aggaacggct catgaccaag aatgtggcag      480
aagagattgc tgagaagctt tgcgaatcag tggaagctag tcttgaagga aagaaattgt      540
catctttcac caggatctct tcaaccgttc aggcagcgat ggaggatgat ctggttcgta      600
tattgactcc aagacgctcc attgatatat taagagatgt tcatgctgcc aaagaacaga      660
ggaaacctta tgtgttggtg tttgttgagg tcaatggagt tgggaaatcc accaatctcg      720
ctaaagtggc gtattggctt cagcagcata aggtcagtgt aatgatggct gcttgtgaca      780
ctttccgttc tggagctggt gagcagttac ggactcatgc tcgtaggtta cagataccga      840
tatttgaaaa gggttatgaa aaggatccag cagtagttgc taaagaagcc atacaagaag      900
caactcgaaa tggatccgat gtcgttcttg ttgacacagc tggtcggatg caggataatg      960
aacctttgat gagagcactc tcaaagctca tcaaccttaa tcagccggac ttggtcttgt      1020
ttgttggtga agctcttgtt ggaaacgatg cagtagacca gctctcgaag ttcaatcaga      1080
aactttcgga tctctcgact tctgggaacc caagactgat cgatggaate ttactgacaa      1140
agtttgatac cattgacgac aaggtcggag cagcgttgtc tatggtttac atatcgggat      1200
caccggttat gttcgtgggt tgtggccagt cttacactga cctgaagaag cttaatgtca      1260
aagccatagt caagacactt ctcaagtgat ctctcttcca tcatcatcat catcatcatc      1320
actatcatca ttaccatcta ctatcaacaa tcaatgtctt atccatcatg ctgttggttt      1380
tggtttttta tttgaagacg gtttctcttt ggaagtgttg tgttttcttt aaaactcaaa      1440
agactggagt cgcaaaaaat accatcccat gactttatat gatgcaacgt aacttttgtt      1500
ttaaattaaa gattaataat catgtc
```

(2) INFORMATION FOR SEQ ID NO:931:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 428 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..428
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499221

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:931:

Asn	Thr	Ser	Ser	Asn	Val	Ala	Val	Asp	Leu	Ser	Lys	Leu	Gln	Lys	Leu
1			5					10						15	
Arg	Ser	Lys	Gly	Val	Arg	Gly	Arg	Gly	Gly	Val	Arg	Lys	Thr	Asp	Ser
		20						25					30		
Ile	Gly	Asn	Lys	Ser	Ser	Lys	Val	Ala	Glu	Pro	Ala	Lys	Lys	Ala	Thr
		35					40					45			
Lys	Lys	Asn	Arg	Val	Trp	Asp	Asp	Ala	Ala	Pro	Lys	Gln	Ser	Lys	Leu
		50				55					60				
Asp	Phe	Thr	Asp	Ser	Ile	Asp	Glu	Asn	Gly	Asn	Asn	Asp	His	Val	Asp
65					70				75						80
Ile	Val	Ala	Ala	Asp	Gln	Gly	Glu	Ser	Met	Met	Asp	Lys	Glu	Glu	Val
				85					90					95	
Phe	Ser	Ser	Asp	Ser	Glu	Ser	Glu	Asp	Asp	Asp	Glu	Pro	Gly	Ser	Asp
			100					105					110		
Glu	Lys	Pro	Ala	Gln	Ala	Lys	Lys	Lys	Gly	Trp	Phe	Ser	Ser	Val	Phe
		115					120					125			
Gln	Ser	Ile	Thr	Gly	Lys	Ala	Asn	Leu	Glu	Arg	Thr	Asp	Leu	Gly	Pro
		130				135					140				
Ala	Leu	Lys	Ala	Leu	Lys	Glu	Arg	Leu	Met	Thr	Lys	Asn	Val	Ala	Glu
145					150					155					160
Glu	Ile	Ala	Glu	Lys	Leu	Cys	Glu	Ser	Val	Glu	Ala	Ser	Leu	Glu	Gly
				165					170					175	
Lys	Lys	Leu	Ser	Ser	Phe	Thr	Arg	Ile	Ser	Ser	Thr	Val	Gln	Ala	Ala
		180						185					190		
Met	Glu	Asp	Ala	Leu	Val	Arg	Ile	Leu	Thr	Pro	Arg	Arg	Ser	Ile	Asp
		195					200					205			
Ile	Leu	Arg	Asp	Val	His	Ala	Ala	Lys	Glu	Gln	Arg	Lys	Pro	Tyr	Val
		210				215					220				
Val	Val	Phe	Val	Gly	Val	Asn	Gly	Val	Gly	Lys	Ser	Thr	Asn	Leu	Ala
225					230					235					240
Lys	Val	Ala	Tyr	Trp	Leu	Gln	Gln	His	Lys	Val	Ser	Val	Met	Met	Ala
				245					250					255	
Ala	Cys	Asp	Thr	Phe	Arg	Ser	Gly	Ala	Val	Glu	Gln	Leu	Arg	Thr	His
			260					265					270		
Ala	Arg	Arg	Leu	Gln	Ile	Pro	Ile	Phe	Glu	Lys	Gly	Tyr	Glu	Lys	Asp
			275				280					285			
Pro	Ala	Val	Val	Ala	Lys	Glu	Ala	Ile	Gln	Glu	Ala	Thr	Arg	Asn	Gly
		290				295					300				
Ser	Asp	Val	Val	Leu	Val	Asp	Thr	Ala	Gly	Arg	Met	Gln	Asp	Asn	Glu
305					310					315					320
Pro	Leu	Met	Arg	Ala	Leu	Ser	Lys	Leu	Ile	Asn	Leu	Asn	Gln	Pro	Asp
				325					330					335	
Leu	Val	Leu	Phe	Val	Gly	Glu	Ala	Leu	Val	Gly	Asn	Asp	Ala	Val	Asp
			340					345					350		
Gln	Leu	Ser	Lys	Phe	Asn	Gln	Lys	Leu	Ser	Asp	Leu	Ser	Thr	Ser	Gly
		355					360					365			
Asn	Pro	Arg	Leu	Ile	Asp	Gly	Ile	Leu	Leu	Thr	Lys	Phe	Asp	Thr	Ile
		370				375					380				
Asp	Asp	Lys	Val	Gly	Ala	Ala	Leu	Ser	Met	Val	Tyr	Ile	Ser	Gly	Ser
385					390					395					400
Pro	Val	Met	Phe	Val	Gly	Cys	Gly	Gln	Ser	Tyr	Thr	Asp	Leu	Lys	Lys
				405					410					415	
Leu	Asn	Val	Lys	Ala	Ile	Val	Lys	Thr	Leu	Leu	Lys				
			420					425							

(2) INFORMATION FOR SEQ ID NO:932:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 339 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..339
 (D) OTHER INFORMATION: / Ceres Seq. ID 1499222

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:932:

Met	Met	Asp	Lys	Glu	Glu	Val	Phe	Ser	Ser	Asp	Ser	Glu	Ser	Glu	Asp
1				5				10						15	
Asp	Asp	Glu	Pro	Gly	Ser	Asp	Glu	Lys	Pro	Ala	Gln	Ala	Lys	Lys	Lys
			20					25					30		
Gly	Trp	Phe	Ser	Ser	Val	Phe	Gln	Ser	Ile	Thr	Gly	Lys	Ala	Asn	Leu
			35				40					45			
Glu	Arg	Thr	Asp	Leu	Gly	Pro	Ala	Leu	Lys	Ala	Leu	Lys	Glu	Arg	Leu
	50					55				60					
Met	Thr	Lys	Asn	Val	Ala	Glu	Glu	Ile	Ala	Glu	Lys	Leu	Cys	Glu	Ser
65					70					75				80	
Val	Glu	Ala	Ser	Leu	Gly	Lys	Lys	Leu	Ser	Ser	Phe	Thr	Arg	Ile	
			85					90					95		
Ser	Ser	Thr	Val	Gln	Ala	Ala	Met	Glu	Asp	Ala	Leu	Val	Arg	Ile	Leu
			100					105					110		
Thr	Pro	Arg	Arg	Ser	Ile	Asp	Ile	Leu	Arg	Asp	Val	His	Ala	Ala	Lys
			115				120						125		
Glu	Gln	Arg	Lys	Pro	Tyr	Val	Val	Val	Phe	Val	Gly	Val	Asn	Gly	Val
			130				135				140				
Gly	Lys	Ser	Thr	Asn	Leu	Ala	Lys	Val	Ala	Tyr	Trp	Leu	Gln	Gln	His
145					150					155				160	
Lys	Val	Ser	Val	Met	Ala	Ala	Cys	Asp	Thr	Phe	Arg	Ser	Gly	Ala	
			165					170					175		
Val	Glu	Gln	Leu	Arg	Thr	His	Ala	Arg	Arg	Leu	Gln	Ile	Pro	Ile	Phe
			180					185					190		
Glu	Lys	Gly	Tyr	Glu	Lys	Asp	Pro	Ala	Val	Val	Ala	Lys	Glu	Ala	Ile
			195				200					205			
Gln	Glu	Ala	Thr	Arg	Asn	Gly	Ser	Asp	Val	Val	Leu	Val	Asp	Thr	Ala
			210			215					220				
Gly	Arg	Met	Gln	Asp	Asn	Glu	Pro	Leu	Met	Arg	Ala	Leu	Ser	Lys	Leu
225					230					235				240	
Ile	Asn	Leu	Asn	Gln	Pro	Asp	Leu	Val	Leu	Phe	Val	Gly	Glu	Ala	Leu
			245					250					255		
Val	Gly	Asn	Asp	Ala	Val	Asp	Gln	Leu	Ser	Lys	Phe	Asn	Gln	Lys	Leu
			260					265					270		
Ser	Asp	Leu	Ser	Thr	Ser	Gly	Asn	Pro	Arg	Leu	Ile	Asp	Gly	Ile	Leu
			275				280						285		
Leu	Thr	Lys	Phe	Asp	Thr	Ile	Asp	Asp	Lys	Val	Gly	Ala	Ala	Leu	Ser
			290				295				300				
Met	Val	Tyr	Ile	Ser	Gly	Ser	Pro	Val	Met	Phe	Val	Gly	Cys	Gly	Gln
305					310					315				320	
Ser	Tyr	Thr	Asp	Leu	Lys	Lys	Leu	Asn	Val	Lys	Ala	Ile	Val	Lys	Thr
			325					330						335	
Leu	Leu	Lys													

(2) INFORMATION FOR SEQ ID NO:933:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 338 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..338
 (D) OTHER INFORMATION: / Ceres Seq. ID 1499223

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:933:

Met Asp Lys Glu Glu Val Phe Ser Ser Asp Ser Glu Ser Glu Asp Asp
1 5 10 15
Asp Glu Pro Gly Ser Asp Glu Lys Pro Ala Gln Ala Lys Lys Lys Gly
20 25 30
Trp Phe Ser Ser Val Phe Gln Ser Ile Thr Gly Lys Ala Asn Leu Glu
35 40 45
Arg Thr Asp Leu Gly Pro Ala Leu Lys Ala Leu Lys Glu Arg Leu Met
50 55 60
Thr Lys Asn Val Ala Glu Ile Ala Glu Lys Leu Cys Glu Ser Val
65 70 75 80
Glu Ala Ser Leu Glu Gly Lys Lys Leu Ser Ser Phe Thr Arg Ile Ser
85 90 95
Ser Thr Val Gln Ala Ala Met Glu Asp Ala Leu Val Arg Ile Leu Thr
100 105 110
Pro Arg Arg Ser Ile Asp Ile Leu Arg Asp Val His Ala Ala Lys Glu
115 120 125
Gln Arg Lys Pro Tyr Val Val Phe Val Gly Val Asn Gly Val Gly
130 135 140
Lys Ser Thr Asn Leu Ala Lys Val Ala Tyr Trp Leu Gln Gln His Lys
145 150 155 160
Val Ser Val Met Met Ala Ala Cys Asp Thr Phe Arg Ser Gly Ala Val
165 170 175
Glu Gln Leu Arg Thr His Ala Arg Arg Leu Gln Ile Pro Ile Phe Glu
180 185 190
Lys Gly Tyr Glu Lys Asp Pro Ala Val Val Ala Lys Glu Ala Ile Gln
195 200 205
Glu Ala Thr Arg Asn Gly Ser Asp Val Val Leu Val Asp Thr Ala Gly
210 215 220
Arg Met Gln Asp Asn Glu Pro Leu Met Arg Ala Leu Ser Lys Leu Ile
225 230 235 240
Asn Leu Asn Gln Pro Asp Leu Val Leu Phe Val Gly Glu Ala Leu Val
245 250 255
Gly Asn Asp Ala Val Asp Gln Leu Ser Lys Phe Asn Gln Lys Leu Ser
260 265 270
Asp Leu Ser Thr Ser Gly Asn Pro Arg Leu Ile Asp Gly Ile Leu Leu
275 280 285
Thr Lys Phe Asp Thr Ile Asp Asp Lys Val Gly Ala Ala Leu Ser Met
290 295 300
Val Tyr Ile Ser Gly Ser Pro Val Met Phe Val Gly Cys Gly Gln Ser
305 310 315 320
Tyr Thr Asp Leu Lys Lys Leu Asn Val Lys Ala Ile Val Lys Thr Leu
325 330 335
Leu Lys

(2) INFORMATION FOR SEQ ID NO:934:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 521 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..521
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499224

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:934:

attgtgatga atcatcatga gcagtgactt catacttgat attacgggtg agaggccact	60
ataaaaaagca ggcgcgtcct cgaagaagaa gaagaagaag taacaaattg gtggaaatca	120
gaagttgaat cggagaataa caacgatgac gacgaacaag caggtcatat tcaaagacca	180
cgtgagvgwr ttccctaagg aatccgattt caatttcacc accaccaccg tcgaacttag	240

ggttccggaa gggttctaaat cggttcttgt gaagaatctc tacctgtcat gcgatcctta 300
tatgcgggtct cgcattgggga aacctgatcc ctccctctgct cttgctcaag cttacgctcc 360
cggcaagcca atctatgggt atggagtgtc tagagtgata gaatctgggc atccagatta 420
caagaaaggt gatttactct ggggaatagt tggatktgag gagtatagtg ttattacacc 480
aatggctcac atgcatttca agatccaaca tacagatgtt c

(2) INFORMATION FOR SEQ ID NO:935:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 125 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..125

(D) OTHER INFORMATION: / Ceres Seq. ID 1499225

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:935:

Met Thr Thr Asn Lys Gln Val Ile Phe Lys Asp His Val Xaa Xaa Phe
1 5 10 15
Pro Lys Glu Ser Asp Phe Asn Phe Thr Thr Thr Val Glu Leu Arg
20 25 30
Val Pro Glu Gly Ser Lys Ser Val Leu Val Lys Asn Leu Tyr Leu Ser
35 40 45
Cys Asp Pro Tyr Met Arg Ser Arg Met Gly Lys Pro Asp Pro Ser Ser
50 55 60
Ala Leu Ala Gln Ala Tyr Ala Pro Gly Lys Pro Ile Tyr Gly Tyr Gly
65 70 75 80
Val Ser Arg Val Ile Glu Ser Gly His Pro Asp Tyr Lys Lys Gly Asp
85 90 95
Leu Leu Trp Gly Ile Val Gly Xaa Glu Glu Tyr Ser Val Ile Thr Pro
100 105 110
Met Ala His Met His Phe Lys Ile Gln His Thr Asp Val
115 120 125

(2) INFORMATION FOR SEQ ID NO:936:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 73 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..73

(D) OTHER INFORMATION: / Ceres Seq. ID 1499226

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:936:

Met Arg Ser Arg Met Gly Lys Pro Asp Pro Ser Ser Ala Leu Ala Gln
1 5 10 15
Ala Tyr Ala Pro Gly Lys Pro Ile Tyr Gly Tyr Gly Val Ser Arg Val
20 25 30
Ile Glu Ser Gly His Pro Asp Tyr Lys Lys Gly Asp Leu Leu Trp Gly
35 40 45
Ile Val Gly Xaa Glu Glu Tyr Ser Val Ile Thr Pro Met Ala His Met
50 55 60
His Phe Lys Ile Gln His Thr Asp Val
65 70

(2) INFORMATION FOR SEQ ID NO:937:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 69 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..69

(D) OTHER INFORMATION: / Ceres Seq. ID 1499227

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:937:

```
Met Gly Lys Pro Asp Pro Ser Ser Ala Leu Ala Gln Ala Tyr Ala Pro
1          5          10          15
Gly Lys Pro Ile Tyr Gly Tyr Gly Val Ser Arg Val Ile Glu Ser Gly
20          25          30
His Pro Asp Tyr Lys Lys Gly Asp Leu Leu Trp Gly Ile Val Gly Xaa
35          40          45
Glu Glu Tyr Ser Val Ile Thr Pro Met Ala His Met His Phe Lys Ile
50          55          60
Gln His Thr Asp Val
65
```

(2) INFORMATION FOR SEQ ID NO:938:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1721 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1721

(D) OTHER INFORMATION: / Ceres Seq. ID 1499228

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:938:

```
aaaaaattca gccatgcct cgaagaaaaa acctcccaa tctgagaaat cggaaaagat      60
gaccacacc gaaaccctaa atctgctcga tgaaatcgag tctcttgtct ccgatcagct      120
tcaagtggta tcttacaaat ggctgagtcg aaatttctcg ctttcatcaa atactgccaa      180
gaggttgctc aaggatttta tagagaaaca tgggaagggt ttggaagttg tatatattgt      240
gtccggattg ctaaagaacg gaccttccga ttaccacgca aggcttgctt ctagtaccga      300
acttcagaa gtagagaaag agttcaatgg aaaatattca gtacatatct acagtgttca      360
agctagtatt ccaatggatc cagcagccat atggaacact gagtttgtac aagcagaaga      420
actcttcagg cagccttctg ccactgataa ttgtttgaaa ggcaacagtt tttgtggcgt      480
ctccaattct tgtgtgaagc gcaatataga gggagccact gaaaatgtta ccgccccgcg      540
aactgaaagt gtgagaacta caggacaatc taaaagtagt tcaaattttc aaaatagtac      600
agtgccgtca aaccagggaa agaatttcca gcactcaagc tctaattgtg gccatcaggc      660
taagagttaa tctattgctg ctccagctaa aaatcggctc gcgaaatcct ctttggataa      720
agaaaaagct tttcatgtgc ccgctaataa aaagaatgga cagggcgaga agagcgtgac      780
tggaactggg ggtttgttga aaaatatgtg gggccgtgtg cctgtgaaaa cagaagatga      840
ttctccaaca gtatagtga aaaatcatat tactaatcat tcggaacccc aaaaaccttc      900
tcatgatgct gacaagaagg gaggcagcga tgatgagact cgagacgcca atttcatgag      960
agcgcctaaa gataacagaa aaagaaaggt gatatttgat ttttcagatg acgagtatga     1020
agatgtaatc agcttagcat ctcatagtag tccaaagggt aattcacgtc cagatgtcga     1080
actcagttcg gaagattcag gtccagagaa gctgacgca gatgtttctc cagagataaa     1140
atctgaggaa ccagaggcca gcaaagaaga caggcaaaac actgcttctg ttgatgcttc     1200
tacgactttg tcaacggaga agatccaggc cattggttct gaagctgaag tgaatccctc     1260
aaagagaaga actactgcag ttcctagttc gccgaaaagg aaaaagggtg tgaagtcaag     1320
gattgatgat cgtgggagag aagtaactga ggtagtgtgg gaggagacag aaacgaacgc     1380
aaagaagaaa gaggacacta atacaagtaa gaagttagat gatggcaaaa ccgcaaattgc     1440
tgtaacagg gcggttgac agaagaagag tccggccatt ggaaacacag cagcgacaaa     1500
cgcaggagga aaagcgggaa gcaagaaagg aggaaacgtc aaagatccaa agcaagggaa     1560
tataatgtcc ttcttcaaga aagtttaaaa aggcttcttt tttgtattta ttgtttgcta     1620
agtttgagtt gaggatatta taggaaaatc agaacttga ttcactctgac tgtatgttct     1680
gatccattgt gtctaagaaa aaaacttttg agccgtttct c
```

(2) INFORMATION FOR SEQ ID NO:939:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 528 amino acids

(B) TYPE: amino acid

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(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..528
(D) OTHER INFORMATION: / Ceres Seq. ID 1499229
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:939:

Lys	Asn	Ser	Ala	Ile	Ala	Ser	Lys	Lys	Lys	Pro	Pro	Lys	Ser	Glu	Lys
1			5					10						15	
Ser	Glu	Lys	Met	Thr	His	Thr	Glu	Thr	Leu	Asn	Leu	Leu	Asp	Glu	Ile
			20					25					30		
Glu	Ser	Leu	Val	Ser	Asp	Gln	Leu	Gln	Val	Val	Ser	Tyr	Lys	Trp	Leu
			35				40					45			
Ser	Arg	Asn	Phe	Ser	Leu	Ser	Ser	Asn	Thr	Ala	Lys	Arg	Leu	Leu	Lys
						55				60					
Asp	Phe	Ile	Glu	Lys	His	Gly	Lys	Gly	Leu	Glu	Val	Val	Tyr	Ile	Val
65					70				75					80	
Ser	Gly	Leu	Leu	Lys	Asn	Gly	Pro	Ser	Asp	Tyr	His	Ala	Arg	Leu	Ala
				85					90					95	
Ser	Ser	Thr	Glu	Leu	Pro	Glu	Val	Glu	Lys	Glu	Phe	Asn	Gly	Lys	Tyr
			100					105					110		
Ser	Val	His	Ile	Tyr	Ser	Val	Gln	Ala	Ser	Ile	Pro	Met	Asp	Pro	Ala
			115				120					125			
Ala	Ile	Trp	Asn	Thr	Glu	Phe	Val	Gln	Ala	Glu	Glu	Leu	Phe	Arg	Gln
			130			135					140				
Pro	Ser	Ala	Thr	Asp	Asn	Cys	Leu	Lys	Gly	Asn	Ser	Phe	Cys	Gly	Val
145				150						155				160	
Ser	Asn	Ser	Cys	Val	Lys	Arg	Asn	Ile	Glu	Gly	Ala	Thr	Glu	Asn	Val
			165						170					175	
Thr	Ala	Pro	Arg	Thr	Glu	Ser	Val	Arg	Thr	Thr	Gly	Gln	Ser	Lys	Ser
			180					185					190		
Ser	Ser	Asn	Phe	Gln	Asn	Ser	Thr	Val	Pro	Ser	Asn	Gln	Gly	Lys	Asn
			195				200					205			
Phe	Gln	His	Ser	Ser	Ser	Asn	Val	Gly	His	Gln	Ala	Lys	Ser	Glu	Ser
			210			215					220				
Ile	Ala	Ala	Pro	Ala	Lys	Asn	Arg	Ser	Ala	Lys	Ser	Ser	Leu	Asp	Lys
225				230						235				240	
Glu	Lys	Ala	Phe	His	Val	Pro	Ala	Asn	Lys	Lys	Asn	Gly	Gln	Gly	Glu
				245					250					255	
Lys	Ser	Val	Thr	Gly	Thr	Gly	Gly	Leu	Lys	Asn	Met	Trp	Gly	Arg	
			260					265					270		
Val	Pro	Val	Lys	Thr	Glu	Asp	Asp	Ser	Pro	Thr	Val	Asp	Val	Lys	Asn
			275			280						285			
His	Ile	Thr	Asn	His	Ser	Glu	Pro	Gln	Lys	Pro	Ser	His	Asp	Ala	Asp
			290			295					300				
Lys	Lys	Gly	Gly	Ser	Asp	Asp	Glu	Thr	Arg	Asp	Ala	Asn	Phe	Met	Arg
305				310						315				320	
Ala	Pro	Lys	Asp	Asn	Arg	Lys	Arg	Lys	Val	Ile	Phe	Asp	Phe	Ser	Asp
				325					330					335	
Asp	Glu	Tyr	Glu	Asp	Val	Ile	Ser	Leu	Ala	Ser	His	Ser	Ser	Pro	Lys
			340					345					350		
Val	Asn	Ser	Arg	Pro	Asp	Val	Glu	Leu	Ser	Ser	Glu	Asp	Ser	Gly	Pro
			355				360					365			
Glu	Lys	Pro	Asp	Ala	Asp	Val	Ser	Pro	Glu	Ile	Lys	Ser	Glu	Glu	Pro
					375						380				
Glu	Ala	Ser	Lys	Glu	Asp	Arg	Gln	Asn	Thr	Ala	Ser	Val	Asp	Ala	Ser
385				390						395				400	
Thr	Thr	Leu	Ser	Thr	Glu	Lys	Ile	Gln	Ala	Ile	Gly	Ser	Glu	Ala	Glu
				405					410					415	
Val	Asn	Pro	Ser	Lys	Arg	Arg	Thr	Thr	Ala	Val	Pro	Ser	Ser	Pro	Lys

			420					425				430			
Arg	Lys	Lys	Val	Leu	Lys	Ser	Arg	Ile	Asp	Asp	Arg	Gly	Arg	Glu	Val
		435					440					445			
Thr	Glu	Val	Val	Trp	Glu	Glu	Thr	Glu	Thr	Asn	Ala	Lys	Lys	Lys	Glu
	450					455					460				
Asp	Thr	Asn	Thr	Ser	Lys	Lys	Leu	Asp	Asp	Gly	Lys	Thr	Ala	Asn	Ala
465					470					475					480
Val	Asn	Arg	Ala	Val	Ala	Gln	Lys	Lys	Ser	Pro	Ala	Ile	Gly	Asn	Thr
			485						490					495	
Ala	Ala	Thr	Asn	Ala	Gly	Gly	Lys	Ala	Gly	Ser	Lys	Lys	Gly	Gly	Asn
			500					505					510		
Val	Lys	Asp	Pro	Lys	Gln	Gly	Asn	Ile	Met	Ser	Phe	Phe	Lys	Lys	Val
		515					520					525			

(2) INFORMATION FOR SEQ ID NO:940:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 509 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..509

(D) OTHER INFORMATION: / Ceres Seq. ID 1499230

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:940:

Met	Thr	His	Thr	Glu	Thr	Leu	Asn	Leu	Leu	Asp	Glu	Ile	Glu	Ser	Leu
1				5					10					15	
Val	Ser	Asp	Gln	Leu	Gln	Val	Val	Ser	Tyr	Lys	Trp	Leu	Ser	Arg	Asn
			20					25					30		
Phe	Ser	Leu	Ser	Ser	Asn	Thr	Ala	Lys	Arg	Leu	Leu	Lys	Asp	Phe	Ile
			35				40					45			
Glu	Lys	His	Gly	Lys	Gly	Leu	Glu	Val	Val	Tyr	Ile	Val	Ser	Gly	Leu
	50					55					60				
Leu	Lys	Asn	Gly	Pro	Ser	Asp	Tyr	His	Ala	Arg	Leu	Ala	Ser	Ser	Thr
65				70						75					80
Glu	Leu	Pro	Glu	Val	Glu	Lys	Glu	Phe	Asn	Gly	Lys	Tyr	Ser	Val	His
				85					90					95	
Ile	Tyr	Ser	Val	Gln	Ala	Ser	Ile	Pro	Met	Asp	Pro	Ala	Ala	Ile	Trp
			100					105					110		
Asn	Thr	Glu	Phe	Val	Gln	Ala	Glu	Glu	Leu	Phe	Arg	Gln	Pro	Ser	Ala
			115				120					125			
Thr	Asp	Asn	Cys	Leu	Lys	Gly	Asn	Ser	Phe	Cys	Gly	Val	Ser	Asn	Ser
	130					135					140				
Cys	Val	Lys	Arg	Asn	Ile	Glu	Gly	Ala	Thr	Glu	Asn	Val	Thr	Ala	Pro
145				150						155					160
Arg	Thr	Glu	Ser	Val	Arg	Thr	Thr	Gly	Gln	Ser	Lys	Ser	Ser	Ser	Asn
				165				170						175	
Phe	Gln	Asn	Ser	Thr	Val	Pro	Ser	Asn	Gln	Gly	Lys	Asn	Phe	Gln	His
			180					185					190		
Ser	Ser	Ser	Asn	Val	Gly	His	Gln	Ala	Lys	Ser	Glu	Ser	Ile	Ala	Ala
			195				200					205			
Pro	Ala	Lys	Asn	Arg	Ser	Ala	Lys	Ser	Ser	Leu	Asp	Lys	Glu	Lys	Ala
	210					215					220				
Phe	His	Val	Pro	Ala	Asn	Lys	Lys	Asn	Gly	Gln	Gly	Glu	Lys	Ser	Val
225				230					235						240
Thr	Gly	Thr	Gly	Gly	Leu	Leu	Lys	Asn	Met	Trp	Gly	Arg	Val	Pro	Val
				245				250						255	
Lys	Thr	Glu	Asp	Ser	Pro	Thr	Val	Asp	Val	Lys	Asn	His	Ile	Thr	
			260				265					270			

Asn	His	Ser	Glu	Pro	Gln	Lys	Pro	Ser	His	Asp	Ala	Asp	Lys	Lys	Gly
		275					280					285			
Gly	Ser	Asp	Asp	Glu	Thr	Arg	Asp	Ala	Asn	Phe	Met	Arg	Ala	Pro	Lys
	290					295				300					
Asp	Asn	Arg	Lys	Arg	Lys	Val	Ile	Phe	Asp	Phe	Ser	Asp	Asp	Glu	Tyr
305					310					315					320
Glu	Asp	Val	Ile	Ser	Leu	Ala	Ser	His	Ser	Ser	Pro	Lys	Val	Asn	Ser
				325					330					335	
Arg	Pro	Asp	Val	Glu	Leu	Ser	Ser	Glu	Asp	Ser	Gly	Pro	Glu	Lys	Pro
			340					345					350		
Asp	Ala	Asp	Val	Ser	Pro	Glu	Ile	Lys	Ser	Glu	Glu	Pro	Glu	Ala	Ser
		355					360					365			
Lys	Glu	Asp	Arg	Gln	Asn	Thr	Ala	Ser	Val	Asp	Ala	Ser	Thr	Thr	Leu
	370					375					380				
Ser	Thr	Glu	Lys	Ile	Gln	Ala	Ile	Gly	Ser	Glu	Ala	Glu	Val	Asn	Pro
385					390					395					400
Ser	Lys	Arg	Arg	Thr	Ala	Val	Pro	Ser	Ser	Pro	Lys	Arg	Lys	Lys	
			405					410					415		
Val	Leu	Lys	Ser	Arg	Ile	Asp	Asp	Arg	Gly	Arg	Glu	Val	Thr	Glu	Val
			420					425					430		
Val	Trp	Glu	Glu	Thr	Glu	Thr	Asn	Ala	Lys	Lys	Lys	Glu	Asp	Thr	Asn
		435					440					445			
Thr	Ser	Lys	Lys	Leu	Asp	Asp	Gly	Lys	Thr	Ala	Asn	Ala	Val	Asn	Arg
	450					455					460				
Ala	Val	Ala	Gln	Lys	Lys	Ser	Pro	Ala	Ile	Gly	Asn	Thr	Ala	Ala	Thr
465					470					475					480
Asn	Ala	Gly	Gly	Lys	Ala	Gly	Ser	Lys	Lys	Gly	Gly	Asn	Val	Lys	Asp
			485					490						495	
Pro	Lys	Gln	Gly	Asn	Ile	Met	Ser	Phe	Phe	Lys	Lys	Val			
		500						505							

(2) INFORMATION FOR SEQ ID NO:941:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 404 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..404

(D) OTHER INFORMATION: / Ceres Seq. ID 1499231

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:941:

Met	Asp	Pro	Ala	Ala	Ile	Trp	Asn	Thr	Glu	Phe	Val	Gln	Ala	Glu	Glu
1			5						10					15	
Leu	Phe	Arg	Gln	Pro	Ser	Ala	Thr	Asp	Asn	Cys	Leu	Lys	Gly	Asn	Ser
		20						25					30		
Phe	Cys	Gly	Val	Ser	Asn	Ser	Cys	Val	Lys	Arg	Asn	Ile	Glu	Gly	Ala
	35					40						45			
Thr	Glu	Asn	Val	Thr	Ala	Pro	Arg	Thr	Glu	Ser	Val	Arg	Thr	Thr	Gly
	50					55					60				
Gln	Ser	Lys	Ser	Ser	Ser	Asn	Phe	Gln	Asn	Ser	Thr	Val	Pro	Ser	Asn
65					70					75				80	
Gln	Gly	Lys	Asn	Phe	Gln	His	Ser	Ser	Ser	Asn	Val	Gly	His	Gln	Ala
			85					90					95		
Lys	Ser	Glu	Ser	Ile	Ala	Ala	Pro	Ala	Lys	Asn	Arg	Ser	Ala	Lys	Ser
		100						105					110		
Ser	Leu	Asp	Lys	Glu	Lys	Ala	Phe	His	Val	Pro	Ala	Asn	Lys	Lys	Asn
	115					120					125				
Gly	Gln	Gly	Glu	Lys	Ser	Val	Thr	Gly	Thr	Gly	Gly	Leu	Leu	Lys	Asn
	130					135				140					
Met	Trp	Gly	Arg	Val	Pro	Val	Lys	Thr	Glu	Asp	Asp	Ser	Pro	Thr	Val

145 150 155 160
Asp Val Lys Asn His Ile Thr Asn His Ser Glu Pro Gln Lys Pro Ser
165 170 175
His Asp Ala Asp Lys Lys Gly Gly Ser Asp Asp Glu Thr Arg Asp Ala
180 185 190
Asn Phe Met Arg Ala Pro Lys Asp Asn Arg Lys Arg Lys Val Ile Phe
195 200 205
Asp Phe Ser Asp Asp Glu Tyr Glu Asp Val Ile Ser Leu Ala Ser His
210 215 220
Ser Ser Pro Lys Val Asn Ser Arg Pro Asp Val Glu Leu Ser Ser Glu
225 230 235 240
Asp Ser Gly Pro Glu Lys Pro Asp Ala Asp Val Ser Pro Glu Ile Lys
245 250 255
Ser Glu Glu Pro Glu Ala Ser Lys Glu Asp Arg Gln Asn Thr Ala Ser
260 265 270
Val Asp Ala Ser Thr Thr Leu Ser Thr Glu Lys Ile Gln Ala Ile Gly
275 280 285
Ser Glu Ala Glu Val Asn Pro Ser Lys Arg Arg Thr Thr Ala Val Pro
290 295 300
Ser Ser Pro Lys Arg Lys Lys Val Leu Lys Ser Arg Ile Asp Asp Arg
305 310 315 320
Gly Arg Glu Val Thr Glu Val Val Trp Glu Glu Thr Glu Thr Asn Ala
325 330 335
Lys Lys Lys Glu Asp Thr Asn Thr Ser Lys Lys Leu Asp Asp Gly Lys
340 345 350
Thr Ala Asn Ala Val Asn Arg Ala Val Ala Gln Lys Lys Ser Pro Ala
355 360 365
Ile Gly Asn Thr Ala Ala Thr Asn Ala Gly Gly Lys Ala Gly Ser Lys
370 375 380
Lys Gly Gly Asn Val Lys Asp Pro Lys Gln Gly Asn Ile Met Ser Phe
385 390 395 400
Phe Lys Lys Val

(2) INFORMATION FOR SEQ ID NO:942:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 779 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..779
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499232

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:942:

atttctgttc atttcacctt tactaaaaag agaactcaca tcaaagaaac agtccatcat 60
tcacatgata tagatgagca tcattactaa ttatcttgta acgaatgata actaatgttt 120
ttgactattc tatgcagctc tagtggcact cctaccacag gaacaccaac tagtgggaca 180
ccaaccagtg ggaccccgac taccggaact ccgaccaccg gaacccccac cactggaact 240
ccaaccagtg ggactccaac tagtggcttc ccaaataccg ggactccgaa cacagggact 300
aacactggga tgccaaattc caacgggatg ccaacttcat cgtcatcttc ggtgttcccg 360
gggactactc ttggaccgac tggtagcggg ggactaggcg atccaaatgc tggagagaag 420
ctgtctgttc gaactaacac attggtcttc ttattaaccg gtgtagcagc aatgcttgtc 480
atatgagggc ttagatgtca cacgcgggta tggttgtaat tgggtttgct gagagatcag 540
atcttgcccta cggtctcattg ttgatagagc catctttttt tcactcgtct ttctaggatt 600
tggacttagg ttggccgaga gacataatgc tggtagtagc tagtattttg ggttatgtac 660
aactttaact aagagcttta cttttgtaaa tccggaggat gagatgctct tttgtttctt 720
atattctttt taatcctttt actttgatct ttcattcttt aatacgtacc atcattgtc

(2) INFORMATION FOR SEQ ID NO:943:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 123 amino acids

- (B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..123
(D) OTHER INFORMATION: / Ceres Seq. ID 1499233
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:943:

Met Phe Leu Thr Ile Leu Cys Ser Ser Ser Gly Thr Pro Thr Thr Gly
1 5 10 15
Thr Pro Thr Ser Gly Thr Pro Thr Ser Gly Thr Pro Thr Thr Gly Thr
20 25 30
Pro Thr Thr Gly Thr Pro Thr Thr Gly Thr Pro Thr Ser Gly Thr Pro
35 40 45
Thr Ser Gly Phe Pro Asn Thr Gly Thr Pro Asn Thr Gly Thr Asn Thr
50 55 60
Gly Met Pro Asn Ser Asn Gly Met Pro Thr Ser Ser Ser Ser Ser Val
65 70 75 80
Phe Pro Gly Thr Thr Leu Gly Pro Thr Gly Ser Gly Gly Leu Gly Asp
85 90 95
Pro Asn Ala Gly Glu Lys Leu Ser Val Arg Thr Asn Thr Leu Val Phe
100 105 110
Leu Leu Thr Gly Val Ala Ala Met Leu Val Ile
115 120

(2) INFORMATION FOR SEQ ID NO:944:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1412 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
(A) NAME/KEY: -
(B) LOCATION: 1..1412
(D) OTHER INFORMATION: / Ceres Seq. ID 1499242
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:944:

actccgagcg tttcctttct cacaagccaa tggcgcaatt tactaattcc atcaattatc 60
tcttttctgt ttctctctta ttatttgtat cgttccactg cttatgtttt cgtttttcat 120
tggttgagcg ttgttcaaac tccaccgagc accaacagat tcaacacccat caccaccgga 180
aatgggttg tccctcaggc cacaaagtca tcaccgtctc acttaacggc cagctcagct 240
ttcgctccgt ccaagacgct gtggattcca taccaaagav caataacaag agcatcacaa 300
tcaagattgc tcccggattt tacagagaga aagtgggtgt tccagctaca aaaccgtaca 360
taaacgttca aaggagctgg tagggatgtg accgctatag agtggcacga ccgtgcgtcc 420
gaccttggcg ctaacggtca acagttacgt acctatcaaa ccgcttccgt caccgtctac 480
gctaattatt tcaccgctag aaacattagc ttcacggtac tctattcaat tctaacgcaa 540
ttatatatat agggaaactt tcacaaaaat gcgagtcctt ctttatttta ttttaaattg 600
tgaagaatac tgcgccggct ccattgccgg gtagtcaagg gtggcaagcg gtggcggtta 660
ggatctccgg cgacaaagct ttcttttccg gctgcgggtt ttacggtgca caagacactt 720
tatgcgacga tgctggccgt cattacttca aggagtgtta cattgaaggc tctatcgact 780
ttatcttttg taatggccgc tccatgtata aagattgtga gttgcattcg atagcgtcaa 840
gattcgggtc gatagcggcg catggtagga catgcccga agagaaaacg ggtttcgcgt 900
tcgtgggttg tcgggtaaca ggtacgggtc cattgtacgt gggccgggccc atgggaccaa 960
tactcacgta tcgtttacgc ctacacttac tttgatgctc tcgtcgctca cgggtggttg 1020
gacgattggg accacaaatc caacaaaagc aagacggcat ttttcggagt gtacaattgc 1080
tatgggccag gagcagcagc gacgagaggg gtgtcttggg ctagagcttt ggactatgaa 1140
tcggcccatc caattatcgc taagagcttc gttaatggga gacattggat cgctcctcga 1200
gatgcttaac caacttcaaa ccttgccggg gtttcttttc ctaattcctc ggttccctcc 1260
agtcccaagt cctaaaagct tactatattt ttatcattcg tttatttctt ttattgttta 1320
ttttttccaa tttatttata cattgtgtga tagtacaaca aagtattgct tcttcttcat 1380
ctgtatccat ttcagttaaa tgttttgagc tt

(2) INFORMATION FOR SEQ ID NO:945:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 126 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..126
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499243

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:945:

Ser Glu Arg Phe Leu Ser His Lys Pro Met Ala Gln Phe Thr Asn Ser
1 5 10 15
Ile Asn Tyr Leu Phe Ser Val Ser Leu Leu Leu Phe Val Ser Phe His
20 25 30
Cys Leu Cys Phe Arg Phe Ser Leu Val Ala Ala Cys Ser Asn Ser Thr
35 40 45
Asp Asp Gln Gln Ile Gln His His His Arg Lys Trp Val Gly Pro
50 55 60
Ser Gly His Lys Val Ile Thr Val Ser Leu Asn Gly His Ala Gln Phe
65 70 75 80
Arg Ser Val Gln Asp Ala Val Asp Ser Ile Pro Lys Xaa Asn Asn Lys
85 90 95
Ser Ile Thr Ile Lys Ile Ala Pro Gly Phe Tyr Arg Glu Lys Val Val
100 105 110
Val Pro Ala Thr Lys Pro Tyr Ile Asn Val Gln Arg Ser Trp
115 120 125

(2) INFORMATION FOR SEQ ID NO:946:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 175 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..175
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499244

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:946:

Met Pro Gly Arg Glu Asn Gly Phe Arg Val Arg Gly Leu Ser Gly Asn
1 5 10 15
Arg Tyr Gly Ser Ile Val Arg Gly Pro Gly His Gly Thr Asn Thr His
20 25 30
Val Ser Phe Thr Pro Thr Leu Thr Leu Met Leu Ser Ser Leu Thr Val
35 40 45
Val Gly Thr Ile Gly Thr Thr Asn Pro Thr Lys Ala Arg Arg His Phe
50 55 60
Ser Glu Cys Thr Ile Ala Met Gly Gln Glu Gln Arg Arg Glu Ala
65 70 75 80
Cys Leu Gly Leu Glu Leu Trp Thr Met Asn Arg Pro Ile His Leu Ser
85 90 95
Leu Arg Ala Ser Leu Met Gly Asp Ile Gly Ser Leu Leu Glu Met Leu
100 105 110
Asn Gln Leu Gln Thr Leu Ala Gly Phe Leu Phe Leu Ile Pro Arg Phe
115 120 125
Leu Pro Val Pro Ser Pro Lys Ser Leu Leu Tyr Phe Tyr His Ser Phe
130 135 140
Ile Ser Phe Ile Val Tyr Phe Phe Gln Phe Ile Tyr Thr Leu Cys Asp
145 150 155 160
Ser Thr Thr Lys Tyr Cys Phe Phe Phe Ile Cys Ile His Phe Ser

165 170 175

(2) INFORMATION FOR SEQ ID NO:947:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 134 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..134

(D) OTHER INFORMATION: / Ceres Seq. ID 1499245

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:947:

Met Leu Ser Ser Leu Thr Val Val Gly Thr Ile Gly Thr Thr Asn Pro
1 5 10 15
Thr Lys Ala Arg Arg His Phe Ser Glu Cys Thr Ile Ala Met Gly Gln
20 25 30
Glu Gln Gln Arg Arg Glu Ala Cys Leu Gly Leu Glu Leu Trp Thr Met
35 40 45
Asn Arg Pro Ile His Leu Ser Leu Arg Ala Ser Leu Met Gly Asp Ile
50 55 60
Gly Ser Leu Leu Glu Met Leu Asn Gln Leu Gln Thr Leu Ala Gly Phe
65 70 75 80
Leu Phe Leu Ile Pro Arg Phe Leu Pro Val Pro Ser Pro Lys Ser Leu
85 90 95
Leu Tyr Phe Tyr His Ser Phe Ile Ser Phe Ile Val Tyr Phe Phe Gln
100 105 110
Phe Ile Tyr Thr Leu Cys Asp Ser Thr Thr Lys Tyr Cys Phe Phe Phe
115 120 125
Ile Cys Ile His Phe Ser
130

(2) INFORMATION FOR SEQ ID NO:948:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1894 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1894

(D) OTHER INFORMATION: / Ceres Seq. ID 1499250

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:948:

aacaccgtga cagctcctta gatctctcct cggttacttc ctttttaatt tccatggctc 60
tctaaaaatc tctctctctt tctctctctc ttacttgat tgttacgata tctgcttgaa 120
gattatggac ggcgcgatg gaaccgttcg cgtcaagcct ggtcgcgat tcgaaacgga 180
gacggatgtt gcggtttcgt cgccagtgc acgtcagaaa gctgctgcag ctaagcaatt 240
catcgagaat cattataaga attacttgca aggcttgac gaacgaatgg agagacgcag 300
ggagtttcag aggaaagtgc aagaagctca gttacctgtt gaggaacaag acgagatgat 360
gaggaatctg gctcgctcgtg aaactgagta tatgagactt cagagacgta aaattgggat 420
tgatgatttt gagcttttga ccgttattgg caaaggtgcc tttgggtgagg ttagattatg 480
tcgtttgaga tctacatctg aagtttatgc catgaagaaa ttgaaaaaaa ctgagatgct 540
tagccgtgga caggtagagc atgtcaggtc cgagaggaac ttacttgacag aagttgacag 600
ccgttacatt gtaaagcttt tttactcttt tcaagattct gaatgtttgt atcttatcat 660
ggagtattta cctgggggtg acatcatgac actactcatg agagaagaca ttctttctga 720
agatgttgcc cgtttttata ttgctgagag cattcttgcc atccattcaa ttcataaaca 780
caactatggt cacagggaca tcaaacctga taatttgata ctagacaaaa gtgggcattt 840
gaagctttca gattttggtt tatgtaagcc acttgatgac aagtattctt cattgctatt 900
agaagacgat gaaatgttgt ctcaggattc agagaaccag tcaggaaaat cagacgctga 960
caaagcacc tggaacatgc ctaaagagca gttactgcag tggaaacgca atcgccgtgc 1020
attggcttat tcaaccgttg gaactcttga ttacatggct ccagaagtag tcctaaagaa 1080

```
aggatatgga atggaatgtg attggtggtc tctcggcgca attttgtatg agatgttagt 1140
tggttatccc ccattctggt ctgatgaccc ccgtataaca tgccgcaaga taattaattg 1200
gagggtatgc ttgaagttcc ctgaacaacc aaaaatatca gatgaagcca gagacttgat 1260
ttgtcggttg ctttgtgatg ttgattcaag gttgggaacc agaggtggtg aggagataaa 1320
gtcgcaccca tggttcaaaag gcaccccatg ggacaaactg tatgacatgg aggcagctta 1380
tagaccatt gtcgatggag aactagacac acaaaatttt gagaagtttc ctgaagttga 1440
aggatcacca tccgaagcac cacaagtgtg tccttggaaga aagatgttga cgtccaagga 1500
caccaacttc ataggattta catttaagaa gtcagacatc acaagatcaa tggaaagttc 1560
agggtgcagac atgaaatcaa atggatcagg ggaagccccg tcgttgatat cattgttagg 1620
tcggatcaat atggaagaag gtgaaggtgg tgagttaaac cacaagacat agggaaaata 1680
caaattattat tgatttttta tccgcttgca gttgttttga tcatttgga gaggaatgg 1740
agaggcgatg gtagtttttt aaccacatca cttatgatgg ggttcataaa aacttctatt 1800
tccttttttt ttcttgtaac atatttgttt ttttttcaat ctaaaaaaga aactgtaaag 1860
catggaagaa taatttctgg aacattttac cccc
```

(2) INFORMATION FOR SEQ ID NO:949:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 515 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..515

(D) OTHER INFORMATION: / Ceres Seq. ID 1499251

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:949:

```
Met Asp Gly Ala Asp Gly Thr Val Arg Val Lys Pro Gly Arg Gly Phe
1      5      10      15
Glu Thr Glu Thr Asp Val Ala Val Ser Ser Pro Val Thr Arg Gln Lys
20      25      30
Ala Ala Ala Ala Lys Gln Phe Ile Glu Asn His Tyr Lys Asn Tyr Leu
35      40      45
Gln Gly Leu His Glu Arg Met Glu Arg Arg Arg Glu Phe Gln Arg Lys
50      55      60
Val Gln Glu Ala Gln Leu Pro Val Glu Glu Gln Asp Glu Met Met Arg
65      70      75      80
Asn Leu Ala Arg Arg Glu Thr Glu Tyr Met Arg Leu Gln Arg Arg Lys
85      90      95
Ile Gly Ile Asp Asp Phe Glu Leu Leu Thr Val Ile Gly Lys Gly Ala
100     105     110
Phe Gly Glu Val Arg Leu Cys Arg Leu Arg Ser Thr Ser Glu Val Tyr
115     120     125
Ala Met Lys Lys Leu Lys Lys Thr Glu Met Leu Ser Arg Gly Gln Val
130     135     140
Glu His Val Arg Ser Glu Arg Asn Leu Leu Ala Glu Val Asp Ser Arg
145     150     155     160
Tyr Ile Val Lys Leu Phe Tyr Ser Phe Gln Asp Ser Glu Cys Leu Tyr
165     170     175
Leu Ile Met Glu Tyr Leu Pro Gly Gly Asp Ile Met Thr Leu Leu Met
180     185     190
Arg Glu Asp Ile Leu Ser Glu Asp Val Ala Arg Phe Tyr Ile Ala Glu
195     200     205
Ser Ile Leu Ala Ile His Ser Ile His Gln His Asn Tyr Val His Arg
210     215     220
Asp Ile Lys Pro Asp Asn Leu Ile Leu Asp Lys Ser Gly His Leu Lys
225     230     235     240
Leu Ser Asp Phe Gly Leu Cys Lys Pro Leu Asp Asp Lys Tyr Ser Ser
245     250     255
Leu Leu Leu Glu Asp Asp Glu Met Leu Ser Gln Asp Ser Glu Asn Gln
260     265     270
Ser Gly Lys Ser Asp Ala Asp Lys Ala Pro Trp Gln Met Pro Lys Glu
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275	280	285
Gln Leu Leu Gln Trp Lys Arg Asn Arg Arg Ala Leu Ala Tyr Ser Thr		
290	295	300
Val Gly Thr Leu Asp Tyr Met Ala Pro Glu Val Leu Leu Lys Lys Gly		
305	310	315
Tyr Gly Met Glu Cys Asp Trp Trp Ser Leu Gly Ala Ile Leu Tyr Glu		
	325	330
Met Leu Val Gly Tyr Pro Pro Phe Cys Ser Asp Asp Pro Arg Ile Thr		
	340	345
Cys Arg Lys Ile Ile Asn Trp Arg Val Cys Leu Lys Phe Pro Glu Gln		
	355	360
Pro Lys Ile Ser Asp Glu Ala Arg Asp Leu Ile Cys Arg Leu Leu Cys		
	370	375
Asp Val Asp Ser Arg Leu Gly Thr Arg Gly Val Glu Glu Ile Lys Ser		
385	390	395
His Pro Trp Phe Lys Gly Thr Pro Trp Asp Lys Leu Tyr Asp Met Glu		
	405	410
Ala Ala Tyr Arg Pro Ile Val Asp Gly Glu Leu Asp Thr Gln Asn Phe		
	420	425
Glu Lys Phe Pro Glu Val Glu Gly Ser Pro Ser Glu Ala Pro Gln Val		
	435	440
Gly Pro Trp Arg Lys Met Leu Thr Ser Lys Asp Thr Asn Phe Ile Gly		
	450	455
Phe Thr Phe Lys Lys Ser Asp Ile Thr Arg Ser Met Glu Ser Ser Gly		
465	470	475
Ala Asp Met Lys Ser Asn Gly Ser Gly Glu Ala Pro Ser Leu Ile Ser		
	485	490
Leu Leu Gly Arg Ile Asn Met Glu Glu Gly Glu Gly Glu Leu Asn		
	500	505
His Lys Thr		510
	515	

(2) INFORMATION FOR SEQ ID NO:950:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 461 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..461

(D) OTHER INFORMATION: / Ceres Seq. ID 1499252

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:950:

Met	Glu	Arg	Arg	Arg	Glu	Phe	Gln	Arg	Lys	Val	Gln	Glu	Ala	Gln	Leu
1				5					10					15	
Pro	Val	Glu	Glu	Gln	Asp	Glu	Met	Met	Arg	Asn	Leu	Ala	Arg	Arg	Glu
			20					25					30		
Thr	Glu	Tyr	Met	Arg	Leu	Gln	Arg	Arg	Lys	Ile	Gly	Ile	Asp	Asp	Phe
		35				40						45			
Glu	Leu	Leu	Thr	Val	Ile	Gly	Lys	Gly	Ala	Phe	Gly	Glu	Val	Arg	Leu
	50					55					60				
Cys	Arg	Leu	Arg	Ser	Thr	Ser	Glu	Val	Tyr	Ala	Met	Lys	Lys	Leu	Lys
65					70					75				80	
Lys	Thr	Glu	Met	Leu	Ser	Arg	Gly	Gln	Val	Glu	His	Val	Arg	Ser	Glu
			85					90						95	
Arg	Asn	Leu	Leu	Ala	Glu	Val	Asp	Ser	Arg	Tyr	Ile	Val	Lys	Leu	Phe
		100						105					110		
Tyr	Ser	Phe	Gln	Asp	Ser	Glu	Cys	Leu	Tyr	Leu	Ile	Met	Glu	Tyr	Leu
		115					120					125			
Pro	Gly	Gly	Asp	Ile	Met	Thr	Leu	Leu	Met	Arg	Glu	Asp	Ile	Leu	Ser
	130					135					140				

Glu Asp Val Ala Arg Phe Tyr Ile Ala Glu Ser Ile Leu Ala Ile His
 145 150 155 160
 Ser Ile His Gln His Asn Tyr Val His Arg Asp Ile Lys Pro Asp Asn
 165 170 175
 Leu Ile Leu Asp Lys Ser Gly His Leu Lys Leu Ser Asp Phe Gly Leu
 180 185 190
 Cys Lys Pro Leu Asp Asp Lys Tyr Ser Ser Leu Leu Leu Glu Asp Asp
 195 200 205
 Glu Met Leu Ser Gln Asp Ser Glu Asn Gln Ser Gly Lys Ser Asp Ala
 210 215 220
 Asp Lys Ala Pro Trp Gln Met Pro Lys Glu Gln Leu Leu Gln Trp Lys
 225 230 235 240
 Arg Asn Arg Arg Ala Leu Ala Tyr Ser Thr Val Gly Thr Leu Asp Tyr
 245 250 255
 Met Ala Pro Glu Val Leu Leu Lys Lys Gly Tyr Gly Met Glu Cys Asp
 260 265 270
 Trp Trp Ser Leu Gly Ala Ile Leu Tyr Glu Met Leu Val Gly Tyr Pro
 275 280 285
 Pro Phe Cys Ser Asp Asp Pro Arg Ile Thr Cys Arg Lys Ile Ile Asn
 290 295 300
 Trp Arg Val Cys Leu Lys Phe Pro Glu Gln Pro Lys Ile Ser Asp Glu
 305 310 315 320
 Ala Arg Asp Leu Ile Cys Arg Leu Leu Cys Asp Val Asp Ser Arg Leu
 325 330 335
 Gly Thr Arg Gly Val Glu Glu Ile Lys Ser His Pro Trp Phe Lys Gly
 340 345 350
 Thr Pro Trp Asp Lys Leu Tyr Asp Met Glu Ala Ala Tyr Arg Pro Ile
 355 360 365
 Val Asp Gly Glu Leu Asp Thr Gln Asn Phe Glu Lys Phe Pro Glu Val
 370 375 380
 Glu Gly Ser Pro Ser Glu Ala Pro Gln Val Gly Pro Trp Arg Lys Met
 385 390 395 400
 Leu Thr Ser Lys Asp Thr Asn Phe Ile Gly Phe Thr Phe Lys Lys Ser
 405 410 415
 Asp Ile Thr Arg Ser Met Glu Ser Ser Gly Ala Asp Met Lys Ser Asn
 420 425 430
 Gly Ser Gly Glu Ala Pro Ser Leu Ile Ser Leu Leu Gly Arg Ile Asn
 435 440 445
 Met Glu Glu Gly Glu Gly Gly Glu Leu Asn His Lys Thr
 450 455 460

(2) INFORMATION FOR SEQ ID NO:951:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 438 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..438

(D) OTHER INFORMATION: / Ceres Seq. ID 1499253

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:951:

Met Met Arg Asn Leu Ala Arg Arg Glu Thr Glu Tyr Met Arg Leu Gln
 1 5 10 15
 Arg Arg Lys Ile Gly Ile Asp Asp Phe Glu Leu Leu Thr Val Ile Gly
 20 25 30
 Lys Gly Ala Phe Gly Glu Val Arg Leu Cys Arg Leu Arg Ser Thr Ser
 35 40 45
 Glu Val Tyr Ala Met Lys Lys Leu Lys Lys Thr Glu Met Leu Ser Arg
 50 55 60
 Gly Gln Val Glu His Val Arg Ser Glu Arg Asn Leu Leu Ala Glu Val

65		70		75		80
Asp Ser Arg Tyr	Ile Val Lys Leu Phe Tyr Ser Phe Gln Asp Ser Glu					
	85			90		95
Cys Leu Tyr Leu	Ile Met Glu Tyr Leu Pro Gly Gly Asp Ile Met Thr					
	100			105		110
Leu Leu Met Arg	Glu Asp Ile Leu Ser Glu Asp Val Ala Arg Phe Tyr					
	115			120		125
Ile Ala Glu Ser	Ile Leu Ala Ile His Ser Ile His Gln His Asn Tyr					
	130			135		140
Val His Arg Asp	Ile Lys Pro Asp Asn Leu Ile Leu Asp Lys Ser Gly					
	145			150		155
His Leu Lys Leu	Ser Asp Phe Gly Leu Cys Lys Pro Leu Asp Asp Lys					
	165			170		175
Tyr Ser Ser Leu	Leu Leu Glu Asp Asp Glu Met Leu Ser Gln Asp Ser					
	180			185		190
Glu Asn Gln Ser	Gly Lys Ser Asp Ala Asp Lys Ala Pro Trp Gln Met					
	195			200		205
Pro Lys Glu Gln	Leu Leu Gln Trp Lys Arg Asn Arg Arg Ala Leu Ala					
	210			215		220
Tyr Ser Thr Val	Gly Thr Leu Asp Tyr Met Ala Pro Glu Val Leu Leu					
	225			230		235
Lys Lys Gly Tyr	Gly Met Glu Cys Asp Trp Trp Ser Leu Gly Ala Ile					
	245			250		255
Leu Tyr Glu Met	Leu Val Gly Tyr Pro Pro Phe Cys Ser Asp Asp Pro					
	260			265		270
Arg Ile Thr Cys	Arg Lys Ile Ile Asn Trp Arg Val Cys Leu Lys Phe					
	275			280		285
Pro Glu Gln Pro	Lys Ile Ser Asp Glu Ala Arg Asp Leu Ile Cys Arg					
	290			295		300
Leu Leu Cys Asp	Val Asp Ser Arg Leu Gly Thr Arg Gly Val Glu Glu					
	305			310		315
Ile Lys Ser His	Pro Trp Phe Lys Gly Thr Pro Trp Asp Lys Leu Tyr					
	325			330		335
Asp Met Glu Ala	Tyr Arg Pro Ile Val Asp Gly Glu Leu Asp Thr					
	340			345		350
Gln Asn Phe Glu	Lys Phe Pro Glu Val Glu Gly Ser Pro Ser Glu Ala					
	355			360		365
Pro Gln Val Gly	Pro Trp Arg Lys Met Leu Thr Ser Lys Asp Thr Asn					
	370			375		380
Phe Ile Gly Phe	Thr Phe Lys Lys Ser Asp Ile Thr Arg Ser Met Glu					
	385			390		395
Ser Ser Gly Ala	Asp Met Lys Ser Asn Gly Ser Gly Glu Ala Pro Ser					
	405			410		415
Leu Ile Ser Leu	Leu Gly Arg Ile Asn Met Glu Glu Gly Glu Gly Gly					
	420			425		430
Glu Leu Asn His	Lys Thr					
	435					

(2) INFORMATION FOR SEQ ID NO:952:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1760 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1760
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499254

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:952:

aagcttttga agctttctcaa caatggcggc tattccttcc cacaacaacc ttcttaccat	60
caaccacaaa aactccataa ccggttcttc ttcccttaac accaatttct cagaaatcaa	120

ttttcccgcc aaattccgag tagctacgag agctttgtcc agaaccgacg agtcgtcttt 180
atccgccgtg atttctcgcc tcgagcgaga aaggcgggaa agacaagggtt tattaatcga 240
ggaagcggaa ggagctggag aactatggat gacggcggaa gatattcgcc ggcgagataa 300
aaaaaccgaa gaagaaagaa gactaagaga cacgtggcgt aagatccaag gagaagacga 360
ttgggcccggg ttaatggatc caatggatcc aattcttaga tcggagctaa tccgttacgg 420
cgaaatggct caagcttggt acgacgcttt cgatttcgat cccgcttcca aatactgcgg 480
cacctccagg ttcacgcgac tcgagttctt cgattctctc ggaatgatcg attccgggta 540
cgaggtggcg cgttacctct acgcgacgtc gaacatcaat ctcccgaact tcttctcgaa 600
atcgcggtgg tctaaagtct ggagcaaaaa cgctaattgg atgggatacg tcgccgtttc 660
agacgacgaa acgtctcgta accgactcgg ccgccgtgat atcgcgattg cgtggagagg 720
aaccgttacg aaacttgaat ggatcgcgga tctaaaggat tattttaaaac cggtaaccga 780
aaacaagatc cgatgccccg acccgggccgt taaagtcgaa tccggattct tagatctcta 840
cactgacaaa gacacaacct gcaaattcgc gagattctca gcgcgtgaac agattttaac 900
ggaggtgaaa cggttagtgg aagaacacgg cgacgacgat gattccgatt taagcatcac 960
cgtgacggga cacagtctcg gcggcgcggtt agcgatatta agcgcgtagc atatagcgga 1020
gatgagattg aatcggagta agaaagggaa agtgattccg gtgacgggtg tgacatacgg 1080
aggaccgaga gttgggaacg ttaggttttag ggagaggatg gaggaattgg gagtgaaggt 1140
gatgagagta gtgaatgttc acgacgtggt tcccaagtcg ccgggattgt ttttgaacga 1200
gagtagacct cacgcgtga tgaagatagc ggagggggtg ccgtggtgtt atagccacgt 1260
gggggaggag ctggcggttg atcatcagaa ctgcgccgtt cttaaaccct ccgttgatgt 1320
ttctactgct cataactctg aagctatgct tcatttactg gacgggtatc atggaaaagg 1380
agagagattt gtgctgtcga gtgggagaga ccatgcgcta gtgaacaaag cgtcggactt 1440
tttgaaagag catttacaaa ttccaccgtt ttggcgctca gacgcgaata aaggaatggt 1500
tcggaacagt gaaggtcggt ggattcaagc cgagcgtctc cgttttgagg atcatcattc 1560
tcctgatatc caccaccatc tctctcagct ccgtcttgat catccttggt aatcacacgc 1620
acatatatat aatatacaca ttttccctaa tttgtaaagt acgcatccat cttttgaaaa 1680
taaaatgtca caatcatctc acttgcaggc tttggtcaac gtacgttccc tattaataaa 1740
acttattacg tttacgaggc

(2) INFORMATION FOR SEQ ID NO:953:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 529 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..529
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499255

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:953:

Met Ala Ala Ile Pro Ser His Asn Asn Leu Leu Thr Ile Asn His Lys
1 5 10 15
Asn Ser Ile Thr Gly Ser Ser Ser Leu Asn Thr Asn Phe Ser Glu Ile
20 25 30
Asn Phe Pro Ala Lys Phe Arg Val Ala Thr Arg Ala Leu Ser Arg Thr
35 40 45
Asp Glu Ser Ser Leu Ser Ala Val Ile Ser Arg Leu Glu Arg Glu Arg
50 55 60
Arg Glu Arg Gln Gly Leu Ile Glu Glu Ala Glu Gly Ala Gly Glu
65 70 75 80
Leu Trp Met Thr Ala Glu Asp Ile Arg Arg Asp Lys Lys Thr Glu
85 90 95
Glu Glu Arg Arg Leu Arg Asp Thr Trp Arg Lys Ile Gln Gly Glu Asp
100 105 110
Asp Trp Ala Gly Leu Met Asp Pro Met Asp Pro Ile Leu Arg Ser Glu
115 120 125
Leu Ile Arg Tyr Gly Glu Met Ala Gln Ala Cys Tyr Asp Ala Phe Asp
130 135 140
Phe Asp Pro Ala Ser Lys Tyr Cys Gly Thr Ser Arg Phe Thr Arg Leu
145 150 155 160
Glu Phe Phe Asp Ser Leu Gly Met Ile Asp Ser Gly Tyr Glu Val Ala

				165					170					175					
Arg	Tyr	Leu	Tyr	Ala	Thr	Ser	Asn	Ile	Asn	Leu	Pro	Asn	Phe	Phe	Ser				
			180					185					190						
Lys	Ser	Arg	Trp	Ser	Lys	Val	Trp	Ser	Lys	Asn	Ala	Asn	Trp	Met	Gly				
		195					200					205							
Tyr	Val	Ala	Val	Ser	Asp	Asp	Glu	Thr	Ser	Arg	Asn	Arg	Leu	Gly	Arg				
	210				215					220									
Arg	Asp	Ile	Ala	Ile	Ala	Trp	Arg	Gly	Thr	Val	Thr	Lys	Leu	Glu	Trp				
225				230					235					240					
Ile	Ala	Asp	Leu	Lys	Asp	Tyr	Leu	Lys	Pro	Val	Thr	Glu	Asn	Lys	Ile				
			245					250					255						
Arg	Cys	Pro	Asp	Pro	Ala	Val	Lys	Val	Glu	Ser	Gly	Phe	Leu	Asp	Leu				
		260						265					270						
Tyr	Thr	Asp	Lys	Asp	Thr	Thr	Cys	Lys	Phe	Ala	Arg	Phe	Ser	Ala	Arg				
	275					280			285										
Glu	Gln	Ile	Leu	Thr	Glu	Val	Lys	Arg	Leu	Val	Glu	Glu	His	Gly	Asp				
290				295					300										
Asp	Asp	Asp	Ser	Asp	Leu	Ser	Ile	Thr	Val	Thr	Gly	His	Ser	Leu	Gly				
305				310					315					320					
Gly	Ala	Leu	Ala	Ile	Leu	Ser	Ala	Tyr	Asp	Ile	Ala	Glu	Met	Arg	Leu				
			325					330					335						
Asn	Arg	Ser	Lys	Lys	Gly	Lys	Val	Ile	Pro	Val	Thr	Val	Leu	Thr	Tyr				
		340					345					350							
Gly	Gly	Pro	Arg	Val	Gly	Asn	Val	Arg	Phe	Arg	Glu	Arg	Met	Glu	Glu				
	355				360				365										
Leu	Gly	Val	Lys	Val	Met	Arg	Val	Val	Asn	Val	His	Asp	Val	Val	Pro				
370				375					380										
Lys	Ser	Pro	Gly	Leu	Phe	Leu	Asn	Glu	Ser	Arg	Pro	His	Ala	Leu	Met				
385			390					395					400						
Lys	Ile	Ala	Glu	Gly	Leu	Pro	Trp	Cys	Tyr	Ser	His	Val	Gly	Glu	Glu				
		405						410					415						
Leu	Ala	Leu	Asp	His	Gln	Asn	Ser	Pro	Phe	Leu	Lys	Pro	Ser	Val	Asp				
		420					425					430							
Val	Ser	Thr	Ala	His	Asn	Leu	Glu	Ala	Met	Leu	His	Leu	Leu	Asp	Gly				
	435					440					445								
Tyr	His	Gly	Lys	Gly	Glu	Arg	Phe	Val	Leu	Ser	Ser	Gly	Arg	Asp	His				
450				455				460											
Ala	Leu	Val	Asn	Lys	Ala	Ser	Asp	Phe	Leu	Lys	Glu	His	Leu	Gln	Ile				
465			470					475					480						
Pro	Pro	Phe	Trp	Arg	Gln	Asp	Ala	Asn	Lys	Gly	Met	Val	Arg	Asn	Ser				
			485					490					495						
Glu	Gly	Arg	Trp	Ile	Gln	Ala	Glu	Arg	Leu	Arg	Phe	Glu	Asp	His	His				
		500					505					510							
Ser	Pro	Asp	Ile	His	His	His	Leu	Ser	Gln	Leu	Arg	Leu	Asp	His	Pro				
	515					520					525								

(2) INFORMATION FOR SEQ ID NO:954:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 447 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..447

(D) OTHER INFORMATION: / Ceres Seq. ID 1499256

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:954:

Met	Thr	Ala	Glu	Asp	Ile	Arg	Arg	Arg	Asp	Lys	Lys	Thr	Glu	Glu	Glu
1			5					10					15		

```

Arg Arg Leu Arg Asp Thr Trp Arg Lys Ile Gln Gly Glu Asp Asp Trp
      20      25      30
Ala Gly Leu Met Asp Pro Met Asp Pro Ile Leu Arg Ser Glu Leu Ile
      35      40      45
Arg Tyr Gly Glu Met Ala Gln Ala Cys Tyr Asp Ala Phe Asp Phe Asp
      50      55      60
Pro Ala Ser Lys Tyr Cys Gly Thr Ser Arg Phe Thr Arg Leu Glu Phe
      65      70      75      80
Phe Asp Ser Leu Gly Met Ile Asp Ser Gly Tyr Glu Val Ala Arg Tyr
      85      90      95
Leu Tyr Ala Thr Ser Asn Ile Asn Leu Pro Asn Phe Phe Ser Lys Ser
      100      105      110
Arg Trp Ser Lys Val Trp Ser Lys Asn Ala Asn Trp Met Gly Tyr Val
      115      120      125
Ala Val Ser Asp Asp Glu Thr Ser Arg Asn Arg Leu Gly Arg Arg Asp
      130      135      140
Ile Ala Ile Ala Trp Arg Gly Thr Val Thr Lys Leu Glu Trp Ile Ala
      145      150      155      160
Asp Leu Lys Asp Tyr Leu Lys Pro Val Thr Glu Asn Lys Ile Arg Cys
      165      170      175
Pro Asp Pro Ala Val Lys Val Glu Ser Gly Phe Leu Asp Leu Tyr Thr
      180      185      190
Asp Lys Asp Thr Thr Cys Lys Phe Ala Arg Phe Ser Ala Arg Glu Gln
      195      200      205
Ile Leu Thr Glu Val Lys Arg Leu Val Glu Glu His Gly Asp Asp Asp
      210      215      220
Asp Ser Asp Leu Ser Ile Thr Val Thr Gly His Ser Leu Gly Gly Ala
      225      230      235      240
Leu Ala Ile Leu Ser Ala Tyr Asp Ile Ala Glu Met Arg Leu Asn Arg
      245      250      255
Ser Lys Lys Gly Lys Val Ile Pro Val Thr Val Leu Thr Tyr Gly Gly
      260      265      270
Pro Arg Val Gly Asn Val Arg Phe Arg Glu Arg Met Glu Glu Leu Gly
      275      280      285
Val Lys Val Met Arg Val Val Asn Val His Asp Val Val Pro Lys Ser
      290      295      300
Pro Gly Leu Phe Leu Asn Glu Ser Arg Pro His Ala Leu Met Lys Ile
      305      310      315      320
Ala Glu Gly Leu Pro Trp Cys Tyr Ser His Val Gly Glu Glu Leu Ala
      325      330      335
Leu Asp His Gln Asn Ser Pro Phe Leu Lys Pro Ser Val Asp Val Ser
      340      345      350
Thr Ala His Asn Leu Glu Ala Met Leu His Leu Leu Asp Gly Tyr His
      355      360      365
Gly Lys Gly Glu Arg Phe Val Leu Ser Ser Gly Arg Asp His Ala Leu
      370      375      380
Val Asn Lys Ala Ser Asp Phe Leu Lys Glu His Leu Gln Ile Pro Pro
      385      390      395      400
Phe Trp Arg Gln Asp Ala Asn Lys Gly Met Val Arg Asn Ser Glu Gly
      405      410      415
Arg Trp Ile Gln Ala Glu Arg Leu Arg Phe Glu Asp His His Ser Pro
      420      425      430
Asp Ile His His His Leu Ser Gln Leu Arg Leu Asp His Pro Cys
      435      440      445

```

(2) INFORMATION FOR SEQ ID NO:955:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 412 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

SEQUENCE: 3564320

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..412

(D) OTHER INFORMATION: / Ceres Seq. ID 1499257

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:955:

Met	Asp	Pro	Met	Asp	Pro	Ile	Leu	Arg	Ser	Glu	Leu	Ile	Arg	Tyr	Gly
1			5						10					15	
Glu	Met	Ala	Gln	Ala	Cys	Tyr	Asp	Ala	Phe	Asp	Phe	Asp	Pro	Ala	Ser
		20						25					30		
Lys	Tyr	Cys	Gly	Thr	Ser	Arg	Phe	Thr	Arg	Leu	Glu	Phe	Phe	Asp	Ser
		35					40					45			
Leu	Gly	Met	Ile	Asp	Ser	Gly	Tyr	Glu	Val	Ala	Arg	Tyr	Leu	Tyr	Ala
	50					55					60				
Thr	Ser	Asn	Ile	Asn	Leu	Pro	Asn	Phe	Phe	Ser	Lys	Ser	Arg	Trp	Ser
65					70					75				80	
Lys	Val	Trp	Ser	Lys	Asn	Ala	Asn	Trp	Met	Gly	Tyr	Val	Ala	Val	Ser
			85						90					95	
Asp	Asp	Glu	Thr	Ser	Arg	Asn	Arg	Leu	Gly	Arg	Arg	Asp	Ile	Ala	Ile
			100					105					110		
Ala	Trp	Arg	Gly	Thr	Val	Thr	Lys	Leu	Glu	Trp	Ile	Ala	Asp	Leu	Lys
		115					120					125			
Asp	Tyr	Leu	Lys	Pro	Val	Thr	Glu	Asn	Lys	Ile	Arg	Cys	Pro	Asp	Pro
		130				135					140				
Ala	Val	Lys	Val	Glu	Ser	Gly	Phe	Leu	Asp	Leu	Tyr	Thr	Asp	Lys	Asp
145					150					155				160	
Thr	Thr	Cys	Lys	Phe	Ala	Arg	Phe	Ser	Ala	Arg	Glu	Gln	Ile	Leu	Thr
			165						170					175	
Glu	Val	Lys	Arg	Leu	Val	Glu	Glu	His	Gly	Asp	Asp	Asp	Asp	Ser	Asp
			180					185					190		
Leu	Ser	Ile	Thr	Val	Thr	Gly	His	Ser	Leu	Gly	Gly	Ala	Leu	Ala	Ile
		195				200						205			
Leu	Ser	Ala	Tyr	Asp	Ile	Ala	Glu	Met	Arg	Leu	Asn	Arg	Ser	Lys	Lys
	210					215					220				
Gly	Lys	Val	Ile	Pro	Val	Thr	Val	Leu	Thr	Tyr	Gly	Gly	Pro	Arg	Val
225					230					235				240	
Gly	Asn	Val	Arg	Phe	Arg	Glu	Arg	Met	Glu	Glu	Leu	Gly	Val	Lys	Val
			245						250					255	
Met	Arg	Val	Val	Asn	Val	His	Asp	Val	Val	Pro	Lys	Ser	Pro	Gly	Leu
		260						265					270		
Phe	Leu	Asn	Glu	Ser	Arg	Pro	His	Ala	Leu	Met	Lys	Ile	Ala	Glu	Gly
		275					280						285		
Leu	Pro	Trp	Cys	Tyr	Ser	His	Val	Gly	Glu	Glu	Leu	Ala	Leu	Asp	His
	290					295					300				
Gln	Asn	Ser	Pro	Phe	Leu	Lys	Pro	Ser	Val	Asp	Val	Ser	Thr	Ala	His
305					310					315				320	
Asn	Leu	Glu	Ala	Met	Leu	His	Leu	Leu	Asp	Gly	Tyr	His	Gly	Lys	Gly
			325						330					335	
Glu	Arg	Phe	Val	Leu	Ser	Ser	Gly	Arg	Asp	His	Ala	Leu	Val	Asn	Lys
		340						345					350		
Ala	Ser	Asp	Phe	Leu	Lys	Glu	His	Leu	Gln	Ile	Pro	Pro	Phe	Trp	Arg
		355					360						365		
Gln	Asp	Ala	Asn	Lys	Gly	Met	Val	Arg	Asn	Ser	Glu	Gly	Arg	Trp	Ile
	370					375					380				
Gln	Ala	Glu	Arg	Leu	Arg	Phe	Glu	Asp	His	His	Ser	Pro	Asp	Ile	His
385					390					395				400	
His	His	Leu	Ser	Gln	Leu	Arg	Leu	Asp	His	Pro	Cys				
			405						410						

(2) INFORMATION FOR SEQ ID NO:956:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1361 base pairs

(B) TYPE: nucleic acid

- (C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
(A) NAME/KEY: -
(B) LOCATION: 1..1361
(D) OTHER INFORMATION: / Ceres Seq. ID 1499258

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:956:

```
ggattaggga gactcgcaact cttcttcttc ttctttgtac ccagaaagaa agtgagctcc      60
aacaatggct gottgcgcta ctcaactcctc tctcatgcta gcatacgccg ccgcatccac      120
tcgttcccag gaccttacct ctactccatc tcttttctct ttgtccagct ccagacccaa      180
ccacttgagc gtcccgttc ttctccttgg gggttccagg gaccggagat gtgctgctat      240
tgacagagct tccaaccaca agtttattgt ctccgccgtg gccgctgagg ctgacctcga      300
cacggaggag gacctggagc agaccgccac cgccgtcctt gatccgcca agcctaagaa      360
aggaaaagcc gctttgggtc tcaagagaga tagaacaagg tctaagaggt ttttggaat      420
ccaaaagcta agggaaacca aaaaggagta tgatgtcaac actgctatct ctttgcttaa      480
acaaactgcc aacacaaggt ttgttgagtc tgttgaagcc catttccgtc tcaacatcga      540
tcctaagtac aatgaccagc agctgcgtgc aacggtgagc ctgcctaagg gaactggcca      600
gactgttata gtcgctgttc ttgcacaagg tgagaagggt gatgaagcca aaagtgcagg      660
ggcagatatt gtgggcagtg atgatttaat cgaacagatt aaaggaggct tcatggagtt      720
tgacaagctg attgcatccc cggatatgat ggtcaagggt gctggcctgg gaaagattct      780
tgaccacgg gggtcatgc caaatcccaa ggctggtaca gtcacagcga acattcccca      840
ggctattgaa gagttcaaga aggggaaagt tgaattcaga gcagacaaaa ctgggattgt      900
tcacattcca tttgggaaag ttaattttac agaggaagac cttctcataa acttccttgc      960
agcagtgaat tcggtggaga caaacaagcc aaaggaggct aaaggagtgt actggaaaag      1020
cgctcacata tgctcgtcaa tggggccttc catcaagttg aacataagag agatgataga      1080
cttcaagcct cccactgcga actaatcgac aacgccattt gtaaattgggg tccttttggg      1140
agacgggcaa tgccagtgt gacagagaag agaaacacca agtctagtct gttagtaatc      1200
ttttcacgcc tcaactgctt gtatcacttt gatggccatt tacttcttgt cgttatttat      1260
ttactattgc ctattaaaat ttggcaaggg gctgtacatg tcaggacgca gaactcttta      1320
gtactctcta aaagaaaaga ccttacattg atctttaggc t
```

(2) INFORMATION FOR SEQ ID NO:957:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 346 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..346
(D) OTHER INFORMATION: / Ceres Seq. ID 1499259

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:957:

```
Met Ala Ala Cys Ala Thr His Ser Ser Leu Met Leu Ala Tyr Ala Ala
1      5      10      15
Ala Ser Thr Arg Ser Gln Asp Leu Thr Pro Thr Pro Ser Leu Phe Ser
20      25      30
Phe Ala Ser Ser Arg Pro Asn His Leu Ser Val Pro Leu Leu Leu
35      40      45
Gly Gly Ser Arg Asp Arg Arg Cys Ala Ala Ile Asp Arg Ala Ser Asn
50      55      60
His Lys Phe Ile Val Ser Ala Val Ala Ala Glu Ala Asp Leu Asp Thr
65      70      75      80
Glu Glu Asp Leu Glu Gln Thr Ala Thr Ala Val Leu Asp Pro Pro Lys
85      90      95
Pro Lys Lys Gly Lys Ala Ala Leu Val Leu Lys Arg Asp Arg Thr Arg
100      105      110
Ser Lys Arg Phe Leu Glu Ile Gln Lys Leu Arg Glu Thr Lys Lys Glu
115      120      125
Tyr Asp Val Asn Thr Ala Ile Ser Leu Leu Lys Gln Thr Ala Asn Thr
130      135      140
```

Arg Phe Val Glu Ser Val Glu Ala His Phe Arg Leu Asn Ile Asp Pro
145 150 155 160
Lys Tyr Asn Asp Gln Leu Arg Ala Thr Val Ser Leu Pro Lys Gly
165 170 175
Thr Gly Gln Thr Val Ile Val Ala Val Leu Ala Gln Gly Glu Lys Val
180 185 190
Asp Glu Ala Lys Ser Ala Gly Ala Asp Ile Val Gly Ser Asp Asp Leu
195 200 205
Ile Glu Gln Ile Lys Gly Gly Phe Met Glu Phe Asp Lys Leu Ile Ala
210 215 220
Ser Pro Asp Met Met Val Lys Val Ala Gly Leu Gly Lys Ile Leu Gly
225 230 235 240
Pro Arg Gly Leu Met Pro Asn Pro Lys Ala Gly Thr Val Thr Ala Asn
245 250 255
Ile Pro Gln Ala Ile Glu Glu Phe Lys Lys Gly Lys Val Glu Phe Arg
260 265 270
Ala Asp Lys Thr Gly Ile Val His Ile Pro Phe Gly Lys Val Asn Phe
275 280 285
Thr Glu Glu Asp Leu Leu Ile Asn Phe Leu Ala Ala Val Lys Ser Val
290 295 300
Glu Thr Asn Lys Pro Lys Gly Ala Lys Gly Val Tyr Trp Lys Ser Ala
305 310 315 320
His Ile Cys Ser Ser Met Gly Pro Ser Ile Lys Leu Asn Ile Arg Glu
325 330 335
Met Ile Asp Phe Lys Pro Pro Thr Ala Asn
340 345

(2) INFORMATION FOR SEQ ID NO:958:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 336 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..336

(D) OTHER INFORMATION: / Ceres Seq. ID 1499260

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:958:

Met Leu Ala Tyr Ala Ala Ala Ser Thr Arg Ser Gln Asp Leu Thr Pro
1 5 10 15
Thr Pro Ser Leu Phe Ser Phe Ala Ser Ser Arg Pro Asn His Leu Ser
20 25 30
Val Pro Leu Leu Leu Leu Gly Gly Ser Arg Asp Arg Arg Cys Ala Ala
35 40 45
Ile Asp Arg Ala Ser Asn His Lys Phe Ile Val Ser Ala Val Ala Ala
50 55 60
Glu Ala Asp Leu Asp Thr Glu Glu Asp Leu Glu Gln Thr Ala Thr Ala
65 70 75 80
Val Leu Asp Pro Pro Lys Pro Lys Lys Gly Lys Ala Ala Leu Val Leu
85 90 95
Lys Arg Asp Arg Thr Arg Ser Lys Arg Phe Leu Glu Ile Gln Lys Leu
100 105 110
Arg Glu Thr Lys Lys Glu Tyr Asp Val Asn Thr Ala Ile Ser Leu Leu
115 120 125
Lys Gln Thr Ala Asn Thr Arg Phe Val Glu Ser Val Glu Ala His Phe
130 135 140
Arg Leu Asn Ile Asp Pro Lys Tyr Asn Asp Gln Gln Leu Arg Ala Thr
145 150 155 160
Val Ser Leu Pro Lys Gly Thr Gly Gln Thr Val Ile Val Ala Val Leu
165 170 175
Ala Gln Gly Glu Lys Val Asp Glu Ala Lys Ser Ala Gly Ala Asp Ile

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	180		185		190
Val Gly Ser Asp Asp Leu Ile Glu Gln Ile Lys Gly Gly Phe Met Glu					
	195		200		205
Phe Asp Lys Leu Ile Ala Ser Pro Asp Met Met Val Lys Val Ala Gly					
	210		215		220
Leu Gly Lys Ile Leu Gly Pro Arg Gly Leu Met Pro Asn Pro Lys Ala					
	225		230		235
Gly Thr Val Thr Ala Asn Ile Pro Gln Ala Ile Glu Glu Phe Lys Lys					
	245		250		255
Gly Lys Val Glu Phe Arg Ala Asp Lys Thr Gly Ile Val His Ile Pro					
	260		265		270
Phe Gly Lys Val Asn Phe Thr Glu Asp Leu Leu Ile Asn Phe Leu					
	275		280		285
Ala Ala Val Lys Ser Val Glu Thr Asn Lys Pro Lys Gly Ala Lys Gly					
	290		295		300
Val Tyr Trp Lys Ser Ala His Ile Cys Ser Ser Met Gly Pro Ser Ile					
	305		310		315
Lys Leu Asn Ile Arg Glu Met Ile Asp Phe Lys Pro Pro Thr Ala Asn					
	325		330		335

(2) INFORMATION FOR SEQ ID NO:959:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1307 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1307
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499261

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:959:

aatttcaccg	ctctttctct	ttcgcttctc	tgagaagttt	caaagcta	tcagctttcg	60
agaaattgca	acaatggaga	aactcgcggc	gtctactgtt	acagatctag	cttgcgtaac	120
ggcgataaac	tcaccaccgc	ctccactatc	accgatctct	gaacaaagct	tcagcaacaa	180
acaccaagaa	gagttcgcag	caagcttcgc	atcactctac	aactcaattt	tctcaccgga	240
atctcaattc	tctcctttct	ctccgtcctc	ttcctcacca	ccatctcgcg	tcgatacaac	300
tacagagcat	cgtcttcttc	aagcgaaact	tatcctcgag	tacgatgaac	tcaacgatca	360
ttacgagctt	tgctttaacc	gtcttcaatc	tctaattgacg	gaacttgact	ctcttcgtca	420
cgaaaacgat	tctctccgct	ttgaaaactc	agatctactc	aaacttattc	atatctctac	480
ttcatcctcc	tctctcgtct	ctcctccggc	gccgatccat	aaccgtcaat	tccgtcacca	540
gatctccgat	tctcgtctcc	cgaagagaaa	caatcaagag	agaaaactcg	tgctaagag	600
catctccgtc	agatctcaag	gatattctcaa	gatcaaccat	ggatttgaag	cttcagatcg	660
ccaaacgagt	caactcagct	ctaactcggg	gttgctcttc	caaaagggtg	gtgtagtaca	720
aaccaaaggg	gagagagaag	cattagagct	tgaggatat	cgtcaaggga	tgatgaagac	780
ggagctttgt	aacaaatggc	aagagactgg	agcttggtgt	tacggcgata	attgccatt	840
cgctcacgga	atcgacgagc	tacgtcctgt	gattagggat	ccacgctaca	aaactgaggt	900
ttgcagaatg	attgtcaccg	gagctatgtg	tccttacggg	caccgttgcc	atttccgtca	960
ctcacttact	gatcaagaga	ggatgatgat	gatgatgctt	actcgtgat	ctggagaaga	1020
agaagaaagg	tcattgaaaa	agagaaataa	ttagtgggtg	tgtacagatt	tcagatttga	1080
taccttataa	atatcgtaac	ttttctgggt	atttgctata	ggaataagga	agagaaagtg	1140
tttaataaat	gtttgatagg	attataggaa	tataattagg	gttgaagaaa	tgtgtggttc	1200
tcggataaag	ctggagagac	ctgaaagagg	atttagattt	aacaaagata	tggaatttgt	1260
attgataaaa	gtttttgact	ttgtgcaaaa	ctatgcaact	ttcttcc		

(2) INFORMATION FOR SEQ ID NO:960:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 311 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..311

(D) OTHER INFORMATION: / Ceres Seq. ID 1499262

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:960:

Met	Glu	Lys	Leu	Ala	Ala	Ser	Thr	Val	Thr	Asp	Leu	Ala	Cys	Val	Thr
1				5					10					15	
Ala	Ile	Asn	Ser	Pro	Pro	Pro	Pro	Leu	Ser	Pro	Ile	Ser	Glu	Gln	Ser
			20					25					30		
Phe	Ser	Asn	Lys	His	Gln	Glu	Glu	Phe	Ala	Ala	Ser	Phe	Ala	Ser	Leu
		35				40						45			
Tyr	Asn	Ser	Ile	Phe	Ser	Pro	Glu	Ser	Gln	Phe	Ser	Pro	Ser	Pro	Pro
	50					55					60				
Ser	Ser	Ser	Ser	Pro	Pro	Ser	Arg	Val	Asp	Thr	Thr	Thr	Glu	His	Arg
65				70					75					80	
Leu	Leu	Gln	Ala	Lys	Leu	Ile	Leu	Glu	Tyr	Asp	Glu	Leu	Asn	Asp	His
			85					90					95		
Tyr	Glu	Leu	Cys	Leu	Asn	Arg	Leu	Gln	Ser	Leu	Met	Thr	Glu	Leu	Asp
		100						105					110		
Ser	Leu	Arg	His	Glu	Asn	Asp	Ser	Leu	Arg	Phe	Glu	Asn	Ser	Asp	Leu
		115					120					125			
Leu	Lys	Leu	Ile	His	Ile	Ser	Thr	Ser	Ser	Ser	Ser	Ser	Val	Ser	Pro
	130					135					140				
Pro	Ala	Pro	Ile	His	Asn	Arg	Gln	Phe	Arg	His	Gln	Ile	Ser	Asp	Ser
145				150					155					160	
Arg	Ser	Ala	Lys	Arg	Asn	Asn	Gln	Glu	Arg	Asn	Ser	Leu	Pro	Lys	Ser
			165					170					175		
Ile	Ser	Val	Arg	Ser	Gln	Gly	Tyr	Leu	Lys	Ile	Asn	His	Gly	Phe	Glu
		180					185					190			
Ala	Ser	Asp	Arg	Gln	Thr	Ser	Gln	Leu	Ser	Ser	Asn	Ser	Val	Leu	Ser
	195					200					205				
Ser	Gln	Lys	Val	Cys	Val	Val	Gln	Thr	Lys	Gly	Glu	Arg	Glu	Ala	Leu
	210					215					220				
Glu	Leu	Glu	Val	Tyr	Arg	Gln	Gly	Met	Met	Lys	Thr	Glu	Leu	Cys	Asn
225				230						235				240	
Lys	Trp	Gln	Glu	Thr	Gly	Ala	Cys	Cys	Tyr	Gly	Asp	Asn	Cys	Gln	Phe
			245					250					255		
Ala	His	Gly	Ile	Asp	Glu	Leu	Arg	Pro	Val	Ile	Arg	His	Pro	Arg	Tyr
		260					265					270			
Lys	Thr	Glu	Val	Cys	Arg	Met	Ile	Val	Thr	Gly	Ala	Met	Cys	Pro	Tyr
	275					280						285			
Gly	His	Arg	Cys	His	Phe	Arg	His	Ser	Leu	Thr	Asp	Gln	Glu	Arg	Met
	290					295					300				
Met	Met	Met	Met	Leu	Thr	Arg									
305				310											

(2) INFORMATION FOR SEQ ID NO:961:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 204 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..204

(D) OTHER INFORMATION: / Ceres Seq. ID 1499263

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:961:

Met	Thr	Glu	Leu	Asp	Ser	Leu	Arg	His	Glu	Asn	Asp	Ser	Leu	Arg	Phe
1			5						10					15	
Glu	Asn	Ser	Asp	Leu	Leu	Lys	Leu	Ile	His	Ile	Ser	Thr	Ser	Ser	Ser

	20		25		30										
Ser	Ser	Val	Ser	Pro	Pro	Ala	Pro	Ile	His	Asn	Arg	Gln	Phe	Arg	His
	35						40					45			
Gln	Ile	Ser	Asp	Ser	Arg	Ser	Ala	Lys	Arg	Asn	Asn	Gln	Glu	Arg	Asn
	50					55					60				
Ser	Leu	Pro	Lys	Ser	Ile	Ser	Val	Arg	Ser	Gln	Gly	Tyr	Leu	Lys	Ile
65					70					75				80	
Asn	His	Gly	Phe	Glu	Ala	Ser	Asp	Arg	Gln	Thr	Ser	Gln	Leu	Ser	Ser
				85					90					95	
Asn	Ser	Val	Leu	Ser	Ser	Gln	Lys	Val	Cys	Val	Val	Gln	Thr	Lys	Gly
		100						105					110		
Glu	Arg	Glu	Ala	Leu	Glu	Leu	Glu	Val	Tyr	Arg	Gln	Gly	Met	Met	Lys
	115						120					125			
Thr	Glu	Leu	Cys	Asn	Lys	Trp	Gln	Glu	Thr	Gly	Ala	Cys	Cys	Tyr	Gly
	130					135					140				
Asp	Asn	Cys	Gln	Phe	Ala	His	Gly	Ile	Asp	Glu	Leu	Arg	Pro	Val	Ile
145					150				155					160	
Arg	His	Pro	Arg	Tyr	Lys	Thr	Glu	Val	Cys	Arg	Met	Ile	Val	Thr	Gly
			165					170						175	
Ala	Met	Cys	Pro	Tyr	Gly	His	Arg	Cys	His	Phe	Arg	His	Ser	Leu	Thr
		180					185						190		
Asp	Gln	Glu	Arg	Met	Met	Met	Met	Met	Leu	Thr	Arg				
	195						200								

(2) INFORMATION FOR SEQ ID NO:962:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1372 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1372
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499264

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:962:

aaaaatagct	ttcttctttt	ggcccttac	ccagagatag	attcttatat	actactgaga	60
atcttcaatt	tctgcaactt	ttgtatctct	tcctgatgga	gtcttcgagt	ccccaccata	120
gtcacattgt	tgagggtta	gttggaat	ctgatgaaga	gagaataatt	gtggcgagta	180
aagtctgtgg	agaagcacca	tgtgggtttt	cagattctaa	gaatgcttcc	ggggatgctc	240
acgaacgctc	tgcttctatg	cggaagcttt	gtatcgccgt	cgtgctgtgt	ctagtgttca	300
tgagtgttga	agttgttggg	gggattaaag	ccaatagttt	agctatatta	accgatgcag	360
ctcatttgct	ctctgacgtt	gctgcctttg	ctatctccct	cttctcattg	tgggctgctg	420
gctgggaagc	gactcctagg	cagacttacg	ggttcttcag	gattgagatt	ttgggtgctc	480
ttgtatctat	ccagctcatt	tgggtgctca	cgggtattct	ggtttatgaa	gcgattatca	540
gaattgttac	agagaccagt	gagggtta	gattcctcat	gtttctgggt	gctgcctttg	600
gtctagtggg	gaacatcata	atggctgttc	tgctagggca	tgatcatggg	cacagtcattg	660
gacatgggca	tggccacggc	catgaccatc	acaatcatag	ccatgggggtg	actgttacca	720
ctcatcacca	tcatacagat	catgaacatg	gccatagtca	tggatcatgga	gaggacaagc	780
atcatgctca	tggggatggt	actgagcaat	tgttggaaca	atcgaagact	caagtcgcag	840
caaaagagaa	aagaaagaga	aacatcaatc	tccaaggagc	ttatctgcat	gtccttgggg	900
attccatcca	gagtgttggg	gttatgattg	gaggagctat	catttggtac	aatccggaat	960
ggaagatagt	ggatctgac	tgcacacttg	ccttttcggg	tattgtccta	ggaacaacca	1020
tcaacatgat	tcgcaacatt	ctagaagtat	tgatggagag	tacaccacga	gagattgacg	1080
ccacaaagct	cgaaaagggt	ttgctcgaaa	tggagaaggt	gggtggctgtt	catgagctcc	1140
acatatgggc	tatcacagt	ggaaaagtgc	tattggcttg	ccatgtcaat	atcagaccag	1200
aagcagatgc	agatatggg	ctcaacaagg	taattgatta	catccgcagg	gagtacaaca	1260
ttagtcatgc	cacgatacaa	atcgagcgct	aaaagctaa	taagatctga	tgaaggggtt	1320
ttgtatcagc	attctcatta	acaataaaat	caataaagtt	tctacatttt	tc	

(2) INFORMATION FOR SEQ ID NO:963:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 398 amino acids

(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..398
(D) OTHER INFORMATION: / Ceres Seq. ID 1499265
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:963:

Met	Glu	Ser	Ser	Ser	Pro	His	His	Ser	His	Ile	Val	Glu	Val	Asn	Val
1				5				10						15	
Gly	Lys	Ser	Asp	Glu	Glu	Arg	Ile	Ile	Val	Ala	Ser	Lys	Val	Cys	Gly
			20				25						30		
Glu	Ala	Pro	Cys	Gly	Phe	Ser	Asp	Ser	Lys	Asn	Ala	Ser	Gly	Asp	Ala
		35				40					45				
His	Glu	Arg	Ser	Ala	Ser	Met	Arg	Lys	Leu	Cys	Ile	Ala	Val	Val	Leu
	50					55				60					
Cys	Leu	Val	Phe	Met	Ser	Val	Glu	Val	Val	Gly	Gly	Ile	Lys	Ala	Asn
65				70					75					80	
Ser	Leu	Ala	Ile	Leu	Thr	Asp	Ala	Ala	His	Leu	Leu	Ser	Asp	Val	Ala
			85					90						95	
Ala	Phe	Ala	Ile	Ser	Leu	Phe	Ser	Leu	Trp	Ala	Ala	Gly	Trp	Glu	Ala
			100					105					110		
Thr	Pro	Arg	Gln	Thr	Tyr	Gly	Phe	Phe	Arg	Ile	Glu	Ile	Leu	Gly	Ala
			115				120						125		
Leu	Val	Ser	Ile	Gln	Leu	Ile	Trp	Leu	Leu	Thr	Gly	Ile	Leu	Val	Tyr
	130					135					140				
Glu	Ala	Ile	Ile	Arg	Ile	Val	Thr	Glu	Thr	Ser	Glu	Val	Asn	Gly	Phe
145					150					155					160
Leu	Met	Phe	Leu	Val	Ala	Ala	Phe	Gly	Leu	Val	Val	Asn	Ile	Ile	Met
			165					170						175	
Ala	Val	Leu	Leu	Gly	His	Asp	His	Gly	His	Ser	His	Gly	His	Gly	His
			180					185					190		
Gly	His	Gly	His	Asp	His	His	Asn	His	Ser	His	Gly	Val	Thr	Val	Thr
	195						200					205			
Thr	His	His	His	His	His	Asp	His	Glu	His	Gly	His	Ser	His	Gly	His
	210					215					220				
Gly	Glu	Asp	Lys	His	His	Ala	His	Gly	Asp	Val	Thr	Glu	Gln	Leu	Leu
225					230				235					240	
Asp	Lys	Ser	Lys	Thr	Gln	Val	Ala	Ala	Lys	Glu	Lys	Arg	Lys	Arg	Asn
			245					250						255	
Ile	Asn	Leu	Gln	Gly	Ala	Tyr	Leu	His	Val	Leu	Gly	Asp	Ser	Ile	Gln
		260					265						270		
Ser	Val	Gly	Val	Met	Ile	Gly	Gly	Ala	Ile	Ile	Trp	Tyr	Asn	Pro	Glu
	275					280						285			
Trp	Lys	Ile	Val	Asp	Leu	Ile	Cys	Thr	Leu	Ala	Phe	Ser	Val	Ile	Val
	290					295				300					
Leu	Gly	Thr	Thr	Ile	Asn	Met	Ile	Arg	Asn	Ile	Leu	Glu	Val	Leu	Met
305					310				315					320	
Glu	Ser	Thr	Pro	Arg	Glu	Ile	Asp	Ala	Thr	Lys	Leu	Glu	Lys	Gly	Leu
			325					330						335	
Leu	Glu	Met	Glu	Glu	Val	Val	Ala	Val	His	Glu	Leu	His	Ile	Trp	Ala
		340					345						350		
Ile	Thr	Val	Gly	Lys	Val	Leu	Leu	Ala	Cys	His	Val	Asn	Ile	Arg	Pro
	355					360						365			
Glu	Ala	Asp	Ala	Asp	Met	Val	Leu	Asn	Lys	Val	Ile	Asp	Tyr	Ile	Arg
	370					375					380				
Arg	Glu	Tyr	Asn	Ile	Ser	His	Val	Thr	Ile	Gln	Ile	Glu	Arg		
385				390						395					

(2) INFORMATION FOR SEQ ID NO:964:
(i) SEQUENCE CHARACTERISTICS:

2025 RELEASE UNDER E.O. 14176

- (A) LENGTH: 344 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..344
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1499266
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:964:

Met Arg Lys Leu Cys Ile Ala Val Val Leu Cys Leu Val Phe Met Ser
1 5 10 15
Val Glu Val Val Gly Gly Ile Lys Ala Asn Ser Leu Ala Ile Leu Thr
20 25 30
Asp Ala Ala His Leu Leu Ser Asp Val Ala Ala Phe Ala Ile Ser Leu
35 40 45
Phe Ser Leu Trp Ala Ala Gly Trp Glu Ala Thr Pro Arg Gln Thr Tyr
50 55 60
Gly Phe Phe Arg Ile Glu Ile Leu Gly Ala Leu Val Ser Ile Gln Leu
65 70 75 80
Ile Trp Leu Leu Thr Gly Ile Leu Val Tyr Glu Ala Ile Ile Arg Ile
85 90 95
Val Thr Glu Thr Ser Glu Val Asn Gly Phe Leu Met Phe Leu Val Ala
100 105 110
Ala Phe Gly Leu Val Val Asn Ile Ile Met Ala Val Leu Leu Gly His
115 120 125
Asp His Gly His Ser His Gly His Gly His Gly His Gly His Asp His
130 135 140
His Asn His Ser His Gly Val Thr Val Thr Thr His His His His His
145 150 155 160
Asp His Glu His Gly His Ser His Gly His Gly Glu Asp Lys His His
165 170 175
Ala His Gly Asp Val Thr Glu Gln Leu Leu Asp Lys Ser Lys Thr Gln
180 185 190
Val Ala Ala Lys Glu Lys Arg Lys Arg Asn Ile Asn Leu Gln Gly Ala
195 200 205
Tyr Leu His Val Leu Gly Asp Ser Ile Gln Ser Val Gly Val Met Ile
210 215 220
Gly Gly Ala Ile Ile Trp Tyr Asn Pro Glu Trp Lys Ile Val Asp Leu
225 230 235 240
Ile Cys Thr Leu Ala Phe Ser Val Ile Val Leu Gly Thr Thr Ile Asn
245 250 255
Met Ile Arg Asn Ile Leu Glu Val Leu Met Glu Ser Thr Pro Arg Glu
260 265 270
Ile Asp Ala Thr Lys Leu Glu Lys Gly Leu Leu Glu Met Glu Glu Val
275 280 285
Val Ala Val His Glu Leu His Ile Trp Ala Ile Thr Val Gly Lys Val
290 295 300
Leu Leu Ala Cys His Val Asn Ile Arg Pro Glu Ala Asp Ala Asp Met
305 310 315 320
Val Leu Asn Lys Val Ile Asp Tyr Ile Arg Arg Glu Tyr Asn Ile Ser
325 330 335
His Val Thr Ile Gln Ile Glu Arg
340

(2) INFORMATION FOR SEQ ID NO:965:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 330 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..330

(D) OTHER INFORMATION: / Ceres Seq. ID 1499267

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:965:

Met	Ser	Val	Glu	Val	Val	Gly	Gly	Ile	Lys	Ala	Asn	Ser	Leu	Ala	Ile
1			5					10					15		
Leu	Thr	Asp	Ala	Ala	His	Leu	Leu	Ser	Asp	Val	Ala	Ala	Phe	Ala	Ile
			20					25					30		
Ser	Leu	Phe	Ser	Leu	Trp	Ala	Ala	Gly	Trp	Glu	Ala	Thr	Pro	Arg	Gln
			35				40					45			
Thr	Tyr	Gly	Phe	Phe	Arg	Ile	Glu	Ile	Leu	Gly	Ala	Leu	Val	Ser	Ile
			50			55					60				
Gln	Leu	Ile	Trp	Leu	Leu	Thr	Gly	Ile	Leu	Val	Tyr	Glu	Ala	Ile	Ile
65					70					75				80	
Arg	Ile	Val	Thr	Glu	Thr	Ser	Glu	Val	Asn	Gly	Phe	Leu	Met	Phe	Leu
				85					90					95	
Val	Ala	Ala	Phe	Gly	Leu	Val	Val	Asn	Ile	Ile	Met	Ala	Val	Leu	Leu
			100					105					110		
Gly	His	Asp	His	Gly	His	Ser	His	Gly	His	Gly	His	Gly	His	Gly	His
			115				120					125			
Asp	His	His	Asn	His	Ser	His	Gly	Val	Thr	Val	Thr	Thr	His	His	His
						135					140				
His	His	Asp	His	Glu	His	Gly	His	Ser	His	Gly	His	Gly	Glu	Asp	Lys
145					150					155				160	
His	His	Ala	His	Gly	Asp	Val	Thr	Glu	Gln	Leu	Leu	Asp	Lys	Ser	Lys
				165					170					175	
Thr	Gln	Val	Ala	Lys	Glu	Lys	Arg	Lys	Arg	Asn	Ile	Asn	Leu	Gln	
			180				185					190			
Gly	Ala	Tyr	Leu	His	Val	Leu	Gly	Asp	Ser	Ile	Gln	Ser	Val	Gly	Val
			195				200					205			
Met	Ile	Gly	Gly	Ala	Ile	Ile	Trp	Tyr	Asn	Pro	Glu	Trp	Lys	Ile	Val
					215						220				
Asp	Leu	Ile	Cys	Thr	Leu	Ala	Phe	Ser	Val	Ile	Val	Leu	Gly	Thr	Thr
225					230					235				240	
Ile	Asn	Met	Ile	Arg	Asn	Ile	Leu	Glu	Val	Leu	Met	Glu	Ser	Thr	Pro
				245					250					255	
Arg	Glu	Ile	Asp	Ala	Thr	Lys	Leu	Glu	Lys	Gly	Leu	Leu	Glu	Met	Glu
			260					265					270		
Glu	Val	Val	Ala	Val	His	Glu	Leu	His	Ile	Trp	Ala	Ile	Thr	Val	Gly
			275				280					285			
Lys	Val	Leu	Leu	Ala	Cys	His	Val	Asn	Ile	Arg	Pro	Glu	Ala	Asp	Ala
			290			295					300				
Asp	Met	Val	Leu	Asn	Lys	Val	Ile	Asp	Tyr	Ile	Arg	Arg	Glu	Tyr	Asn
305					310					315					320
Ile	Ser	His	Val	Thr	Ile	Gln	Ile	Glu	Arg						
					325				330						

(2) INFORMATION FOR SEQ ID NO:966:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 945 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..945

(D) OTHER INFORMATION: / Ceres Seq. ID 1499310

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:966:

accaaacc	caac	gcctc	aactaat	cggtc	agatc	aggtc	atcg	ggga	aggcc	gccat	60	
ggacgac	gag	gagc	acgag	tttac	ggcca	ggagat	ccct	gaggac	ggcg	atatgg	acg	120

```
cgctgacggtt gatatggccg ccgcccggga cgacgcggcg aacttcagga gcttgacgag      180
atgaagcgca astganagga gatggaggag gaggccgcgc cctccgcga tatgcaggcc      240
aaggctcgcca aggagatgca aggaggtgac cctagtatat ctacagctga rgcgaaggag      300
cagggtggatg cccggtctgt gtatgttgga aatgttgatt atgcttgac cccagaagaa      360
gtgcagcagc atttccaagc ttgtggaact gtcaacaggg tgacaatctt gactgacaag      420
tttgggcagc caaaaagggtt tgcttatgtt gaatttctgg aacaagaagc tgtccaggaa      480
gctctgaact tgaatgaatc ggaattgcat ggtcgacaga ttaaggttgc gccgaagagg      540
actaatgtcc ctgggatgaa gcagcgtcca ccacgcgggt ataatcccta ccatggctac      600
ccttatagat catatggagc accgtacttc cccccatacg gttatgggag ggctcctaga      660
ttccgcgcgc ctatgcgcta cagaccttac ttctgaagta cgtgcggggg aataatgttc      720
aatgcaaaac cagccatggt tagtggtcag tctcgggaat aattaaacct actgctgtat      780
cgtttgcgct gttcaatagt tgacatcggt gcggttcaat gctcctttac cagctgcctt      840
ttctgacctc tgttctcgca taagcgacat gtagacacag gacgtagggt tacaattgtt      900
tgcattttct gtcattcttg attctgatga ccctatacag cactc
```

(2) INFORMATION FOR SEQ ID NO:967:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 164 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..164

(D) OTHER INFORMATION: / Ceres Seq. ID 1499311

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:967:

```
Met Glu Glu Glu Ala Ala Leu Arg Asp Met Gln Ala Lys Val Ala
 1             5             10             15
Lys Glu Met Gln Gly Gly Asp Pro Ser Ile Ser Thr Ala Xaa Ala Lys
 20             25             30
Glu Gln Val Asp Ala Arg Ser Val Tyr Val Gly Asn Val Asp Tyr Ala
 35             40             45
Cys Thr Pro Glu Glu Val Gln Gln His Phe Gln Ala Cys Gly Thr Val
 50             55             60
Asn Arg Val Thr Ile Leu Thr Asp Lys Phe Gly Gln Pro Lys Gly Phe
 65             70             75             80
Ala Tyr Val Glu Phe Leu Glu Gln Glu Ala Val Gln Glu Ala Leu Asn
 85             90             95
Leu Asn Glu Ser Glu Leu His Gly Arg Gln Ile Lys Val Ala Pro Lys
100            105            110
Arg Thr Asn Val Pro Gly Met Lys Gln Arg Pro Pro Arg Gly Tyr Asn
115            120            125
Pro Tyr His Gly Tyr Pro Tyr Arg Ser Tyr Gly Ala Pro Tyr Phe Pro
130            135            140
Pro Tyr Gly Tyr Gly Arg Ala Pro Arg Phe Arg Arg Pro Met Arg Tyr
145            150            155            160
Arg Pro Tyr Phe
```

(2) INFORMATION FOR SEQ ID NO:968:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 154 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..154

(D) OTHER INFORMATION: / Ceres Seq. ID 1499312

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:968:

```
Met Gln Ala Lys Val Ala Lys Glu Met Gln Gly Gly Asp Pro Ser Ile
```

1	5	10	15
Ser Thr Ala Xaa	Ala Lys Glu Gln Val	Asp Ala Arg Ser Val	Tyr Val
20	25	30	
Gly Asn Val Asp	Tyr Ala Cys Thr Pro	Glu Glu Val Gln	Gln His Phe
35	40	45	
Gln Ala Cys Gly	Thr Val Asn Arg Val	Thr Ile Leu Thr	Asp Lys Phe
50	55	60	
Gly Gln Pro Lys	Gly Phe Ala Tyr Val	Glu Phe Leu Glu	Gln Glu Ala
65	70	75	80
Val Gln Glu Ala	Leu Asn Leu Asn Glu	Ser Glu Leu His	Gly Arg Gln
85	90	95	
Ile Lys Val Ala	Pro Lys Arg Thr Asn	Val Pro Gly Met	Lys Gln Arg
100	105	110	
Pro Pro Arg Gly	Tyr Asn Pro Tyr His	Gly Tyr Pro Tyr	Arg Ser Tyr
115	120	125	
Gly Ala Pro Tyr	Phe Pro Pro Tyr Gly	Tyr Gly Arg Ala	Pro Arg Phe
130	135	140	
Arg Arg Pro Met	Arg Tyr Arg Pro	Tyr Phe	
145	150		

(2) INFORMATION FOR SEQ ID NO:969:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 146 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..146

(D) OTHER INFORMATION: / Ceres Seq. ID 1499313

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:969:

Met Gln Gly Gly	Asp Pro Ser Ile Ser	Thr Ala Xaa Ala	Lys Glu Gln
1	5	10	15
Val Asp Ala Arg	Ser Val Tyr Val Gly	Asn Val Asp Tyr	Ala Cys Thr
20	25	30	
Pro Glu Glu Val	Gln Gln His Phe	Gln Ala Cys Gly	Thr Val Asn Arg
35	40	45	
Val Thr Ile Leu	Thr Asp Lys Phe	Gly Gln Pro Lys	Gly Phe Ala Tyr
50	55	60	
Val Glu Phe Leu	Glu Gln Glu Ala	Val Gln Glu Ala	Leu Asn Leu Asn
65	70	75	80
Glu Ser Glu Leu	His Gly Arg Gln	Ile Lys Val Ala	Pro Lys Arg Thr
85	90	95	
Asn Val Pro Gly	Met Lys Gln Arg	Pro Pro Arg Gly	Tyr Asn Pro Tyr
100	105	110	
His Gly Tyr Pro	Tyr Arg Ser Tyr	Gly Ala Pro Tyr	Phe Pro Pro Tyr
115	120	125	
Gly Tyr Gly Arg	Ala Pro Arg Phe	Arg Arg Pro Met	Arg Tyr Arg Pro
130	135	140	
Tyr Phe			
145			

(2) INFORMATION FOR SEQ ID NO:970:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 917 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..917

(D) OTHER INFORMATION: / Ceres Seq. ID 1499314

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:970:

atgggggttrg cctagttgtg cccgttgagc actagcagcc tccttgaaac ctccagatct	60
gtgcctccaa ggcccccggt cctcggcaac aagtcaccatc tgamggacct tgttccctgt	120
rcccgscac gtggcctcct ctgcagccgt ccagatggac accgcccgcg ccttgcaact	180
gaaagcctgc gccggcgacg ccgcgagaaa gctgctgctc gccgtcgcag ccgaggggtcc	240
tatctgtrgt gtgccagact tcaagatgag gggaaagaag agtgatgarc tcgaacctgt	300
cgatrtctggc gatgaagatg atgatggtgg tgacgatggg gacgaggatg gtgacttttg	360
ggaggagggt gaagaggacg tctcagaagg ggagggatat gacaacccaa agggcaatga	420
gaccaagawg camagagggtg atcctgagga aaatggtgag gaagatgagg aagaaccaga	480
agatcaggag ggtggcgcg acgacgatga tgacgacgat gacgatgatg agaacgggga	540
tgacgaggac gacgacaatg gggatgacga tgaggagggt gtagatgaag aagacgatga	600
ccaggacgag gatgaggag aagatgatga tgaagactcg ctccagcccc caaagaagag	660
gaagaagtga agatcttctg ccgctttagt taccgtgcgc tgagttctgc ctggcttttc	720
gtcatatcct cgcatttcaa ctttcccata gagagttaag aaggatccac acgttcagca	780
gcacgtgtgg gctttagtag gctttatgat ttgaggcaat tagggacaac tcttatgtca	840
ttgttgcttg cttctgtgga gtcgaacaga tgtttcgcta acataattcg acttgagtga	900
tgaaagcctc cagattg	

(2) INFORMATION FOR SEQ ID NO:971:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 171 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..171

(D) OTHER INFORMATION: / Ceres Seq. ID 1499315

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:971:

Met	Asp	Thr	Ala	Ala	Pro	Leu	Gln	Leu	Lys	Ala	Cys	Ala	Gly	Asp	Ala	
1				5					10					15		
Ala	Glu	Lys	Leu	Leu	Ala	Val	Ala	Ala	Glu	Gly	Pro	Ile	Cys	Xaa		
			20					25					30			
Val	Pro	Asp	Phe	Lys	Met	Arg	Gly	Lys	Lys	Ser	Asp	Xaa	Leu	Glu	Pro	
			35				40					45				
Val	Asp	Xaa	Gly	Asp	Glu	Asp	Asp	Asp	Gly	Gly	Asp	Asp	Gly	Asp	Glu	
			50			55					60					
Asp	Gly	Asp	Phe	Gly	Glu	Glu	Gly	Glu	Glu	Asp	Val	Ser	Glu	Gly	Glu	
65				70					75					80		
Gly	Tyr	Asp	Asn	Pro	Lys	Gly	Asn	Glu	Thr	Lys	Xaa	Xaa	Arg	Gly	Asp	
			85					90						95		
Pro	Glu	Glu	Asn	Gly	Glu	Glu	Asp	Glu	Glu	Glu	Pro	Glu	Asp	Gln	Glu	
			100					105					110			
Gly	Gly	Gly	Asp	Asp	Asp	Asp	Asp	Asp	Asp	Asp	Asp	Asp	Glu	Asn	Gly	
			115					120				125				
Asp	Asp	Glu	Asp	Asp	Asp	Asn	Gly	Asp	Asp	Asp	Glu	Glu	Gly	Val	Asp	
			130			135					140					
Glu	Glu	Asp	Asp	Asp	Gln	Asp	Glu	Asp	Glu	Glu	Asp	Asp	Asp	Asp	Glu	
145				150					155						160	
Asp	Ser	Leu	Gln	Pro	Pro	Lys	Lys	Arg	Lys	Lys						
			165						170							

(2) INFORMATION FOR SEQ ID NO:972:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 134 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide

(B) LOCATION: 1..134

(D) OTHER INFORMATION: / Ceres Seq. ID 1499316

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:972:

Met Arg Gly Lys Lys Ser Asp Xaa Leu Glu Pro Val Asp Xaa Gly Asp
1 5 10 15
Glu Asp Asp Asp Gly Gly Asp Asp Gly Asp Glu Asp Gly Asp Phe Gly
20 25 30
Glu Glu Gly Glu Glu Asp Val Ser Glu Gly Glu Gly Tyr Asp Asn Pro
35 40 45
Lys Gly Asn Glu Thr Lys Xaa Xaa Arg Gly Asp Pro Glu Glu Asn Gly
50 55 60
Glu Glu Asp Glu Glu Glu Pro Glu Asp Gln Glu Gly Gly Gly Asp Asp
65 70 75 80
Asp Asp Asp Asp Asp Asp Asp Asp Glu Asn Gly Asp Asp Glu Asp Asp
85 90 95
Asp Asn Gly Asp Asp Asp Glu Glu Gly Val Asp Glu Glu Asp Asp Asp
100 105 110
Gln Asp Glu Asp Glu Glu Glu Asp Asp Glu Asp Ser Leu Gln Pro
115 120 125
Pro Lys Lys Arg Lys Lys
130

(2) INFORMATION FOR SEQ ID NO:973:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 99 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..99

(D) OTHER INFORMATION: / Ceres Seq. ID 1499317

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:973:

Met Xaa Ser Asn Leu Ser Xaa Leu Ala Met Lys Met Met Met Val Val
1 5 10 15
Thr Met Gly Thr Arg Met Val Thr Leu Gly Arg Arg Val Lys Arg Thr
20 25 30
Ser Gln Lys Gly Arg Asp Met Thr Thr Gln Arg Ala Met Arg Pro Arg
35 40 45
Xaa Xaa Glu Val Ile Leu Arg Lys Met Val Arg Lys Met Arg Lys Asn
50 55 60
Gln Lys Ile Arg Arg Val Ala Ala Thr Thr Met Met Thr Thr Met Thr
65 70 75 80
Met Met Arg Thr Gly Met Thr Arg Thr Thr Thr Met Gly Met Thr Met
85 90 95
Arg Arg Val

(2) INFORMATION FOR SEQ ID NO:974:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 948 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..948

(D) OTHER INFORMATION: / Ceres Seq. ID 1499344

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:974:

ctycgtyccc ctctctgvt cctcgcgac cttctttact gcccgagagt tctgactagc 60
cacatccagt caagcagtaa aggcgcacca tggaggcggc ggcggagaat aaggaggccg 120

```
agcaggagga gcagcagcta ccgcacgcgc agaaggataa cgcgcccgcc gccgcccagg 180
aagacgaagc ggattcggag gagaccgagc gccgcaaccg cgacctcaag tccggccttc 240
acccccttag gcacaaactc gtgctctggt acactcgccg gacgcctgga gcgaggtcgc 300
agtcgtacga ggacaacatc aagaagatca tcgatttcag cacagtcgaa tcgttctggg 360
tttgctactg ccaccttgcg cgccttctt ccctgccgag cccactgac cttcatctct 420
tcaaggatgg catccgtccc ctctgggagg atcctgcaaa ccagaatggt ggcaagtgga 480
taattagatt caaaaaggca gtttcaggtc gattttggga ggatttggtg ctagtggtag 540
taggcgacca gcttgagtat agcgatgatg tctgtggtgt tgtgcttagt gtcctgttca 600
atgaagacat tctgagcgtc tggaaaccgga acgcatcaga ccatcaggct gtgatggcat 660
tgagggattc tatcaagagg cacctcaagc tgccgcacag ctatctgatg gagtacaaac 720
cccatgatst tcgcggcgtg acaactcgtc ctacaggaac acatggctga gaggatagat 780
aaacctcatg atactcgga gcttcactgc gacggttctg aagcaaagag actcttttat 840
gtaccaagaa cgcagactat tatgcaatgt agtactacta ctactactac tcaaaagccc 900
ctacaatgtg acgcgcaaca attttactat ctaatgtgtt ttttttgc
```

(2) INFORMATION FOR SEQ ID NO:975:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 160 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..160
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499345

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:975:

```
Xaa Arg Xaa Pro Pro Xaa Leu Leu Ala Ile Leu Leu Tyr Cys Pro Arg
1      5      10      15
Val Leu Thr Ser His Ile Gln Ser Ser Ser Lys Gly Ala Pro Trp Arg
20     25     30
Arg Arg Arg Arg Ile Arg Arg Pro Ser Arg Arg Ser Ser Ser Tyr Arg
35     40     45
Thr Arg Arg Arg Ile Thr Arg Pro Pro Pro Pro Arg Lys Thr Lys Arg
50     55     60
Ile Arg Arg Arg Pro Ser Ala Ala Thr Ala Thr Ser Ser Pro Ala Phe
65     70     75     80
Thr Pro Leu Gly Thr Asn Ser Cys Ser Gly Thr Leu Ala Gly Arg Leu
85     90     95
Glu Arg Gly Arg Ser Arg Thr Arg Thr Thr Ser Arg Arg Ser Ser Ile
100    105    110
Ser Ala Gln Ser Asn Arg Ser Gly Phe Ala Thr Ala Thr Leu Arg Ala
115    120    125
Leu Leu Pro Cys Arg Ala Pro Leu Thr Phe Ile Ser Ser Arg Met Ala
130    135    140
Ser Val Pro Ser Gly Arg Ile Leu Gln Thr Arg Met Val Ala Ser Gly
145    150    155    160
```

(2) INFORMATION FOR SEQ ID NO:976:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 226 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..226
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499346

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:976:

```
Met Glu Ala Ala Ala Glu Asn Lys Glu Ala Glu Gln Glu Glu Gln Gln
```

1 5 10 15
Leu Pro His Ala Gln Lys Asp Asn Ala Pro Ala Ala Ala Glu Glu Asp
20 25 30
Glu Ala Asp Ser Glu Glu Thr Glu Arg Arg Asn Arg Asp Leu Lys Ser
35 40 45
Gly Leu His Pro Leu Arg His Lys Leu Val Leu Trp Tyr Thr Arg Arg
50 55 60
Thr Pro Gly Ala Arg Ser Gln Ser Tyr Glu Asp Asn Ile Lys Lys Ile
65 70 75 80
Ile Asp Phe Ser Thr Val Glu Ser Phe Trp Val Cys Tyr Cys His Leu
85 90 95
Ala Arg Pro Ser Ser Leu Pro Ser Pro Thr Asp Leu His Leu Phe Lys
100 105 110
Asp Gly Ile Arg Pro Leu Trp Glu Asp Pro Ala Asn Gln Asn Gly Gly
115 120 125
Lys Trp Ile Ile Arg Phe Lys Lys Ala Val Ser Gly Arg Phe Trp Glu
130 135 140
Asp Leu Val Leu Val Val Val Gly Asp Gln Leu Glu Tyr Ser Asp Asp
145 150 155 160
Val Cys Gly Val Val Leu Ser Val Arg Phe Asn Glu Asp Ile Leu Ser
165 170 175
Val Trp Asn Arg Asn Ala Ser Asp His Gln Ala Val Met Ala Leu Arg
180 185 190
Asp Ser Ile Lys Arg His Leu Lys Leu Pro His Ser Tyr Leu Met Glu
195 200 205
Tyr Lys Pro His Asp Xaa Arg Gly Val Thr Thr Arg Pro Thr Gly Thr
210 215 220
His Gly
225

(2) INFORMATION FOR SEQ ID NO:977:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 537 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..537
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499353

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:977:

aaaaacacca cacaacacaa cacaataata cagcaaagga ggctagcaga agtgcaggat	60
taataagcta agctagtaga aattaagcaa agcataggca cagccatggc tacctcctct	120
ggttcttgcc ttattattag cctgtwgtg gtggtggtg cggcggcgct gtcggcctca	180
acggcgctcg cacagctgtc gtcgacgttc tacgacacgt cgtgccccag cgcgatgtcc	240
accatcagca gcggcgtgaa ctccgccgtg gcgcasaggc tcgtgtgggg gcgtcgctgc	300
tccggctcca cttccacgac tgcttcgtcc aagggtgcga cgcgtccatt ctgctgaacg	360
acacgtccgg ggagcagacc cagccgccga acctaacctt gaacccgagg gccttcgacg	420
tcgtcaacag catcaaggcg caggtggagg cggcgtgccc gggcgctcgtc tcctgcgccg	480
acatcctcgc cgtcgccgcc cgcgacgagt tgctgcgctc ggcgggcctt cgtggac	

(2) INFORMATION FOR SEQ ID NO:978:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 83 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..83
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499354

[illegible]

(A) LENGTH: 460 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(D) OTHER INFORMATION: / Ceres Seq. ID 1499362

accatagca	gccagtcgcc	cgcacgactc	tttcccggt	accacaccg	cgcgagatct	60
ccgatccccg	cccaaattcc	acgacgccgg	cggsgccatg	ggcggaagg	acctgacgga	120
ggaccagatc	gcctcgatgc	gggaggcctt	ctcgtgttc	gacacggacg	gggacggccg	180
catcgcgccc	tcggagctgg	gcgtcctcat	gcgtccctc	ggcggaacc	ccacgcaggc	240
gcastccggg	acatcgcgcc	gcaggagaag	ctcaccgcac	ccttogactt	cccgcgcttt	300
ctcgacctca	tgcgcgccca	cctcaagccc	gagcccttcg	accgchcget	ccgcgamgcc	360
ttcmcgctcc	tcgacaaggga	cggctccggc	accgtcgccg	tmgcmrasct	ccgccacgtc	420
ctcacctcca	tcggcgagaa	gctcgaggcc	cacgagttcg			

(A) LENGTH: 153 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(D) OTHER INFORMATION: / Ceres Seq. ID 1499363

Thr 1	His	Ser	Ser	Gln 5	Ser	Pro	Ala	Arg	Leu 10	Phe	Pro	Gly	Tyr	Pro 15	His
Arg	Ala	Arg	Ser 20	Pro	Ile	Pro	Ala	Gln 25	Ile	Pro	Arg	Arg	Arg	Arg	Xaa
His	Gly	Arg 35	Gln	Gly	Pro	Asp	Gly 40	Gly	Pro	Asp	Arg	Leu	Asp	Ala	Gly
Gly	Leu 50	Leu	Ala	Val	Arg	His 55	Gly	Arg	Gly	Arg	Pro 60	His	Arg	Ala	Leu
Gly 65	Ala	Gly	Arg	Pro	His 70	Ala	Leu	Pro	Arg	Arg	Glu 75	Pro	His	Ala	Gly 80
Ala	Xaa	Arg	Asp 85	Ile	Ala	Ala	Gln	Glu	Lys 90	Leu	Thr	Ala	Pro	Phe	Asp
Phe	Pro	Arg	Phe 100	Leu	Asp	Leu	Met	Arg 105	Ala	His	Leu	Lys	Pro 110	Glu	Pro
Phe	Asp	Arg 115	Xaa	Leu	Arg	Xaa	Ala 120	Phe	Xaa	Val	Leu	Asp 125	Lys	Asp	Gly

Ser Gly Thr Val Ala Xaa Xaa Xaa Leu Arg His Val Leu Thr Ser Ile
130 135 140
Gly Glu Lys Leu Glu Ala His Glu Phe
145 150

(2) INFORMATION FOR SEQ ID NO:981:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 153 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..153
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499364

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:981:

Pro Ile Ala Ala Ser Arg Pro His Asp Ser Phe Pro Ala Thr His Thr
1 5 10 15
Ala Arg Asp Leu Arg Ser Pro Pro Lys Ser His Asp Ala Gly Xaa Ala
20 25 30
Met Gly Gly Lys Asp Leu Thr Glu Asp Gln Ile Ala Ser Met Arg Glu
35 40 45
Ala Phe Ser Leu Phe Asp Thr Asp Gly Asp Gly Arg Ile Ala Pro Ser
50 55 60
Glu Leu Gly Val Leu Met Arg Ser Leu Gly Gly Asn Pro Thr Gln Ala
65 70 75 80
Xaa Ser Gly Thr Ser Arg Arg Arg Arg Ser Ser Pro His Pro Ser Thr
85 90 95
Ser Arg Ala Phe Ser Thr Ser Cys Ala Pro Thr Ser Ser Pro Ser Pro
100 105 110
Ser Thr Xaa Arg Ser Ala Xaa Pro Xaa Ala Ser Ser Thr Arg Thr Ala
115 120 125
Pro Ala Pro Ser Pro Xaa Xaa Xaa Ser Ala Thr Ser Ser Pro Pro Ser
130 135 140
Ala Arg Ser Ser Arg Pro Thr Ser Ser
145 150

(2) INFORMATION FOR SEQ ID NO:982:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 121 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..121
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499365

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:982:

Met Gly Gly Lys Asp Leu Thr Glu Asp Gln Ile Ala Ser Met Arg Glu
1 5 10 15
Ala Phe Ser Leu Phe Asp Thr Asp Gly Asp Gly Arg Ile Ala Pro Ser
20 25 30
Glu Leu Gly Val Leu Met Arg Ser Leu Gly Gly Asn Pro Thr Gln Ala
35 40 45
Xaa Ser Gly Thr Ser Arg Arg Arg Arg Ser Ser Pro His Pro Ser Thr
50 55 60
Ser Arg Ala Phe Ser Thr Ser Cys Ala Pro Thr Ser Ser Pro Ser Pro
65 70 75 80
Ser Thr Xaa Arg Ser Ala Xaa Pro Xaa Ala Ser Ser Thr Arg Thr Ala
85 90 95
Pro Ala Pro Ser Pro Xaa Xaa Xaa Ser Ala Thr Ser Ser Pro Pro Ser

100 105
Ala Arg Ser Ser Arg Pro Thr Ser Ser
115 120

110

(2) INFORMATION FOR SEQ ID NO:983:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 736 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..736
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499370

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:983:

gcattcgtac	aaccgcagcc	gagacggttg	accaacgctg	ccacgattcc	gtccacacgc	60
cgacgcggcg	ggctcctggc	cgacgagcac	tcccctccga	acgcgcggtt	ggccggcccc	120
gccccacgag	gccacgatgc	agtagcagcg	ttcacaccat	ctgtctgtct	caagtgtcac	180
ggcgtccgtc	attcgattca	accccccaacc	ccccatgggc	ctggccggtat	aaatcaaccg	240
ccggtgaagt	ctagtcgtct	cgtcgctcgg	tccaccacct	cagctccgcc	gcttgccccg	300
ttttgtctct	tccctcccgg	ctctcggctt	cttctacacg	ctaccgtctc	acagccgtaa	360
acgccccctc	cggatcccgc	tagttcgcca	ccgcgcggcg	cccgcgcggc	gttcgcctca	420
tcattggcgc	ctcgtcgacc	gcccacctcc	gtccatgact	tcatcgtaaa	ggatggaggt	480
ggcggccgtg	gaggcgggcg	tggcggtatac	ggtggcgggc	gccgtgatgg	aggcggttac	540
ggcgggtggc	gtggaggcta	cggcggtggt	cgtggaggct	acggcgggcg	tgggggatac	600
ggtggtgcaa	accgcggcg	cggctacggc	aacaacgacg	ggaactggag	gaactgagcg	660
gtggggtcgc	ctgaggccta	gttatcttgt	tcgcttctgc	taccgtgttc	accctagtct	720
agaggggggt	tatctt					

(2) INFORMATION FOR SEQ ID NO:984:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 119 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..119
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499371

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:984:

Ala	Phe	Val	Gln	Pro	Gln	Pro	Arg	Arg	Leu	Thr	Asn	Ala	Ala	Thr	Ile	
1				5					10						15	
Pro	Ser	Thr	Arg	Arg	Arg	Gly	Gly	Leu	Leu	Ala	Asp	Glu	His	Ser	Pro	
			20					25						30		
Pro	Asn	Ala	Ala	Leu	Ala	Gly	Pro	Ala	Pro	Arg	Gly	His	Asp	Ala	Val	
			35					40						45		
Ala	Ala	Phe	Thr	Pro	Ser	Val	Cys	Leu	Lys	Cys	His	Gly	Val	Arg	His	
			50					55						60		
Ser	Ile	Gln	Pro	Pro	Thr	Pro	His	Gly	Pro	Gly	Arg	Ile	Asn	Gln	Pro	
65						70				75					80	
Pro	Val	Lys	Ser	Ser	Arg	Leu	Val	Ala	Arg	Ser	Thr	Thr	Ser	Ala	Pro	
						85				90					95	
Pro	Leu	Ala	Arg	Phe	Cys	Ser	Leu	Pro	Pro	Gly	Ser	Arg	Leu	Leu	Leu	
						100				105					110	
His	Ala	Thr	Val	Ser	Gln	Pro										
						115										

(2) INFORMATION FOR SEQ ID NO:985:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 94 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:

- (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..94
 (D) OTHER INFORMATION: / Ceres Seq. ID 1499372

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:985:

```
Met Thr Ser Ser Arg Met Glu Val Ala Ala Val Glu Ala Ala Val
1      5      10      15
Ala Asp Thr Val Ala Gly Ala Val Met Glu Ala Ala Thr Ala Val Ala
20      25      30
Val Glu Ala Thr Ala Val Val Val Glu Ala Thr Ala Ala Val Gly Asp
35      40      45
Thr Val Val Gln Thr Ala Ala Ala Thr Ala Thr Thr Thr Gly Thr
50      55      60
Gly Gly Thr Glu Arg Trp Gly Pro Leu Arg Pro Ser Tyr Leu Val Arg
65      70      75      80
Phe Cys Tyr Arg Val His Pro Ser Leu Glu Gly Val Tyr Leu
85      90
```

(2) INFORMATION FOR SEQ ID NO:986:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 88 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..88
 (D) OTHER INFORMATION: / Ceres Seq. ID 1499373

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:986:

```
Met Glu Val Ala Ala Val Glu Ala Ala Val Ala Asp Thr Val Ala Gly
1      5      10      15
Ala Val Met Glu Ala Ala Thr Ala Val Ala Val Glu Ala Thr Ala Val
20      25      30
Val Val Glu Ala Thr Ala Ala Val Gly Asp Thr Val Val Gln Thr Ala
35      40      45
Ala Ala Ala Thr Ala Thr Thr Thr Gly Thr Gly Gly Thr Glu Arg Trp
50      55      60
Gly Pro Leu Arg Pro Ser Tyr Leu Val Arg Phe Cys Tyr Arg Val His
65      70      75      80
Pro Ser Leu Glu Gly Val Tyr Leu
85
```

(2) INFORMATION FOR SEQ ID NO:987:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 914 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
 (A) NAME/KEY: -
 (B) LOCATION: 1..914
 (D) OTHER INFORMATION: / Ceres Seq. ID 1499380

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:987:

```
gnacccctgc gccgcacccg cacggcaaca gcatcgacct aggcccggtc ccgtgtcgct      60
tcgtagttcg tccccttccc cgcgcccccga gcagcagcgg attcccctcg agagatccgg      120
cccttggcgc ggtcgcccga gagagcggca tggggctctg ggactcgctc ctcaactggc      180
tccggagctt gtttttcaag caagaaatgg agctctccct cgttggttg cagaatgctg      240
ggaagacgtc gctggtcaat gctgttgcta caggtggcta cagcgaggac atgattccaa      300
cggtaggctt caatatgcgg aaggtcacca agggaaatgt cagattaag ctttgggata      360
```

ttggtgggca gcgagattc cgcactatgt gggagcgccta ttgccgtgga gtttctgcta	420
ttctatatgt tgtggacgct gctgaccgag atagtgtccc aatcgcgaaa agtgagttgc	480
atgatctgct gacgaaacag tctttggctg ggattccctt gcttgtcctt ggcaacaaaa	540
ttgacaagtc agaagcgctt tcgaagcagg ccttggttga tcaacttgga ctggaattga	600
taaaggaccg tgaggtttgt tgctacatga tctcctgtaa ggattctgtg aacatagacg	660
tcgtcatcga ctggcttata aagcactcta gaacagcgaa gtaggctttc tgtgtgtttg	720
tatcgcttga tgcacggtgt tttatctttt gtgaatctga gcctggttcc ttggtcccga	780
tggtaaaagc ggccaccttg taatttatga cctctttggt gtcacagacg aactgcatgg	840
tatctagact agaaacatgt cttccctttg taaatccctt gaacctttga ttattcttac	900
tgtgaatgcc gtcc	

(2) INFORMATION FOR SEQ ID NO:988:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 233 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..233

(D) OTHER INFORMATION: / Ceres Seq. ID 1499381

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:988:

Thr	Pro	Ala	Pro	His	Pro	His	Gly	Asn	Ser	Ile	Asp	Leu	Gly	Pro	Val
1			5					10						15	
Pro	Cys	Arg	Phe	Val	Val	Arg	Pro	Leu	Pro	Arg	Ala	Pro	Ser	Ser	Ser
			20					25					30		
Gly	Phe	Pro	Ser	Arg	Asp	Pro	Ala	Leu	Gly	Ala	Val	Ala	Gly	Glu	Ser
		35					40					45			
Gly	Met	Gly	Leu	Trp	Asp	Ser	Leu	Leu	Asn	Trp	Leu	Arg	Ser	Leu	Phe
	50					55					60				
Phe	Lys	Gln	Glu	Met	Glu	Leu	Ser	Leu	Val	Gly	Leu	Gln	Asn	Ala	Gly
65					70					75					80
Lys	Thr	Ser	Leu	Val	Asn	Ala	Val	Ala	Thr	Gly	Gly	Tyr	Ser	Glu	Asp
				85					90					95	
Met	Ile	Pro	Thr	Val	Gly	Phe	Asn	Met	Arg	Lys	Val	Thr	Lys	Gly	Asn
			100					105						110	
Val	Thr	Ile	Lys	Leu	Trp	Asp	Leu	Gly	Gly	Gln	Arg	Arg	Phe	Arg	Thr
		115					120					125			
Met	Trp	Glu	Arg	Tyr	Cys	Arg	Gly	Val	Ser	Ala	Ile	Leu	Tyr	Val	Val
		130				135					140				
Asp	Ala	Ala	Asp	Arg	Asp	Ser	Val	Pro	Ile	Ala	Lys	Ser	Glu	Leu	His
145					150					155					160
Asp	Leu	Leu	Thr	Lys	Gln	Ser	Leu	Ala	Gly	Ile	Pro	Leu	Leu	Val	Leu
			165						170					175	
Gly	Asn	Lys	Ile	Asp	Lys	Ser	Glu	Ala	Leu	Ser	Lys	Gln	Ala	Leu	Val
		180						185					190		
Asp	Gln	Leu	Gly	Leu	Glu	Leu	Ile	Lys	Asp	Arg	Glu	Val	Cys	Cys	Tyr
		195					200				205				
Met	Ile	Ser	Cys	Lys	Asp	Ser	Val	Asn	Ile	Asp	Val	Val	Ile	Asp	Trp
	210					215					220				
Leu	Ile	Lys	His	Ser	Arg	Thr	Ala	Lys							
225					230										

(2) INFORMATION FOR SEQ ID NO:989:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 184 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..184

(D) OTHER INFORMATION: / Ceres Seq. ID 1499382

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:989:

Met Gly Leu Trp Asp Ser Leu Leu Asn Trp Leu Arg Ser Leu Phe Phe
1 5 10 15
Lys Gln Glu Met Glu Leu Ser Leu Val Gly Leu Gln Asn Ala Gly Lys
20 25 30
Thr Ser Leu Val Asn Ala Val Ala Thr Gly Gly Tyr Ser Glu Asp Met
35 40 45
Ile Pro Thr Val Gly Phe Asn Met Arg Lys Val Thr Lys Gly Asn Val
50 55 60
Thr Ile Lys Leu Trp Asp Leu Gly Gly Gln Arg Arg Phe Arg Thr Met
65 70 75 80
Trp Glu Arg Tyr Cys Arg Gly Val Ser Ala Ile Leu Tyr Val Val Asp
85 90 95
Ala Ala Asp Arg Asp Ser Val Pro Ile Ala Lys Ser Glu Leu His Asp
100 105 110
Leu Leu Thr Lys Gln Ser Leu Ala Gly Ile Pro Leu Leu Val Leu Gly
115 120 125
Asn Lys Ile Asp Lys Ser Glu Ala Leu Ser Lys Gln Ala Leu Val Asp
130 135 140
Gln Leu Gly Leu Glu Leu Ile Lys Asp Arg Glu Val Cys Cys Tyr Met
145 150 155 160
Ile Ser Cys Lys Asp Ser Val Asn Ile Asp Val Val Ile Asp Trp Leu
165 170 175
Ile Lys His Ser Arg Thr Ala Lys
180

(2) INFORMATION FOR SEQ ID NO:990:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 165 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..165

(D) OTHER INFORMATION: / Ceres Seq. ID 1499383

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:990:

Met Glu Leu Ser Leu Val Gly Leu Gln Asn Ala Gly Lys Thr Ser Leu
1 5 10 15
Val Asn Ala Val Ala Thr Gly Gly Tyr Ser Glu Asp Met Ile Pro Thr
20 25 30
Val Gly Phe Asn Met Arg Lys Val Thr Lys Gly Asn Val Thr Ile Lys
35 40 45
Leu Trp Asp Leu Gly Gly Gln Arg Arg Phe Arg Thr Met Trp Glu Arg
50 55 60
Tyr Cys Arg Gly Val Ser Ala Ile Leu Tyr Val Val Asp Ala Ala Asp
65 70 75 80
Arg Asp Ser Val Pro Ile Ala Lys Ser Glu Leu His Asp Leu Leu Thr
85 90 95
Lys Gln Ser Leu Ala Gly Ile Pro Leu Leu Val Leu Gly Asn Lys Ile
100 105 110
Asp Lys Ser Glu Ala Leu Ser Lys Gln Ala Leu Val Asp Gln Leu Gly
115 120 125
Leu Glu Leu Ile Lys Asp Arg Glu Val Cys Cys Tyr Met Ile Ser Cys
130 135 140
Lys Asp Ser Val Asn Ile Asp Val Val Ile Asp Trp Leu Ile Lys His
145 150 155 160
Ser Arg Thr Ala Lys
165

(2) INFORMATION FOR SEQ ID NO:991:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 536 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..536
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499384

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:991:

acacagcgag ccaatcgccg taatcatgaa ggtcctcatc gttctcgccg cgtgcgttgc	60
cgccgcccctg gctggcatcc cctccgagtc tgagatccag gtcattggg agagcttcaa	120
ggctacccac ggcaagacct acgccaatgc cgtcgaggag gcctacaggg ccaaggtgtt	180
caaggaaaac gccatcagga tcgccaaagca caatgaccgt ttcgccagcg gsagngtcac	240
cttcaaggtc ggctacaacc agtacgctga catgcacacc cagcaggtca ccgagaagat	300
gaacggtttc cgcattggaga tgaagaaacc ctccgctaac gtgcacgagg gcaacgactc	360
ctggcccttg agcaagaagg tcgactggag atccaagggc tacgtcaccc ccatcaagga	420
ccagggacag tgcggttcct gctggctctt ctctgccact ggttccctcg agggtcagct	480
cttcaagata ccggcaagct ggtctccctc tctgagcaga acctggtcga ctgctc	

(2) INFORMATION FOR SEQ ID NO:992:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 178 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..178
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499385

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:992:

His Ser Glu Pro Ile Ala Val Ile Met Lys Val Leu Ile Val Leu Ala	
1 5 10 15	
Ala Cys Val Ala Ala Leu Ala Gly Ile Pro Ser Glu Ser Glu Ile	
20 25 30	
Gln Ala His Trp Glu Ser Phe Lys Ala Thr His Gly Lys Thr Tyr Ala	
35 40 45	
Asn Ala Val Glu Glu Ala Tyr Arg Ala Lys Val Phe Lys Glu Asn Ala	
50 55 60	
Ile Arg Ile Ala Lys His Asn Asp Arg Phe Ala Ser Xaa Xaa Val Thr	
65 70 75 80	
Phe Lys Val Gly Tyr Asn Gln Tyr Ala Asp Met His Thr His Glu Val	
85 90 95	
Thr Glu Lys Met Asn Gly Phe Arg Met Glu Met Lys Lys Pro Ser Ala	
100 105 110	
Asn Val His Glu Gly Asn Asp Ser Trp Pro Trp Ser Lys Lys Val Asp	
115 120 125	
Trp Arg Ser Lys Gly Tyr Val Thr Pro Ile Lys Asp Gln Gly Gln Cys	
130 135 140	
Gly Ser Cys Trp Ser Phe Ser Ala Thr Gly Ser Leu Glu Gly Gln Leu	
145 150 155 160	
Phe Lys Ile Pro Ala Ser Trp Ser Pro Ser Leu Ser Arg Thr Trp Ser	
165 170 175	
Thr Ala	

(2) INFORMATION FOR SEQ ID NO:993:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 170 amino acids
- (B) TYPE: amino acid

(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..170
(D) OTHER INFORMATION: / Ceres Seq. ID 1499386
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:993:
Met Lys Val Leu Ile Val Leu Ala Ala Cys Val Ala Ala Ala Leu Ala
1 5 10 15
Gly Ile Pro Ser Glu Ser Glu Ile Gln Ala His Trp Glu Ser Phe Lys
20 25 30
Ala Thr His Gly Lys Thr Tyr Ala Asn Ala Val Glu Glu Ala Tyr Arg
35 40 45
Ala Lys Val Phe Lys Glu Asn Ala Ile Arg Ile Ala Lys His Asn Asp
50 55 60
Arg Phe Ala Ser Xaa Xaa Val Thr Phe Lys Val Gly Tyr Asn Gln Tyr
65 70 75 80
Ala Asp Met His Thr His Glu Val Thr Glu Lys Met Asn Gly Phe Arg
85 90 95
Met Glu Met Lys Lys Pro Ser Ala Asn Val His Glu Gly Asn Asp Ser
100 105 110
Trp Pro Trp Ser Lys Lys Val Asp Trp Arg Ser Lys Gly Tyr Val Thr
115 120 125
Pro Ile Lys Asp Gln Gly Gln Cys Gly Ser Cys Trp Ser Phe Ser Ala
130 135 140
Thr Gly Ser Leu Glu Gly Gln Leu Phe Lys Ile Pro Ala Ser Trp Ser
145 150 155 160
Pro Ser Leu Ser Arg Thr Trp Ser Thr Ala
165 170

(2) INFORMATION FOR SEQ ID NO:994:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 470 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
(B) LOCATION: 1..470
(D) OTHER INFORMATION: / Ceres Seq. ID 1499389

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:994:

gaccctttct	ttcccaaagc	cgagcagcga	ccagcgaggg	tgccactgcc	accgcccgcc	60
ccccagtccc	ccactcactc	actagctagc	ttgctagctg	cgactacg	gctacgccga	120
gctagagtcc	ggcgatcaca	gcccggcagg	ccggccatgg	ccaccgcgcc	cgctcgtcgtc	180
ctagtcctgc	acgtttctgct	aggcgctgca	gcggccgcct	gcgccgcggc	ggcagggagt	240
agcagcaagg	tgccggcgat	gtacgtgttc	ggcgactcca	cggcggacgt	gggcaccaac	300
aactacttgc	cgggcggcgc	cgaagtgccg	cgtgccaaact	tccccacaa	cggcgtcgac	360
ttccccasgg	sgcgcmccac	cggcagggttc	agcaacgggt	tcaacggcgt	cgacttcttg	420
gccgtgaaca	tgggcttcaa	gcgcasmtccc	cgccgttctc	cgcmgtggcc		

(2) INFORMATION FOR SEQ ID NO:995:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 156 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..156
(D) OTHER INFORMATION: / Ceres Seq. ID 1499390

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:995:

Asp Pro Phe Phe Pro Lys Ala Glu Gln Arg Pro Ala Arg Val Pro Leu
1 5 10 15
Pro Pro Pro Ala Pro Gln Ser Pro Thr His Ser Leu Ala Ser Leu Leu
20 25 30
Ala Ala His Tyr Gly Leu Arg Arg Ala Arg Val Arg Arg Ser Gln Pro
35 40 45
Gly Arg Pro Ala Met Ala Thr Ala Pro Val Val Val Leu Val Leu His
50 55 60
Val Leu Leu Gly Ala Ala Ala Ala Cys Ala Ala Ala Ala Gly Ser
65 70 75 80
Ser Ser Lys Val Pro Ala Met Tyr Val Phe Gly Asp Ser Thr Ala Asp
85 90 95
Val Gly Thr Asn Asn Tyr Leu Pro Gly Gly Ala Glu Val Pro Arg Ala
100 105 110
Asn Phe Pro His Asn Gly Val Asp Phe Pro Xaa Xaa Arg Xaa Thr Gly
115 120 125
Arg Phe Ser Asn Gly Phe Asn Gly Val Asp Phe Leu Ala Val Asn Met
130 135 140
Gly Phe Lys Arg Xaa Pro Arg Arg Ser Ser Xaa Trp
145 150 155

(2) INFORMATION FOR SEQ ID NO:996:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 104 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..104
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499391

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:996:

Met Ala Thr Ala Pro Val Val Val Leu Val Leu His Val Leu Leu Gly
1 5 10 15
Ala Ala Ala Ala Ala Cys Ala Ala Ala Ala Gly Ser Ser Ser Lys Val
20 25 30
Pro Ala Met Tyr Val Phe Gly Asp Ser Thr Ala Asp Val Gly Thr Asn
35 40 45
Asn Tyr Leu Pro Gly Gly Ala Glu Val Pro Arg Ala Asn Phe Pro His
50 55 60
Asn Gly Val Asp Phe Pro Xaa Xaa Arg Xaa Thr Gly Arg Phe Ser Asn
65 70 75 80
Gly Phe Asn Gly Val Asp Phe Leu Ala Val Asn Met Gly Phe Lys Arg
85 90 95
Xaa Pro Arg Arg Ser Ser Xaa Trp
100

(2) INFORMATION FOR SEQ ID NO:997:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 519 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..519
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499402

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:997:

cagascagaa ascagccgca gccccagccc ccacaagacg aggcaacaat ggcgctagaa 60
gcagccaccg cccccgcgc actcctcgcc gcgtgcctcg tcctgctggt cctcggcggc 120

```
ggcaccggcc cgctcgctggt gctgcgcggc gccggggcgc aggccggcag gggagccgga 180
tccaggatac gtcattgtatc cggcatgggg ccccgccgtc cactaatcgt cgctcggtcga 240
ggcgacgac gacgctccgc cgccaacgac ggcgagtgcc acatgcctat gctctcgtgt 300
gggccccgta cgttattgag cgctactagt actagggaaa gtgtacgtgt gatgtgtgtc 360
actcagtgtc gattgatcaa tgatgctcat ttctgagcag acccaggaat gctgagtgtc 420
gagagcagag cgtntgttct acaagtgcac cgaggaataa agtggacaga aatgttggct 480
ggttcacgtg ccttctgagt aataaaatgg acatcttcg
```

(2) INFORMATION FOR SEQ ID NO:998:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 165 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..165

(D) OTHER INFORMATION: / Ceres Seq. ID 1499403

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:998:

```
Gln Xaa Arg Xaa Gln Pro Gln Pro Gln Pro Gln Asp Glu Ala Thr
1      5      10      15
Met Ala Leu Glu Ala Ala Thr Ala Pro Arg Ala Leu Leu Ala Ala Cys
20     25     30
Leu Val Leu Leu Val Leu Gly Gly Gly Thr Gly Pro Ser Ser Val Leu
35     40     45
Arg Gly Ala Gly Ala Gln Ala Gly Arg Gly Ala Gly Ser Arg Ile Arg
50     55     60
His Val Ser Gly Met Gly Pro Arg Arg Pro Leu Ile Val Val Val Arg
65     70     75     80
Gly Arg Arg Arg Arg Ser Ala Ala Asn Asp Gly Glu Cys His Met Pro
85     90     95
Met Leu Ser Cys Gly Pro Arg Thr Leu Leu Ser Ala Thr Ser Thr Arg
100    105    110
Glu Ser Val Arg Val Met Cys Val Thr Gln Cys Arg Leu Ile Asn Asp
115    120    125
Ala His Phe Arg Ala Asp Pro Gly Met Leu Ser Ala Glu Ser Arg Ala
130    135    140
Xaa Val Leu Gln Val His Arg Gly Ile Lys Trp Thr Glu Met Leu Ala
145    150    155    160
Gly Ser Arg Ala Phe
165
```

(2) INFORMATION FOR SEQ ID NO:999:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 108 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..108

(D) OTHER INFORMATION: / Ceres Seq. ID 1499404

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:999:

```
Xaa Gln Lys Xaa Ala Ala Ala Pro Ala Pro Thr Arg Arg Gly Asn Asn
1      5      10      15
Gly Ala Arg Ser Ser His Arg Pro Pro Arg Thr Pro Arg Arg Val Pro
20     25     30
Arg Pro Ala Gly Pro Arg Arg Arg His Arg Pro Val Val Gly Ala Ala
35     40     45
Arg Arg Arg Gly Ala Gly Arg Gln Gly Ser Arg Ile Gln Asp Thr Ser
50     55     60
```

Cys Ile Arg His Gly Ala Pro Pro Ser Thr Asn Arg Arg Arg Ser Arg
65 70 75 80
Ala Thr Thr Thr Leu Arg Arg Gln Arg Arg Arg Val Pro His Ala Tyr
85 90 95
Ala Leu Val Trp Ala Pro Tyr Val Ile Glu Arg Tyr
100 105

(2) INFORMATION FOR SEQ ID NO:1000:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 149 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..149

(D) OTHER INFORMATION: / Ceres Seq. ID 1499405

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1000:

Met Ala Leu Glu Ala Ala Thr Ala Pro Arg Ala Leu Leu Ala Ala Cys
1 5 10 15
Leu Val Leu Leu Val Leu Gly Gly Gly Thr Gly Pro Ser Ser Val Leu
20 25 30
Arg Gly Ala Gly Ala Gln Ala Gly Arg Gly Ala Gly Ser Arg Ile Arg
35 40 45
His Val Ser Gly Met Gly Pro Arg Arg Pro Leu Ile Val Val Val Arg
50 55 60
Gly Arg Arg Arg Arg Ser Ala Ala Asn Asp Gly Glu Cys His Met Pro
65 70 75 80
Met Leu Ser Cys Gly Pro Arg Thr Leu Leu Ser Ala Thr Ser Thr Arg
85 90 95
Glu Ser Val Arg Val Met Cys Val Thr Gln Cys Arg Leu Ile Asn Asp
100 105 110
Ala His Phe Arg Ala Asp Pro Gly Met Leu Ser Ala Glu Ser Arg Ala
115 120 125
Xaa Val Leu Gln Val His Arg Gly Ile Lys Trp Thr Glu Met Leu Ala
130 135 140
Gly Ser Arg Ala Phe
145

(2) INFORMATION FOR SEQ ID NO:1001:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1040 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1040

(D) OTHER INFORMATION: / Ceres Seq. ID 1499406

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1001:

gcattctcct cggcgcggggt tgccgagacg cgtacgggca ttctccttag gtgcgggggt 60
tcctctcgag tctcggaac gacgaaaacg aaaataccga gtcgagtcag cgatgaatcc 120
cttcgcaaaa aaaccaactc cgcgagaggt gatgcggasa gcaagcggga cctgacgaat 180
gctacgcgag ggatcgagag ggacattgcg tcattacagc aggaggagaa gaaactcggt 240
gctgaaatta aaaggacagc aaaaactggc aatgaggcag caacgaaaat tctagcccgt 300
cagctgatca gggttaaggc gcagatttct aatttgcaag gtagccgagc tcagattcgg 360
gggattgcga cacatactca ggcaatgcat gccaacactt cagtggctac tggtttataa 420
agtgcgagca aagcaatggg agctttgaat aagcaaatgg aacctaccaa gcagatgaaa 480
ataatgcaag aattccaaaa gcagtcagca caaatggata tgacaaatga gatgatgtct 540
gattcaatcg atgatgtctt agacgatgac caggccgagg aagaaaactga agaacttgct 600
aatcaggttc tggatgagat tgggtgtagac attgcatcac agttgtcctc ggctcccaaa 660

ggaaaaattg ctggaagaa ggttcaggtt gatggaagtt cggagttgga ggaactagag 720
aagagactgg ctgctctaaa aaatgcataa gatcagttta caaccctctc ctctatgcac 780
atagcaagcc tgccgtgtac cttaattcca aatcttcatt cgacacgcaa agtcactgtg 840
atttgatgt atcaaaagga agatgatgca aacccccaaag tttttgggcg aatcgatgtt 900
gctgctgttc gtacacactc acgcataaga tggggctgtg ctgccttatt agcgacatga 960
ttcagagcaa gggattccat agtcttgtaa agaagtttga ttatttttac atgacagcct 1020
tttgtttttg gtcgttcggt

(2) INFORMATION FOR SEQ ID NO:1002:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 249 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..249

(D) OTHER INFORMATION: / Ceres Seq. ID 1499407

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1002:

Ala Phe Ser Ser Ala Arg Val Ala Glu Thr Arg Thr Gly Ile Leu Leu
1 5 10 15
Arg Cys Gly Gly Ser Ser Arg Val Ser Ala Thr Thr Lys Thr Lys Ile
20 25 30
Pro Ser Arg Val Ser Asp Glu Ser Leu Arg Gln Lys Thr Asn Ser Ala
35 40 45
Arg Gly Asp Ala Xaa Ser Lys Arg Asp Leu Thr Asn Ala Thr Arg Gly
50 55 60
Ile Glu Arg Asp Ile Ala Ser Leu Gln Gln Glu Lys Lys Leu Val
65 70 75 80
Ala Glu Ile Lys Arg Thr Ala Lys Thr Gly Asn Glu Ala Ala Thr Lys
85 90 95
Ile Leu Ala Arg Gln Leu Ile Arg Leu Arg Gln Gln Ile Ser Asn Leu
100 105 110
Gln Gly Ser Arg Ala Gln Ile Arg Gly Ile Ala Thr His Thr Gln Ala
115 120 125
Met His Ala Asn Thr Ser Val Ala Thr Gly Leu Gln Ser Ala Ser Lys
130 135 140
Ala Met Gly Ala Leu Asn Lys Gln Met Glu Pro Thr Lys Gln Met Lys
145 150 155 160
Ile Met Gln Glu Phe Gln Lys Gln Ser Ala Gln Met Asp Met Thr Asn
165 170 175
Glu Met Met Ser Asp Ser Ile Asp Asp Val Leu Asp Asp Asp Gln Ala
180 185 190
Glu Glu Glu Thr Glu Glu Leu Ala Asn Gln Val Leu Asp Glu Ile Gly
195 200 205
Val Asp Ile Ala Ser Gln Leu Ser Ser Ala Pro Lys Gly Lys Ile Ala
210 215 220
Gly Lys Lys Val Gln Val Asp Gly Ser Ser Glu Leu Glu Glu Leu Glu
225 230 235 240
Lys Arg Leu Ala Ala Leu Lys Asn Ala
245

(2) INFORMATION FOR SEQ ID NO:1003:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 485 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..485

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1003:

(2) INFORMATION FOR SEQ ID NO:1004:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 53 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..53

(D) OTHER INFORMATION: / Ceres Seq. ID 1499409

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1004:

[illegible]

(2) INFORMATION FOR SEQ ID NO:1005:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 90 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..90

(D) OTHER INFORMATION: / Ceres Seq. ID 1499410

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1005:

Cys 1	Ser	Leu	Ser	Arg 5	Val	Pro	Ala	Phe	Gln 10	Trp	Gly	Ala	Phe	Met 15	Ala
Gly	Gln	Ser	Asp 20	Pro	His	Leu	Ser	Ile 25	Phe	Ser	Pro	Ser	Glu 30	Val	Glu
Phe	Val	Ala 35	Glu	Asp	Glu	Ile	Val 40	Glu	Ile	Val	Pro	Asn 45	Ile	Arg	Met
Asp	Ala 50	Leu	Asn	Met	Ile	Cys 55	Gly	Asp	Phe	Gly	Pro 60	Phe	Phe	Pro	Gln
Ile 65	Pro	Thr	Lys	Val	Pro 70	Leu	Trp	Leu	Ala	Val 75	Ala	Leu	Lys	Lys	Arg 80
Xaa	Ser	Ala	Pro	Ser 85	Ala	Pro	Arg	Thr	Gly 90						

(2) INFORMATION FOR SEO ID NO:1006:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 76 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..76

(D) OTHER INFORMATION: / Ceres Seq. ID 1499411

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1006:

```
Met Ala Gly Gln Ser Asp Pro His Leu Ser Ile Phe Ser Pro Ser Glu
1           5           10           15
Val Glu Phe Val Ala Glu Asp Glu Ile Val Glu Ile Val Pro Asn Ile
20           25           30
Arg Met Asp Ala Leu Asn Met Ile Cys Gly Asp Phe Gly Pro Phe Phe
35           40           45
Pro Gln Ile Pro Thr Lys Val Pro Leu Trp Leu Ala Val Ala Leu Lys
50           55           60
Lys Arg Xaa Ser Ala Pro Ser Ala Pro Arg Thr Gly
65           70           75
```

(2) INFORMATION FOR SEQ ID NO:1007:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 468 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..468

(D) OTHER INFORMATION: / Ceres Seq. ID 1499412

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1007:

```
agcctctatc tcattccact ccgacattca cgtgcagctg tcgggagcag gcaatggcgc      60
cggatctaag cgaactcgcc gccgccgctc cagcccgtgg cgcctacctc gccggcgctg      120
gtgtggaaag agaaagagag agagaggaga ggtgcgagct ggtgagatgg atcggttgga      180
ggagcggaac attaagaara aggavaagga ggatgganga ngcgcgcaag gaagangagc      240
ggaargagga ggcgggggac aggaataccc aggagccgca gcaagggtcaa ggcctcarcc      300
tmwvactcgm caacggcagc kacasgncag gtctgcaatg ttgccgatgt cgaacccttc      360
agctaattccc acacagctta caattttcta tggtggatca gtatgtgtgt atgactcggg      420
tgccaccaga aaaggctcag gcaatcatgc ttatagctgc agctgcgg
```

(2) INFORMATION FOR SEQ ID NO:1008:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 155 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..155

(D) OTHER INFORMATION: / Ceres Seq. ID 1499413

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1008:

```
Ala Ser Ile Ser Phe His Ser Asp Ile His Val Gln Leu Ser Gly Ala
1           5           10           15
Gly Asn Gly Ala Gly Ser Lys Arg Thr Arg Arg Arg Arg Ser Ser Pro
20           25           30
Trp Arg Leu Pro Arg Arg Arg Arg Cys Gly Lys Arg Lys Arg Glu Arg
35           40           45
Gly Glu Val Arg Ala Gly Glu Met Asp Arg Leu Glu Glu Arg Asn Ile
50           55           60
Lys Xaa Lys Xaa Lys Glu Asp Gly Xaa Xaa Ala Gln Gly Arg Xaa Ala
65           70           75           80
Glu Xaa Gly Gly Gly Gly Gln Glu Tyr Pro Gly Ala Ala Ala Arg Ser
85           90           95
Arg Pro Xaa Pro Xaa Thr Xaa Gln Arg Gln Xaa Xaa Xaa Arg Ser Ala
```

	100		105		110										
Met	Leu	Pro	Met	Ser	Asn	Pro	Ser	Ala	Asn	Pro	Thr	Gln	Leu	Thr	Ile
	115						120					125			
Phe	Tyr	Gly	Gly	Ser	Val	Cys	Val	Tyr	Asp	Ser	Gly	Ala	Thr	Arg	Lys
	130					135					140				
Gly	Ser	Gly	Asn	His	Ala	Tyr	Ser	Cys	Ser	Cys					
145					150					155					

(2) INFORMATION FOR SEQ ID NO:1009:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 155 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..155

(D) OTHER INFORMATION: / Ceres Seq. ID 1499414

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1009:

Pro	Leu	Ser	His	Ser	Thr	Pro	Thr	Phe	Thr	Cys	Ser	Cys	Arg	Glu	Gln
1			5						10					15	
Ala	Met	Ala	Pro	Asp	Leu	Ser	Glu	Leu	Ala	Ala	Ala	Ala	Pro	Ala	Arg
			20					25					30		
Gly	Ala	Tyr	Leu	Ala	Gly	Val	Gly	Val	Glu	Arg	Glu	Arg	Glu	Arg	Glu
		35				40						45			
Glu	Arg	Cys	Glu	Leu	Val	Arg	Trp	Ile	Gly	Trp	Arg	Ser	Gly	Thr	Leu
	50					55					60				
Arg	Xaa	Arg	Xaa	Arg	Arg	Met	Xaa	Xaa	Ala	Arg	Lys	Glu	Xaa	Glu	Arg
65					70				75					80	
Xaa	Glu	Glu	Ala	Gly	Asp	Arg	Asn	Thr	Gln	Glu	Pro	Gln	Gln	Gly	Gln
			85					90						95	
Gly	Leu	Xaa	Xaa	Xaa	Leu	Xaa	Asn	Gly	Ser	Xaa	Xaa	Xaa	Gly	Leu	Gln
			100					105					110		
Cys	Cys	Arg	Cys	Arg	Thr	Leu	Gln	Leu	Ile	Pro	His	Ser	Leu	Gln	Phe
		115					120					125			
Ser	Met	Val	Asp	Gln	Tyr	Val	Cys	Met	Thr	Arg	Val	Pro	Pro	Glu	Lys
	130					135					140				
Ala	Gln	Ala	Ile	Met	Leu	Ile	Ala	Ala	Ala	Ala					
145					150					155					

(2) INFORMATION FOR SEQ ID NO:1010:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 138 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..138

(D) OTHER INFORMATION: / Ceres Seq. ID 1499415

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1010:

Met	Ala	Pro	Asp	Leu	Ser	Glu	Leu	Ala	Ala	Ala	Ala	Pro	Ala	Arg	Gly
1				5					10					15	
Ala	Tyr	Leu	Ala	Gly	Val	Gly	Val	Glu	Arg	Glu	Arg	Glu	Arg	Glu	Glu
		20					25					30			
Arg	Cys	Glu	Leu	Val	Arg	Trp	Ile	Gly	Trp	Arg	Ser	Gly	Thr	Leu	Arg
		35				40						45			
Xaa	Arg	Xaa	Arg	Arg	Met	Xaa	Xaa	Ala	Arg	Lys	Glu	Xaa	Glu	Arg	Xaa
	50					55				60					
Glu	Glu	Ala	Gly	Asp	Arg	Asn	Thr	Gln	Glu	Pro	Gln	Gln	Gly	Gln	Gly
65					70					75				80	

Leu Xaa Xaa Xaa Leu Xaa Asn Gly Ser Xaa Xaa Xaa Gly Leu Gln Cys
85 90 95
Cys Arg Cys Arg Thr Leu Gln Leu Ile Pro His Ser Leu Gln Phe Ser
100 105 110
Met Val Asp Gln Tyr Val Cys Met Thr Arg Val Pro Pro Glu Lys Ala
115 120 125
Gln Ala Ile Met Leu Ile Ala Ala Ala
130 135

(2) INFORMATION FOR SEQ ID NO:1011:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 392 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..392
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499416

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1011:

cgtgccacac atccatcccc gttagcctct tctcctcct cctgccgggt ccttaataaa	60
gagcagcagc gcaagaggtt ggtagagcga gcgagaagaa ggcaatggcg gcggagagct	120
tcctgttcac ctccgaggtc gtgaacgarg ggcacccaga caagctgtgc gaccaggtgt	180
cggacgcggt gctggacgcc tgccctggcgc aggacccga cagcaaggtg gcctgcgaga	240
cctgcaccaa gacgaacatg gtgatgggtg tcggcgagat caccaccaag gcgagcgtgg	300
actacgagaa gatcgtdcgc gacacctgcc gcgagatcgg gttcacctcc gacgacgtgg	360
ggctcgacgc cgaccgctgc aargtgctgg tg	

(2) INFORMATION FOR SEQ ID NO:1012:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 47 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..47
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499417

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1012:

Arg Ala Thr His Pro Ser Pro Phe Ala Ser Ser Pro Pro Ser Cys Arg	
1 5 10 15	
Val Leu Asn Lys Glu Gln Gln Arg Lys Arg Leu Val Glu Arg Ala Arg	
20 25 30	
Arg Arg Gln Trp Arg Arg Arg Ala Ser Cys Ser Pro Arg Ser Pro	
35 40 45	

(2) INFORMATION FOR SEQ ID NO:1013:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 96 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..96
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499418

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1013:

Met Ala Ala Glu Ser Phe Leu Phe Thr Ser Glu Ser Val Asn Xaa Gly	
1 5 10 15	
His Pro Asp Lys Leu Cys Asp Gln Val Ser Asp Ala Val Leu Asp Ala	
20 25 30	

Cys	Leu	Ala	Gln	Asp	Pro	Asp	Ser	Lys	Val	Ala	Cys	Glu	Thr	Cys	Thr
	35						40					45			
Lys	Thr	Asn	Met	Val	Met	Val	Phe	Gly	Glu	Ile	Thr	Thr	Lys	Ala	Ser
	50					55					60				
Val	Asp	Tyr	Glu	Lys	Ile	Xaa	Arg	Asp	Thr	Cys	Arg	Glu	Ile	Gly	Phe
65					70					75				80	
Thr	Ser	Asp	Asp	Val	Gly	Leu	Asp	Ala	Asp	Arg	Cys	Xaa	Val	Leu	Val
				85					90					95	

(2) INFORMATION FOR SEQ ID NO:1014:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 486 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..486
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499422

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1014:

gaacaggttt	acaggcgcgc	tcccgcacgc	atgccccaac	ccttttttga	caagctcagc	60
gtccaccaact	aaatggcggc	ggagacaaaa	ccggctgcgg	ccatcggggg	tgccggcgag	120
atggaggtgg	aggcataccg	ccgcctattc	ccagtggcct	tcctggagcg	ccacctgggt	180
gagtcgcgtcc	gcatacgatgc	ccgccgcctg	aragaggccc	gcaccaccac	cgtcgcacctc	240
ggcgccgtgt	cctccgcgca	tggttccgct	ctcgccgcgc	ttggcgacac	cgccatgctc	300
gcgtcgggtca	agctcgagggt	gatgtcgccc	tcggccgagt	acccagacga	aggatccgtc	360
tctgttgagt	tccacatgcc	gcccactctgc	tccccgctgg	ttaggccagg	ccgatctgcg	420
gaggtggcac	cagtcactctc	caaggccctt	gaagacgttt	tggatgagtt	ccagaatgct	480
aaatttt						

(2) INFORMATION FOR SEQ ID NO:1015:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 69 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..69
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499423

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1015:

Asn	Arg	Phe	Thr	Gly	Ala	Leu	Pro	His	Ala	Cys	Pro	Asn	Pro	Phe	Leu
1				5					10					15	
Thr	Ser	Ser	Ala	Ser	Thr	Thr	Lys	Trp	Arg	Arg	Arg	Pro	Asn	Arg	Leu
			20				25					30			
Arg	Pro	Ser	Gly	Leu	Pro	Ala	Arg	Trp	Arg	Trp	Arg	His	Thr	Ala	Ala
		35				40					45				
Tyr	Ser	Gln	Trp	Pro	Ser	Trp	Ser	Ala	Thr	Trp	Val	Ser	Pro	Ser	Ala
	50				55					60					
Ser	Met	Pro	Ala	Ala											
65															

(2) INFORMATION FOR SEQ ID NO:1016:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 138 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide
(B) LOCATION: 1..138
(D) OTHER INFORMATION: / Ceres Seq. ID 1499424

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1016:

```
Met Ala Ala Glu Thr Lys Pro Ala Ala Ile Gly Val Ala Gly Glu
1      5      10      15
Met Glu Val Glu Ala Tyr Arg Arg Leu Phe Pro Val Ala Phe Leu Glu
      20      25      30
Arg His Leu Gly Glu Ser Val Arg Ile Asp Ala Arg Arg Leu Xaa Glu
      35      40      45
Ala Arg Thr Thr Thr Val Ala Leu Gly Ala Val Ser Ser Ala His Gly
      50      55      60
Ser Ala Leu Val Arg Val Gly Asp Thr Ala Met Leu Ala Ser Val Lys
65      70      75      80
Leu Glu Val Met Ser Pro Ser Ala Glu Tyr Pro Asp Glu Gly Ser Val
      85      90      95
Ser Val Glu Phe His Met Pro Pro Ile Cys Ser Pro Leu Val Arg Pro
      100     105     110
Gly Arg Ser Ala Glu Val Ala Pro Val Ile Ser Lys Ala Leu Glu Asp
      115     120     125
Val Leu Asp Glu Phe Gln Asn Ala Lys Phe
      130     135
```

(2) INFORMATION FOR SEQ ID NO:1017:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 122 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide
(B) LOCATION: 1..122
(D) OTHER INFORMATION: / Ceres Seq. ID 1499425

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1017:

```
Met Glu Val Glu Ala Tyr Arg Arg Leu Phe Pro Val Ala Phe Leu Glu
1      5      10      15
Arg His Leu Gly Glu Ser Val Arg Ile Asp Ala Arg Arg Leu Xaa Glu
      20      25      30
Ala Arg Thr Thr Thr Val Ala Leu Gly Ala Val Ser Ser Ala His Gly
      35      40      45
Ser Ala Leu Val Arg Val Gly Asp Thr Ala Met Leu Ala Ser Val Lys
      50      55      60
Leu Glu Val Met Ser Pro Ser Ala Glu Tyr Pro Asp Glu Gly Ser Val
65      70      75      80
Ser Val Glu Phe His Met Pro Pro Ile Cys Ser Pro Leu Val Arg Pro
      85      90      95
Gly Arg Ser Ala Glu Val Ala Pro Val Ile Ser Lys Ala Leu Glu Asp
      100     105     110
Val Leu Asp Glu Phe Gln Asn Ala Lys Phe
      115     120
```

(2) INFORMATION FOR SEQ ID NO:1018:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1617 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -
(B) LOCATION: 1..1617
(D) OTHER INFORMATION: / Ceres Seq. ID 1499446

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1018:

aaactgaaag	ttaggacctt	tcatttccaa	tctctaaacc	catttctcta	cgattagaga	60
agctgacatc	aaaattgaaa	cttggaatt	tttagatttg	ttcttcttct	atggcaactg	120
aagacgatgg	tgaattgtca	gctcgttacc	agaacacggt	ggatgcattg	tcgtctttga	180
tcacaaaacg	tggccgttta	gctagtaaca	accaatctca	ccgattccgt	ttgctctttc	240
attatctcaa	ggttcttgag	cttgaagatg	cagtttcaca	aatgaaaatc	attcatgtgg	300
ccggaactaa	aggaaagga	tcaacatgta	catttgcgga	gtctattctt	cgttgttacg	360
gtcttcgaac	tggctcttct	acatctcctc	acttaatcga	tgtccgagag	agattccgctc	420
ttaacggcat	tgagataagc	caggagaaat	ttgtgaacta	cttttggtgt	tcctttcata	480
agctcaagga	gaaaaccagc	aatgaggttg	atgttggtat	actagaagtt	ggcttaggtg	540
ggagattcga	tgcgactaat	gtgattcaga	aacctgtcgt	ctgtggtatt	tcttctctag	600
ggtatgacca	tatggagatt	cttgataca	cacttgctga	aattgctgca	gagaaagccg	660
gtatcttcaa	gagtggagtt	cctgctttta	cagtggctca	acctgatgaa	gcaatgcgtg	720
tactcaatga	aaaagcttca	aaattggagg	tgaatcttca	ggtggtggaa	ccgttggaact	780
caagccagag	actcgggctt	caaggcgaac	atcaatatct	aaacgctggt	cttgctgttg	840
cgttgtgctc	tacatttctt	aaagagattg	gtattgagga	caagaatggt	ttggatcaga	900
caaacggttt	acccgaaaaa	ttcatctctg	gattgtcaaa	tgcttatttg	atgggacgag	960
ctatgatagt	gcctgattca	gaactccctg	aagagattgt	gtattacctt	gatggagctc	1020
atagtcttga	aagcatggaa	gcttgcgcta	tatggttttc	aaaacagatc	aaacaaaacc	1080
aagaaagaaa	ccagaaaaga	tcagagcaga	tactcttggt	caattgtatg	tctgttcctg	1140
acccgagttt	gcttcttccg	cgattaagga	gtaaattgcat	tgatcaagga	gttgatttca	1200
agagagccgt	ttttgtgcca	aacgtatcag	tgtacaacca	agtgggatct	tcgacaaaacg	1260
ttggcacacg	tgctcgagtcg	atgtcgtggc	agttcggctc	tcagaggatt	tgggagagtt	1320
tagctcgagg	tgaagcaaaa	tctaattcaa	aaagtgattc	taaaggcaaa	gaagaagaga	1380
agagtttcgt	tttctcgtca	cttcctgtgg	ctgttgactg	gctccggggac	aatgctcgcc	1440
aaagtaaaca	agttcgtttt	caggtgttgg	taactggttc	attacatttg	gtgggtgatc	1500
tcttgagatt	tatcaagaaa	tgaatatggt	tctgccatgt	attcttggcc	aatctttgcc	1560
tgtaatgact	atatatctca	caacatgatt	taacaaaaga	aaagaaaaga	tatttcg	

(2) INFORMATION FOR SEQ ID NO:1019:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 470 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..470

(D) OTHER INFORMATION: / Ceres Seq. ID 1499447

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1019:

Met	Ala	Thr	Glu	Asp	Asp	Gly	Glu	Leu	Ser	Ala	Arg	Tyr	Gln	Asn	Thr
1				5				10						15	
Leu	Asp	Ala	Leu	Ser	Ser	Leu	Ile	Thr	Lys	Arg	Gly	Arg	Leu	Ala	Ser
			20					25					30		
Asn	Asn	Gln	Ser	His	Arg	Phe	Arg	Leu	Leu	Phe	His	Tyr	Leu	Lys	Val
		35					40				45				
Leu	Glu	Leu	Glu	Asp	Ala	Val	Ser	Gln	Met	Lys	Ile	Ile	His	Val	Ala
	50					55				60					
Gly	Thr	Lys	Gly	Lys	Gly	Ser	Thr	Cys	Thr	Phe	Ala	Glu	Ser	Ile	Leu
65				70					75					80	
Arg	Cys	Tyr	Gly	Leu	Arg	Thr	Gly	Leu	Phe	Thr	Ser	Pro	His	Leu	Ile
			85					90						95	
Asp	Val	Arg	Glu	Arg	Phe	Arg	Leu	Asn	Gly	Ile	Glu	Ile	Ser	Gln	Glu
		100					105						110		
Lys	Phe	Val	Asn	Tyr	Phe	Trp	Cys	Ser	Phe	His	Lys	Leu	Lys	Glu	Lys
		115					120						125		
Thr	Ser	Asn	Glu	Val	Asp	Val	Val	Ile	Leu	Glu	Val	Gly	Leu	Gly	Gly
	130					135					140				
Arg	Phe	Asp	Ala	Thr	Asn	Val	Ile	Gln	Lys	Pro	Val	Val	Cys	Gly	Ile
145					150				155					160	
Ser	Ser	Leu	Gly	Tyr	Asp	His	Met	Glu	Ile	Leu	Gly	Tyr	Thr	Leu	Ala

```

      165      170      175
Glu Ile Ala Ala Glu Lys Ala Gly Ile Phe Lys Ser Gly Val Pro Ala
      180      185      190
Phe Thr Val Ala Gln Pro Asp Glu Ala Met Arg Val Leu Asn Glu Lys
      195      200      205
Ala Ser Lys Leu Glu Val Asn Leu Gln Val Val Glu Pro Leu Asp Ser
      210      215      220
Ser Gln Arg Leu Gly Leu Gln Gly Glu His Gln Tyr Leu Asn Ala Gly
225      230      235      240
Leu Ala Val Ala Leu Cys Ser Thr Phe Leu Lys Glu Ile Gly Ile Glu
      245      250      255
Asp Lys Asn Gly Leu Asp Gln Thr Asn Gly Leu Pro Glu Lys Phe Ile
      260      265      270
Ser Gly Leu Ser Asn Ala Tyr Leu Met Gly Arg Ala Met Ile Val Pro
      275      280      285
Asp Ser Glu Leu Pro Glu Glu Ile Val Tyr Tyr Leu Asp Gly Ala His
290      295      300
Ser Pro Glu Ser Met Glu Ala Cys Ala Ile Trp Phe Ser Lys Gln Ile
305      310      315      320
Lys Gln Asn Gln Glu Arg Asn Gln Lys Arg Ser Glu Gln Ile Leu Leu
      325      330      335
Phe Asn Cys Met Ser Val Arg Asp Pro Ser Leu Leu Leu Pro Arg Leu
      340      345      350
Arg Ser Lys Cys Ile Asp Gln Gly Val Asp Phe Lys Arg Ala Val Phe
      355      360      365
Val Pro Asn Val Ser Val Tyr Asn Gln Val Gly Ser Ser Thr Asn Val
370      375      380
Gly Thr Arg Val Glu Ser Met Ser Trp Gln Phe Gly Leu Gln Arg Ile
385      390      395      400
Trp Glu Ser Leu Ala Arg Gly Glu Ala Lys Ser Asn Ser Lys Ser Asp
      405      410      415
Ser Lys Gly Lys Glu Glu Glu Lys Ser Phe Val Phe Ser Ser Leu Pro
      420      425      430
Val Ala Val Asp Trp Leu Arg Asp Asn Ala Arg Gln Ser Lys Gln Val
      435      440      445
Arg Phe Gln Val Leu Val Thr Gly Ser Leu His Leu Val Gly Asp Leu
450      455      460
Leu Arg Phe Ile Lys Lys
465      470

```

(2) INFORMATION FOR SEQ ID NO:1020:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 413 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..413

(D) OTHER INFORMATION: / Ceres Seq. ID 1499448

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1020:

```

Met Lys Ile Ile His Val Ala Gly Thr Lys Gly Lys Gly Ser Thr Cys
1      5      10      15
Thr Phe Ala Glu Ser Ile Leu Arg Cys Tyr Gly Leu Arg Thr Gly Leu
      20      25      30
Phe Thr Ser Pro His Leu Ile Asp Val Arg Glu Arg Phe Arg Leu Asn
      35      40      45
Gly Ile Glu Ile Ser Gln Glu Lys Phe Val Asn Tyr Phe Trp Cys Ser
50      55      60
Phe His Lys Leu Lys Glu Lys Thr Ser Asn Glu Val Asp Val Val Ile
65      70      75      80

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Leu Glu Val Gly Leu Gly Gly Arg Phe Asp Ala Thr Asn Val Ile Gln
      85                      90                      95
Lys Pro Val Val Cys Gly Ile Ser Ser Leu Gly Tyr Asp His Met Glu
      100                      105                      110
Ile Leu Gly Tyr Thr Leu Ala Glu Ile Ala Ala Glu Lys Ala Gly Ile
      115                      120                      125
Phe Lys Ser Gly Val Pro Ala Phe Thr Val Ala Gln Pro Asp Glu Ala
      130                      135                      140
Met Arg Val Leu Asn Glu Lys Ala Ser Lys Leu Glu Val Asn Leu Gln
      145                      150                      155                      160
Val Val Glu Pro Leu Asp Ser Ser Gln Arg Leu Gly Leu Gln Gly Glu
      165                      170                      175
His Gln Tyr Leu Asn Ala Gly Leu Ala Val Ala Leu Cys Ser Thr Phe
      180                      185                      190
Leu Lys Glu Ile Gly Ile Glu Asp Lys Asn Gly Leu Asp Gln Thr Asn
      195                      200                      205
Gly Leu Pro Glu Lys Phe Ile Ser Gly Leu Ser Asn Ala Tyr Leu Met
      210                      215                      220
Gly Arg Ala Met Ile Val Pro Asp Ser Glu Leu Pro Glu Glu Ile Val
      225                      230                      235                      240
Tyr Tyr Leu Asp Gly Ala His Ser Pro Glu Ser Met Glu Ala Cys Ala
      245                      250                      255
Ile Trp Phe Ser Lys Gln Ile Lys Gln Asn Gln Glu Arg Asn Gln Lys
      260                      265                      270
Arg Ser Glu Gln Ile Leu Leu Phe Asn Cys Met Ser Val Arg Asp Pro
      275                      280                      285
Ser Leu Leu Leu Pro Arg Leu Arg Ser Lys Cys Ile Asp Gln Gly Val
      290                      295                      300
Asp Phe Lys Arg Ala Val Phe Val Pro Asn Val Ser Val Tyr Asn Gln
      305                      310                      315                      320
Val Gly Ser Ser Thr Asn Val Gly Thr Arg Val Glu Ser Met Ser Trp
      325                      330                      335
Gln Phe Gly Leu Gln Arg Ile Trp Glu Ser Leu Ala Arg Gly Glu Ala
      340                      345                      350
Lys Ser Asn Ser Lys Ser Asp Ser Lys Gly Lys Glu Glu Lys Ser
      355                      360                      365
Phe Val Phe Ser Ser Leu Pro Val Ala Val Asp Trp Leu Arg Asp Asn
      370                      375                      380
Ala Arg Gln Ser Lys Gln Val Arg Phe Gln Val Leu Val Thr Gly Ser
      385                      390                      395                      400
Leu His Leu Val Gly Asp Leu Leu Arg Phe Ile Lys Lys
      405                      410

```

(2) INFORMATION FOR SEQ ID NO:1021:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 303 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..303
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499449

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1021:

```

Met Glu Ile Leu Gly Tyr Thr Leu Ala Glu Ile Ala Ala Glu Lys Ala
1      5                      10                      15
Gly Ile Phe Lys Ser Gly Val Pro Ala Phe Thr Val Ala Gln Pro Asp
      20                      25                      30
Glu Ala Met Arg Val Leu Asn Glu Lys Ala Ser Lys Leu Glu Val Asn
      35                      40                      45
Leu Gln Val Val Glu Pro Leu Asp Ser Ser Gln Arg Leu Gly Leu Gln

```


50	55	60
Gly Glu His Gln Tyr	Leu Asn Ala Gly Leu Ala	Val Ala Leu Cys Ser
65	70	75
Thr Phe Leu Lys Glu	Ile Gly Ile Glu Asp Lys	Asn Gly Leu Asp Gln
	85	90
Thr Asn Gly Leu Pro	Glu Lys Phe Ile Ser Gly	Leu Ser Asn Ala Tyr
	100	105
Leu Met Gly Arg Ala	Met Ile Val Pro Asp Ser	Glu Leu Pro Glu Glu
	115	120
Ile Val Tyr Tyr Leu	Asp Gly Ala His Ser Pro	Glu Ser Met Glu Ala
	130	135
Cys Ala Ile Trp Phe	Ser Lys Gln Ile Lys Gln	Asn Gln Glu Arg Asn
145	150	155
Gln Lys Arg Ser Glu	Gln Ile Leu Leu Phe Asn	Cys Met Ser Val Arg
	165	170
Asp Pro Ser Leu Leu	Leu Pro Arg Leu Arg Ser	Lys Cys Ile Asp Gln
	180	185
Gly Val Asp Phe Lys	Arg Ala Val Phe Val Pro	Asn Val Ser Val Tyr
	195	200
Asn Gln Val Gly Ser	Ser Thr Asn Val Gly Thr	Arg Val Glu Ser Met
	210	215
Ser Trp Gln Phe Gly	Leu Gln Arg Ile Trp Glu	Ser Leu Ala Arg Gly
225	230	235
Glu Ala Lys Ser Asn	Ser Lys Ser Asp Ser Lys	Gly Lys Glu Glu Glu
	245	250
Lys Ser Phe Val Phe	Ser Ser Leu Pro Val Ala	Val Asp Trp Leu Arg
	260	265
Asp Asn Ala Arg Gln	Ser Lys Gln Val Arg Phe	Gln Val Leu Val Thr
	275	280
Gly Ser Leu His Leu	Val Gly Asp Leu Leu Arg	Phe Ile Lys Lys
	290	295
		300

(2) INFORMATION FOR SEQ ID NO:1022:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1755 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1755
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499450

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1022:

atctcacaca	ccgaaagtta	ttttcgaatc	cactaacgaa	tcttcacag	caaaaaactt	60
tcgtgttcct	ctgtaatttc	tcagtatata	tagataccaa	atcgagcagt	gaaaaaatgg	120
ctatggcgag	tttatatcgg	cgatctcttc	cttctcctcc	ggccattgac	ttttcttccg	180
ccgaagaagn	ctaattcttc	atgaagcgct	tcagaaagga	actatggaag	gattttttcag	240
gttgatttcg	tatttttcaga	cacaatccga	acctgcgtat	tgtggtttgg	ctagtctctc	300
agtgggtgtg	aatgctcttt	ctatcgatcc	tggacgtaaa	tggaaagggc	cttgaggtg	360
gtttgatgaa	tcaatgttgg	attgctgcga	acctctggaa	gtagtgaagg	aaaaaggcat	420
ttcatttgga	aaagttgtct	gtttggctca	ttgttcagga	gcaaaagttg	aggctttccg	480
tacaagtcag	agcaccattg	atgattttcc	gcamayttgt	cgtgaaatgc	acgagttctg	540
agaattgcc	tatgatctca	acatatcaca	gaggtgtatt	taagcagact	gggactggtc	600
acttttcacc	tattggtggc	tataatgctg	agagagatat	ggctttgatt	cttgatgttg	660
ctcgtttcaa	gtatccccct	cactgggttc	ctcttaaaat	tctttgggaa	gccatggaca	720
gtattgatca	gtcaacaggg	aaacgtagag	ggttcattgct	catatctaga	ccacacagag	780
aaccggtatt	gctctatact	ctgagctgca	aggatgaaag	ctggatcgaa	atagccaagt	840
atttgaagga	agatgttcct	cgtcttgtaa	gttcacagca	tgtagattct	gtggagaaaa	900
tcatatcagt	tgtgttcaag	tcacttccat	caaatttcaa	ccaattcatc	agatgggtgg	960
ctgagatccg	aattacagag	gactcaaac	aaaatctcag	cgcagaggag	aagtctaggc	1020
tgaaactaaa	gcaattggtg	ctgaagggaag	tgcacgaaac	tgaactgttc	aaacacatca	1080

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ataagttctt atccacagtg ggttatgaag acagtctgac ttatgctgct gcaaaggctt 1140
gttgccaagg agctgaaatc ttatccggaa gctcatcaaa agagttttgt tgcgggaaa 1200
cttgcgtaga atgcatcaaa ggctctgatg actctgaagg cacagtgggtg actggagttg 1260
tgggtgcgtga tgggaatgaa caaaagggtg atctgttagt gccatcgacg caaactgagt 1320
gtgaatgtgg tcctgaagca acttatccag caggaaacga tgtgttctact gcacttctat 1380
tggctttacc tccacagaca tggtcaggga tcaaagacca agctcttatg catgaaatga 1440
agcagctcat ttccatggct tccctcccaa ctttgcttca agaagaggta ttgcatcttc 1500
gacggcaact tcagctgcta aaacgatgcc aagagaacaa ggaagaggat gatctcgctg 1560
ctcctgccta ttagttcatt gtcccaaate cactctcttc cccatttgaa tcccacgttc 1620
tcaacacttg attgttagaa agtctcttta ttgtctgtac gattcaaact ctatttgcaa 1680
tgagagatat ttgtaaacad attcattcta tgaattgtta atcacataaa gtaaagaatc 1740
ttagaatcat atttc
```

(2) INFORMATION FOR SEQ ID NO:1023:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 357 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..357

(D) OTHER INFORMATION: / Ceres Seq. ID 1499451

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1023:

```
Met Ile Phe Arg Xaa Xaa Val Val Lys Cys Thr Ser Ser Glu Asn Cys
1           5           10           15
His Met Ile Ser Thr Tyr His Arg Gly Val Phe Lys Gln Thr Gly Thr
20           25           30
Gly His Phe Ser Pro Ile Gly Gly Tyr Asn Ala Glu Arg Asp Met Ala
35           40           45
Leu Ile Leu Asp Val Ala Arg Phe Lys Tyr Pro Pro His Trp Val Pro
50           55           60
Leu Lys Leu Leu Trp Glu Ala Met Asp Ser Ile Asp Gln Ser Thr Gly
65           70           75           80
Lys Arg Arg Gly Phe Met Leu Ile Ser Arg Pro His Arg Glu Pro Gly
85           90           95
Leu Leu Tyr Thr Leu Ser Cys Lys Asp Glu Ser Trp Ile Glu Ile Ala
100          105          110
Lys Tyr Leu Lys Glu Asp Val Pro Arg Leu Val Ser Ser Gln His Val
115          120          125
Asp Ser Val Glu Lys Ile Ile Ser Val Val Phe Lys Ser Leu Pro Ser
130          135          140
Asn Phe Asn Gln Phe Ile Arg Trp Val Ala Glu Ile Arg Ile Thr Glu
145          150          155          160
Asp Ser Asn Gln Asn Leu Ser Ala Glu Glu Lys Ser Arg Leu Lys Leu
165          170          175
Lys Gln Leu Val Leu Lys Glu Val His Glu Thr Glu Leu Phe Lys His
180          185          190
Ile Asn Lys Phe Leu Ser Thr Val Gly Tyr Glu Asp Ser Leu Thr Tyr
195          200          205
Ala Ala Ala Lys Ala Cys Cys Gln Gly Ala Glu Ile Leu Ser Gly Ser
210          215          220
Ser Ser Lys Glu Phe Cys Cys Arg Glu Thr Cys Val Lys Cys Ile Lys
225          230          235          240
Gly Pro Asp Asp Ser Glu Gly Thr Val Val Thr Gly Val Val Val Arg
245          250          255
Asp Gly Asn Glu Gln Lys Val Asp Leu Val Pro Ser Thr Gln Thr
260          265          270
Glu Cys Glu Cys Gly Pro Glu Ala Thr Tyr Pro Ala Gly Asn Asp Val
275          280          285
Phe Thr Ala Leu Leu Leu Ala Leu Pro Pro Gln Thr Trp Ser Gly Ile
```

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290	295	300
Lys Asp Gln Ala Leu Met His Glu Met Lys Gln Leu Ile Ser Met Ala		
305	310	315
Ser Leu Pro Thr Leu Leu Gln Glu Glu Val Leu His Leu Arg Arg Gln		
	325	330
Leu Gln Leu Leu Lys Arg Cys Gln Glu Asn Lys Glu Glu Asp Asp Leu		
	340	345
Ala Ala Pro Ala Tyr		350
355		

(2) INFORMATION FOR SEQ ID NO:1024:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 340 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..340

(D) OTHER INFORMATION: / Ceres Seq. ID 1499452

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1024:

Met	Ile	Ser	Thr	Tyr	His	Arg	Gly	Val	Phe	Lys	Gln	Thr	Gly	Thr	Gly
1				5					10					15	
His	Phe	Ser	Pro	Ile	Gly	Gly	Tyr	Asn	Ala	Glu	Arg	Asp	Met	Ala	Leu
			20					25					30		
Ile	Leu	Asp	Val	Ala	Arg	Phe	Lys	Tyr	Pro	Pro	His	Trp	Val	Pro	Leu
		35					40					45			
Lys	Leu	Leu	Trp	Glu	Ala	Met	Asp	Ser	Ile	Asp	Gln	Ser	Thr	Gly	Lys
	50					55				60					
Arg	Arg	Gly	Phe	Met	Leu	Ile	Ser	Arg	Pro	His	Arg	Glu	Pro	Gly	Leu
65				70					75					80	
Leu	Tyr	Thr	Leu	Ser	Cys	Lys	Asp	Glu	Ser	Trp	Ile	Glu	Ile	Ala	Lys
			85					90						95	
Tyr	Leu	Lys	Glu	Asp	Val	Pro	Arg	Leu	Val	Ser	Ser	Gln	His	Val	Asp
		100						105					110		
Ser	Val	Glu	Lys	Ile	Ile	Ser	Val	Val	Phe	Lys	Ser	Leu	Pro	Ser	Asn
	115						120					125			
Phe	Asn	Gln	Phe	Ile	Arg	Trp	Val	Ala	Glu	Ile	Arg	Ile	Thr	Glu	Asp
	130					135					140				
Ser	Asn	Gln	Asn	Leu	Ser	Ala	Glu	Glu	Lys	Ser	Arg	Leu	Lys	Leu	Lys
145				150					155					160	
Gln	Leu	Val	Leu	Lys	Glu	Val	His	Glu	Thr	Glu	Leu	Phe	Lys	His	Ile
			165					170						175	
Asn	Lys	Phe	Leu	Ser	Thr	Val	Gly	Tyr	Glu	Asp	Ser	Leu	Thr	Tyr	Ala
		180						185					190		
Ala	Ala	Lys	Ala	Cys	Cys	Gln	Gly	Ala	Glu	Ile	Leu	Ser	Gly	Ser	Ser
	195					200					205				
Ser	Lys	Glu	Phe	Cys	Cys	Arg	Glu	Thr	Cys	Val	Lys	Cys	Ile	Lys	Gly
	210					215					220				
Pro	Asp	Asp	Ser	Glu	Gly	Thr	Val	Val	Thr	Gly	Val	Val	Val	Arg	Asp
225				230						235				240	
Gly	Asn	Glu	Gln	Lys	Val	Asp	Leu	Leu	Val	Pro	Ser	Thr	Gln	Thr	Glu
			245						250					255	
Cys	Glu	Cys	Gly	Pro	Glu	Ala	Thr	Tyr	Pro	Ala	Gly	Asn	Asp	Val	Phe
	260							265					270		
Thr	Ala	Leu	Leu	Ala	Leu	Pro	Pro	Gln	Thr	Trp	Ser	Gly	Ile	Lys	
	275					280					285				
Asp	Gln	Ala	Leu	Met	His	Glu	Met	Lys	Gln	Leu	Ile	Ser	Met	Ala	Ser
	290					295					300				
Leu	Pro	Thr	Leu	Leu	Gln	Glu	Glu	Val	Leu	His	Leu	Arg	Arg	Gln	Leu
305					310					315					320

Gln Leu Leu Lys Arg Cys Gln Glu Asn Lys Glu Glu Asp Asp Leu Ala
325 330 335
Ala Pro Ala Tyr
340

(2) INFORMATION FOR SEQ ID NO:1025:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 311 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..311

(D) OTHER INFORMATION: / Ceres Seq. ID 1499453

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1025:

Met Ala Leu Ile Leu Asp Val Ala Arg Phe Lys Tyr Pro Pro His Trp
1 5 10 15
Val Pro Leu Lys Leu Leu Trp Glu Ala Met Asp Ser Ile Asp Gln Ser
20 25 30
Thr Gly Lys Arg Arg Gly Phe Met Leu Ile Ser Arg Pro His Arg Glu
35 40 45
Pro Gly Leu Leu Tyr Thr Leu Ser Cys Lys Asp Glu Ser Trp Ile Glu
50 55 60
Ile Ala Lys Tyr Leu Lys Glu Asp Val Pro Arg Leu Val Ser Ser Gln
65 70 75 80
His Val Asp Ser Val Glu Lys Ile Ile Ser Val Val Phe Lys Ser Leu
85 90 95
Pro Ser Asn Phe Asn Gln Phe Ile Arg Trp Val Ala Glu Ile Arg Ile
100 105 110
Thr Glu Asp Ser Asn Gln Asn Leu Ser Ala Glu Glu Lys Ser Arg Leu
115 120 125
Lys Leu Lys Gln Leu Val Leu Lys Glu Val His Glu Thr Glu Leu Phe
130 135 140
Lys His Ile Asn Lys Phe Leu Ser Thr Val Gly Tyr Glu Asp Ser Leu
145 150 155 160
Thr Tyr Ala Ala Ala Lys Ala Cys Cys Gln Gly Ala Glu Ile Leu Ser
165 170 175
Gly Ser Ser Ser Lys Glu Phe Cys Cys Arg Glu Thr Cys Val Lys Cys
180 185 190
Ile Lys Gly Pro Asp Asp Ser Glu Gly Thr Val Val Thr Gly Val Val
195 200 205
Val Arg Asp Gly Asn Glu Gln Lys Val Asp Leu Leu Val Pro Ser Thr
210 215 220
Gln Thr Glu Cys Glu Cys Gly Pro Glu Ala Thr Tyr Pro Ala Gly Asn
225 230 235 240
Asp Val Phe Thr Ala Leu Leu Leu Ala Leu Pro Pro Gln Thr Trp Ser
245 250 255
Gly Ile Lys Asp Gln Ala Leu Met His Glu Met Lys Gln Leu Ile Ser
260 265 270
Met Ala Ser Leu Pro Thr Leu Leu Gln Glu Glu Val Leu His Leu Arg
275 280 285
Arg Gln Leu Gln Leu Leu Lys Arg Cys Gln Glu Asn Lys Glu Glu Asp
290 295 300
Asp Leu Ala Ala Pro Ala Tyr
305 310

(2) INFORMATION FOR SEQ ID NO:1026:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1283 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

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      (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
      (A) NAME/KEY: -
      (B) LOCATION: 1..1283
      (D) OTHER INFORMATION: / Ceres Seq. ID 1499458

```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1026:

gaaggaccag	acccgagaga	agttgagctg	tatgtggaag	agatactgtc	actgatgcag	60
ttgggtgagg	actataccga	gttcatggtg	tcaaaaatca	agtctttgac	gtcggtagat	120
cctgaattgt	tgccaacggc	tacaaaggca	tttagaaata	agagttttag	caaagcgatt	180
caggatgtga	cgagatatta	tgttatacta	gaagggttct	ttatggttga	gaatgtgagg	240
aaagctatta	ggatcgatga	gcattgtacc	gacagcctta	ccacttcaat	ggtaggacgat	300
gtgtcttacg	tgttgcagag	ttgtctgagg	agagcgattt	caacttcaaa	cataagttct	360
gtgatttgctg	tggtgagcta	tgctgtgtagc	ttgttgggca	atgattacca	tgaagctcta	420
caacagaaga	ttagagagcc	taaccttggg	gctagggttg	tcttgggttg	tataggatatg	480
gaaaacaccg	gaactgagat	tgcaactgct	ttgaacaata	tggacgtgag	ctgcgagtac	540
attctcaaac	taaaacatga	aatcgaggag	caatgtactg	aggattttcc	tgcaccagca	600
gatcgagaga	ggataaaatc	atgtctatcc	gagctaggcg	agttaagcag	cacgttcaag	660
cagttactca	actcaggcat	ggaacagcta	gtagcaaccg	taacacagta	aatccgtccg	720
gttctagaca	ccgtggctac	cataagctac	gagttaacag	aaaccgagta	cgcagagaat	780
gaggtgaacg	acccttgggt	ccaaagactt	ctccactcag	tcgaacaaaa	tgcgcgtgg	840
ctccaaccac	taatgacatc	caacaactac	gactcgtttc	tgcattctcat	aattgatttc	900
atagttaaga	gactcgaagt	cataatgatg	cagaaacggg	ttanccagct	tggtagggctt	960
cagcttgatc	gagacacaag	ggctttgggt	agccattttct	cgggtatgac	tcaaagaaca	1020
gtgagagata	agtttgctcg	gttaacgcag	atggcgacga	tactgaactt	ggaaaaggctc	1080
tcagagattt	tggacttttg	gggagaaaac	tcaggaccca	tgacttggag	actcacacca	1140
gctgaggtta	gacgggtttt	gggtctccgg	gtcgagttca	aaccgcgaatc	aattgctgct	1200
ctcaagttgt	gatgttactt	cttttcttta	ttatgtcatc	tacacaactc	gaaccaatttc	1260
tttcgaaatc	tgattgggttc	ccc				

(2) INFORMATION FOR SEQ ID NO:1027:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 403 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..403

(D) OTHER INFORMATION: / Ceres Seq. ID 1499459

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1027:

Glu	Gly	Pro	Asp	Pro	Arg	Glu	Val	Glu	Leu	Tyr	Val	Glu	Glu	Ile	Leu
1				5					10					15	
Ser	Leu	Met	Gln	Leu	Gly	Glu	Asp	Tyr	Thr	Glu	Phe	Met	Val	Ser	Lys
			20					25					30		
Ile	Lys	Ser	Leu	Thr	Ser	Val	Asp	Pro	Glu	Leu	Leu	Pro	Thr	Ala	Thr
			35				40					45			
Lys	Ala	Phe	Arg	Asn	Lys	Ser	Phe	Ser	Lys	Ala	Ile	Gln	Asp	Val	Thr
	50					55					60				
Arg	Tyr	Tyr	Val	Ile	Leu	Glu	Gly	Phe	Phe	Met	Val	Glu	Asn	Val	Arg
65				70						75					80
Lys	Ala	Ile	Arg	Ile	Asp	Glu	His	Val	Pro	Asp	Ser	Leu	Thr	Thr	Ser
				85					90					95	
Met	Val	Asp	Asp	Val	Phe	Tyr	Val	Leu	Gln	Ser	Cys	Leu	Arg	Arg	Ala
			100					105					110		
Ile	Ser	Thr	Ser	Asn	Ile	Ser	Ser	Val	Ile	Ala	Val	Leu	Ser	Tyr	Ala
			115				120					125			
Gly	Ser	Leu	Leu	Gly	Asn	Asp	Tyr	His	Glu	Ala	Leu	Gln	Gln	Lys	Ile
	130					135					140				
Arg	Glu	Pro	Asn	Leu	Gly	Ala	Arg	Leu	Phe	Leu	Gly	Gly	Ile	Gly	Met
145				150						155					160

Glu Asn Thr Gly Thr Glu Ile Ala Thr Ala Leu Asn Asn Met Asp Val
165 170 175
Ser Cys Glu Tyr Ile Leu Lys Leu Lys His Glu Ile Glu Glu Gln Cys
180 185 190
Thr Glu Val Phe Pro Ala Pro Ala Asp Arg Glu Arg Ile Lys Ser Cys
195 200 205
Leu Ser Glu Leu Gly Glu Leu Ser Ser Thr Phe Lys Gln Leu Leu Asn
210 215 220
Ser Gly Met Glu Gln Leu Val Ala Thr Val Thr Pro Arg Ile Arg Pro
225 230 235 240
Val Leu Asp Thr Val Ala Thr Ile Ser Tyr Glu Leu Thr Glu Thr Glu
245 250 255
Tyr Ala Glu Asn Glu Val Asn Asp Pro Trp Val Gln Arg Leu Leu His
260 265 270
Ser Val Glu Thr Asn Ala Ala Trp Leu Gln Pro Leu Met Thr Ser Asn
275 280 285
Asn Tyr Asp Ser Phe Leu His Leu Ile Ile Asp Phe Ile Val Lys Arg
290 295 300
Leu Glu Val Ile Met Met Gln Lys Arg Phe Xaa Gln Leu Gly Gly Leu
305 310 315 320
Gln Leu Asp Arg Asp Thr Arg Ala Leu Val Ser His Phe Ser Gly Met
325 330 335
Thr Gln Arg Thr Val Arg Asp Lys Phe Ala Arg Leu Thr Gln Met Ala
340 345 350
Thr Ile Leu Asn Leu Glu Lys Val Ser Glu Ile Leu Asp Phe Trp Gly
355 360 365
Glu Asn Ser Gly Pro Met Thr Trp Arg Leu Thr Pro Ala Glu Val Arg
370 375 380
Arg Val Leu Gly Leu Arg Val Glu Phe Lys Pro Glu Ser Ile Ala Ala
385 390 395 400
Leu Lys Leu

(2) INFORMATION FOR SEQ ID NO:1028:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 385 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..385

(D) OTHER INFORMATION: / Ceres Seq. ID 1499460

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1028:

Met Gln Leu Gly Glu Asp Tyr Thr Glu Phe Met Val Ser Lys Ile Lys
1 5 10 15
Ser Leu Thr Ser Val Asp Pro Glu Leu Leu Pro Thr Ala Thr Lys Ala
20 25 30
Phe Arg Asn Lys Ser Phe Ser Lys Ala Ile Gln Asp Val Thr Arg Tyr
35 40 45
Tyr Val Ile Leu Glu Gly Phe Phe Met Val Glu Asn Val Arg Lys Ala
50 55 60
Ile Arg Ile Asp Glu His Val Pro Asp Ser Leu Thr Thr Ser Met Val
65 70 75 80
Asp Asp Val Phe Tyr Val Leu Gln Ser Cys Leu Arg Arg Ala Ile Ser
85 90 95
Thr Ser Asn Ile Ser Ser Val Ile Ala Val Leu Ser Tyr Ala Gly Ser
100 105 110
Leu Leu Gly Asn Asp Tyr His Glu Ala Leu Gln Gln Lys Ile Arg Glu
115 120 125
Pro Asn Leu Gly Ala Arg Leu Phe Leu Gly Gly Ile Gly Met Glu Asn

130	135	140
Thr Gly Thr Glu Ile Ala Thr Ala Leu Asn Asn Met Asp Val Ser Cys		
145	150	155
Glu Tyr Ile Leu Lys Leu Lys His Glu Ile Glu Glu Gln Cys Thr Glu		160
	165	170
Val Phe Pro Ala Pro Ala Asp Arg Glu Arg Ile Lys Ser Cys Leu Ser		175
	180	185
Glu Leu Gly Glu Leu Ser Ser Thr Phe Lys Gln Leu Leu Asn Ser Gly		190
	195	200
Met Glu Gln Leu Val Ala Thr Val Thr Pro Arg Ile Arg Pro Val Leu		205
	210	215
Asp Thr Val Ala Thr Ile Ser Tyr Glu Leu Thr Glu Thr Glu Tyr Ala		220
225	230	235
Glu Asn Glu Val Asn Asp Pro Trp Val Gln Arg Leu Leu His Ser Val		240
	245	250
Glu Thr Asn Ala Ala Trp Leu Gln Pro Leu Met Thr Ser Asn Asn Tyr		255
	260	265
Asp Ser Phe Leu His Leu Ile Ile Asp Phe Ile Val Lys Arg Leu Glu		270
	275	280
Val Ile Met Met Gln Lys Arg Phe Xaa Gln Leu Gly Gly Leu Gln Leu		285
290	295	300
Asp Arg Asp Thr Arg Ala Leu Val Ser His Phe Ser Gly Met Thr Gln		310
305	315	320
Arg Thr Val Arg Asp Lys Phe Ala Arg Leu Thr Gln Met Ala Thr Ile		325
	330	335
Leu Asn Leu Glu Lys Val Ser Glu Ile Leu Asp Phe Trp Gly Glu Asn		340
	345	350
Ser Gly Pro Met Thr Trp Arg Leu Thr Pro Ala Glu Val Arg Arg Val		355
	360	365
Leu Gly Leu Arg Val Glu Phe Lys Pro Glu Ser Ile Ala Ala Leu Lys		370
	375	380

Leu
385

(2) INFORMATION FOR SEQ ID NO:1029:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 375 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..375

(D) OTHER INFORMATION: / Ceres Seq. ID 1499461

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1029:

Met Val Ser Lys Ile Lys Ser Leu Thr Ser Val Asp Pro Glu Leu Leu		
1	5	10
Pro Thr Ala Thr Lys Ala Phe Arg Asn Lys Ser Phe Ser Lys Ala Ile		15
	20	25
Gln Asp Val Thr Arg Tyr Tyr Val Ile Leu Glu Gly Phe Phe Met Val		30
	35	40
Glu Asn Val Arg Lys Ala Ile Arg Ile Asp Glu His Val Pro Asp Ser		45
	50	55
Leu Thr Thr Ser Met Val Asp Asp Val Phe Tyr Val Leu Gln Ser Cys		60
65	70	75
Leu Arg Arg Ala Ile Ser Thr Ser Asn Ile Ser Ser Val Ile Ala Val		80
	85	90
Leu Ser Tyr Ala Gly Ser Leu Leu Gly Asn Asp Tyr His Glu Ala Leu		95
	100	105
Gln Gln Lys Ile Arg Glu Pro Asn Leu Gly Ala Arg Leu Phe Leu Gly		110
	115	120
		125

Gly Ile Gly Met Glu Asn Thr Gly Thr Glu Ile Ala Thr Ala Leu Asn
130 135 140
Asn Met Asp Val Ser Cys Glu Tyr Ile Leu Lys Leu Lys His Glu Ile
145 150 155 160
Glu Glu Gln Cys Thr Glu Val Phe Pro Ala Pro Ala Asp Arg Glu Arg
165 170 175
Ile Lys Ser Cys Leu Ser Glu Leu Gly Glu Leu Ser Ser Thr Phe Lys
180 185 190
Gln Leu Leu Asn Ser Gly Met Glu Gln Leu Val Ala Thr Val Thr Pro
195 200 205
Arg Ile Arg Pro Val Leu Asp Thr Val Ala Thr Ile Ser Tyr Glu Leu
210 215 220
Thr Glu Thr Glu Tyr Ala Glu Asn Glu Val Asn Asp Pro Trp Val Gln
225 230 235 240
Arg Leu Leu His Ser Val Glu Thr Asn Ala Ala Trp Leu Gln Pro Leu
245 250 255
Met Thr Ser Asn Asn Tyr Asp Ser Phe Leu His Leu Ile Ile Asp Phe
260 265 270
Ile Val Lys Arg Leu Glu Val Ile Met Met Gln Lys Arg Phe Xaa Gln
275 280 285
Leu Gly Gly Leu Gln Leu Asp Arg Asp Thr Arg Ala Leu Val Ser His
290 295 300
Phe Ser Gly Met Thr Gln Arg Thr Val Arg Asp Lys Phe Ala Arg Leu
305 310 315 320
Thr Gln Met Ala Thr Ile Leu Asn Leu Glu Lys Val Ser Glu Ile Leu
325 330 335
Asp Phe Trp Gly Glu Asn Ser Gly Pro Met Thr Trp Arg Leu Thr Pro
340 345 350
Ala Glu Val Arg Arg Val Leu Gly Leu Arg Val Glu Phe Lys Pro Glu
355 360 365
Ser Ile Ala Ala Leu Lys Leu
370 375

(2) INFORMATION FOR SEQ ID NO:1030:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 348 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..348
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499462

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1030:

atattattca cgatttctcat caaatcatct ccgataactca caaccgaaat aactaacc	60
tcctcaacaa aaaacaacaa aacatgtaca ctccatcata cttaaaatat tcaataatct	120
caattatata cgtattattc ctccaaggaa ctcatggaga cgacggaggt tggcaagggtg	180
gtcacgccgt aaaacgtggc gtgaccacct tgccaacctc cgtcgtccct tattaataatt	240
acctgccagt ttacttttct ctcttcttgt tttctgtgtt ggaagattct caagttattt	300
attccgcaaa aaacggttta tcatttacaa ttagttgaat tttggtcg	

(2) INFORMATION FOR SEQ ID NO:1031:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..34
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499463

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1031:

Ile Leu Phe Thr
1 5 10 15
Ile Thr Asn Pro Ser Ser Thr Lys Asn Asn Lys Thr Cys Thr Leu His
20 25 30
His Thr

(2) INFORMATION FOR SEQ ID NO:1032:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..50
(D) OTHER INFORMATION: / Ceres Seq. ID 1499464

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1032:

[illegible]

(2) INFORMATION FOR SEQ ID NO:1033:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1004 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
(B) LOCATION: 1..1004
(D) OTHER INFORMATION: / Ceres Seq. ID 1499465

(xi) SEQUENCE DESCRIPTION: SEO ID NO:1033:

aagagacaaa	agaaaaaaa	atctttttct	ttctgtatga	atcgtatcta	ttagctatga	60
gcctgaggtg	atgatcatgt	caacataacc	atcaacgttc	taccatggct	agtcctagca	120
acaaaggcaa	aggcatagca	gaaggatcgt	ctcaaccgca	atcgcaaccg	caaccacaac	180
cacaccaact	gcaatcacct	cctaaccgcg	cagcgtaaag	ccggtacgag	tcacagaaac	240
gacgagactg	gaacacgttt	tgtcaatacc	tgcgtaacca	acagccaccg	gttcacatct	300
cgcagtggtg	atcaaacccac	atcctcgatt	tcctccaata	tctcgaccag	tttggaaga	360
caaaggttca	tatccatgga	tgcgttttct	tcggacaggt	tgagccagcg	ggacagtgtg	420
actgtccttt	aaaacaagcg	tggggagatt	tagatgcttt	gatcggacgg	ctaaagcgg	480
ctttcgagga	gaacggagga	ttggcggaga	gaaacccttt	tgccggcggc	ggaattaggg	540
tttttctgag	ggaagtgaga	gattcacagg	cgaaggcaag	aggagtccg	tacaagaaaa	600
gaaaaaagag	gaagaagagg	aatcctatga	agagtcatga	tggtgaagat	ggtactacgg	660
gaactagtag	tagctccaac	ttggcttctt	agcgggaagca	aacaaaaaat	ctataataaa	720
acaaaagtgg	aattagttaa	tggtaaagcat	ttaatactct	ccataatctc	tattaattttt	780
cagtacttta	atcctatttt	gtgatctatt	tacaatttta	catatagagt	gaaaagaaac	840
aattctacat	ttgtttcttg	atagtcagct	cttaatgcat	agttgaattt	tatacgtatc	900
atacccaaac	tataagatta	actttgatct	tagatcatat	acatatatca	tcatgggtgtg	960
taccctaagt	ttcataatca	tttttcttaa	ctattttatgt	qqat		

(2) INFORMATION FOR SEO ID NO:1034:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 195 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:

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      (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:

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(A) NAME/KEY: peptide
(B) LOCATION: 1..195
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(D) OTHER INFORMATION: / Ceres Seq. ID 1499466

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1034:

[illegible]

(2) INFORMATION FOR SEQ ID NO:1035:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1049 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1049

(D) OTHER INFORMATION: / Ceres Seq. ID 1499467

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1035:

actttgtaat	aataaccaca	acttcccaat	cttcttcac	agattttgct	agttcgtcac	60
acacacggat	caacgtcatc	atcttctctt	cttcttctcc	acaagcccac	ctacaatttc	120
catttcgccg	cttcctctgt	tcccacttac	atcaattccg	ctcgatttcg	aatttcgagc	180
tcaatcttcc	ctttggatcg	aagaagaaga	agaagaatct	ggtctgtctc	tggctttaaa	240
tctatggccg	atttagtaaa	aaccaatgct	cgcagagacg	gtgaagaacg	atttcaagcg	300
cttgagcaag	aggctttcat	caataattcg	tctccggagc	tccagaacga	gttggtatcc	360
gacgccggag	gtgggattga	agcaatcgct	aatcgctcga	ctgcattttt	gtcaaatggc	420
agagcaaagt	gattgtagca	gctctgtttg	gatccgtttc	gcttctacga	catgatggtg	480
cagctttgtg	ggctgtgatt	ggatcggttt	caaattccgt	gctctcagta	gctttgaaac	540
gtatacttaa	ccaagagaga	cctgttgcta	ctctccgttc	tgatcctggg	atgccttctt	600
ctcatgccca	atccatttct	ttcatctctg	tgttttctgt	cttctccggt	atggagtggc	660
ttggaaccaa	tgtactctct	ctgttcctta	gcggcttcac	cctcgcattg	ggttcttatt	720
tcacgtgggt	aagggttttc	cagaagcttc	acacgacaa	tcaagtggtc	gtaggtgcaa	780
tcgtgggttc	tgtttactcc	accttatggt	atgtaacttg	gaactctctt	gttcttgaag	840
cctttacctc	aacattctca	gtacaaatag	ctgtctttct	ggttgctgct	gcgtctgctt	900
taggttttgc	agtttatgtg	ctacttaact	ggtttaaaga	tgacagatga	cagatgcacg	960

aatgataatt ttacgtactt aggatgtata aggaatgcat ttgattctcc ttataattca 1020
tattgattga gctattttta cattcaatg

(2) INFORMATION FOR SEQ ID NO:1036:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 78 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..78
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499468

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1036:

Phe	Val	Ile	Ile	Thr	Thr	Thr	Ser	Gln	Ser	Ser	Ser	Ser	Asp	Phe	Ala
1				5				10						15	
Ser	Ser	Ser	His	Thr	Arg	Ile	Asn	Val	Ile	Ile	Phe	Ser	Ser	Ser	Ser
			20				25					30			
Pro	Gln	Ala	His	Leu	Gln	Phe	Pro	Phe	Arg	Arg	Phe	Leu	Cys	Ser	His
		35				40					45				
Leu	His	Gln	Phe	Arg	Ser	Ile	Ser	Asn	Phe	Glu	Leu	Asn	Leu	Pro	Phe
	50					55				60					
Gly	Ser	Lys	Lys	Lys	Lys	Lys	Asn	Leu	Val	Cys	Leu	Trp	Leu		
65				70						75					

(2) INFORMATION FOR SEQ ID NO:1037:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 119 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..119
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499469

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1037:

Met	Pro	Ser	Ser	His	Ala	Gln	Ser	Ile	Ser	Phe	Ile	Ser	Val	Phe	Ser
1				5				10						15	
Val	Phe	Ser	Val	Met	Glu	Trp	Leu	Gly	Thr	Asn	Val	Leu	Ser	Leu	Phe
			20				25					30			
Leu	Ser	Gly	Phe	Ile	Leu	Ala	Leu	Gly	Ser	Tyr	Phe	Thr	Trp	Leu	Arg
		35				40				45					
Val	Ser	Gln	Lys	Leu	His	Thr	Ser	Gln	Val	Val	Val	Gly	Ala	Ile	
	50					55				60					
Val	Gly	Ser	Val	Tyr	Ser	Thr	Leu	Trp	Tyr	Val	Thr	Trp	Asn	Ser	Leu
65				70						75				80	
Val	Leu	Glu	Ala	Phe	Thr	Ser	Thr	Phe	Ser	Val	Gln	Ile	Ala	Val	Phe
			85					90					95		
Leu	Val	Ala	Ala	Ala	Ser	Ala	Leu	Gly	Phe	Ala	Val	Tyr	Val	Leu	Leu
			100				105						110		
Asn	Trp	Phe	Lys	Asp	Asp	Arg									

(2) INFORMATION FOR SEQ ID NO:1038:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 99 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide

(B) LOCATION: 1..99

(D) OTHER INFORMATION: / Ceres Seq. ID 1499470

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1038:

Met Glu Trp Leu Gly Thr Asn Val Leu Ser Leu Phe Leu Ser Gly Phe
1 5 10 15
Ile Leu Ala Leu Gly Ser Tyr Phe Thr Trp Leu Arg Val Ser Gln Lys
20 25 30
Leu His Thr Thr Ser Gln Val Val Val Gly Ala Ile Val Gly Ser Val
35 40 45
Tyr Ser Thr Leu Trp Tyr Val Thr Trp Asn Ser Leu Val Leu Glu Ala
50 55 60
Phe Thr Ser Thr Phe Ser Val Gln Ile Ala Val Phe Leu Val Ala Ala
65 70 75 80
Ala Ser Ala Leu Gly Phe Ala Val Tyr Val Leu Leu Asn Trp Phe Lys
85 90 95
Asp Asp Arg

(2) INFORMATION FOR SEQ ID NO:1039:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1232 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1232

(D) OTHER INFORMATION: / Ceres Seq. ID 1499474

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1039:

tcttcttctt ccacacagct agaaacacag tctctctatc ttctgagcaa aaaaatggaa 60
gtggctcttc tatnvtcttc ttcttctctg tctctctctc gtcaccagcg aatctcaact 120
ctcacaccca aaacctcgaa ttccccaat taccctcgcc tcccggtcat cagatccgcg 180
gtgacagaga ggagacaagg aagaagagaa ggagatggtg aactagggga acaacaagg 240
ggagatcaag gattggaaga tttttttcaa aaaggttcaa gtgattgaca aacagtatga 300
taagctagac aagcttctaa agaaactgca ggcttccat gaggagtcaa aatctgtgac 360
caaagctcct gccatgaagg cgataaagaa gacaatggaa aaagacgttg atgaagttgg 420
aagtattgcc cgtttcrtaa aggggaaact cgaggagttg gacagagaga acttgggcaa 480
atagacaaaa acctggatgt gcaaaaggat ctggtgtgga tcgatcaaga acagcaacaa 540
cactttcctt aaagaagaag ttgaaagaca agatggccga gtttcagggt ctacgagaga 600
acattcaaca agagtatcgc gatgttggtg ataggcgagt ttatacagta actggggagc 660
ggcggatga agatactatt gatgaattga ttgaaactgg aaacagcgaa cagatcttcc 720
agaaagcgat tcaggagcaa ggaagaggac aggtaatgga caccttggcg gaaatccaag 780
aacgtcatga tgcgtgcaga gacttggaag agaaacttct tgacttacia caaatattct 840
tgatgatggc agttttggtt gatgcacaag gagaaatgct tgacaatata gaatctcagg 900
tgtcaagtgc agtagatcac gtgcaatcgg gaaacacggc acttcaaaga gcaaaagagct 960
tgcakgaaga actcaagaaa atggatgtgt attgcaatta tcctctctct cattgtgggt 1020
gcagtgatcg ttgttggtgt tctcaagcct tggaaaaaca aagagtgcct gaggaaagaa 1080
agaatgtaca aaaagaatat caaatcctta ttcacggctt tgagtgcagag tgttttgttt 1140
atgatgtgtg tgtttttttt ttaccaagaa acgaaaaaaa aagaaacara attctacatt 1200
cttttaattg gatcaacaaa accaatttcc cc

(2) INFORMATION FOR SEQ ID NO:1040:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 95 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..95

(D) OTHER INFORMATION: / Ceres Seq. ID 1499475

(2) INFORMATION FOR SEQ ID NO:1041:

(A) LENGTH: 184 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..184

(D) OTHER INFORMATION: / Ceres Seq. ID 1499476

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1041:

(2) INFORMATION FOR SEQ ID NO:1042:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 123 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..123

(D) OTHER INFORMATION: / Ceres Seq. ID 1499477

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1042:

[illegible]

Met Asp Thr Leu Ala Glu Ile Gln Glu Arg His Asp Ala Val Arg Asp
1 5 10 15
Leu Glu Lys Lys Leu Leu Asp Leu Gln Gln Ile Phe Leu Asp Met Ala
20 25 30
Val Leu Val Asp Ala Gln Gly Glu Met Leu Asp Asn Ile Glu Ser Gln
35 40 45
Val Ser Ser Ala Val Asp His Val Gln Ser Gly Asn Thr Ala Leu Gln
50 55 60
Arg Ala Lys Ser Leu Xaa Glu Glu Leu Lys Lys Met Asp Val Tyr Cys
65 70 75 80
Asn Tyr His Pro Pro His Cys Gly Cys Ser Asp Arg Cys Trp Cys Ser
85 90 95
Gln Ala Leu Glu Lys Gln Arg Val Leu Glu Glu Arg Lys Asn Val Gln
100 105 110
Lys Glu Tyr Gln Ile Leu Ile His Gly Phe Glu
115 120

(2) INFORMATION FOR SEQ ID NO:1043:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 591 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..591
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499486

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1043:

gccttttagtt aaaccacacg atctaaaaat cccttctctc tttctttctt tctttttttc	60
tctccctctc ttctcaggcg agtatgcaaa gcaagaacat gatcgtggct tcatctcatc	120
agcagcaaca acaacagcaa ccgcagcagc cacaaccgca acttaaattgc cctcgttgcg	180
attctttcaa cacaaagttc tgctactaca acaactacag cctctctcaa ccacggcact	240
tttgcaaggc ttgcaagagg tactggacga gaggtgggac tctcaggaac gttcccgtan	300
gggntagcta tcggaagaac aaacgtgtaa agcggccatc aaccgcaacc acaaccactg	360
cctccaccgt ctgcagcact aattcttcat cccctaataa ccctcatcag atctctcatt	420
tctcttccat gaatcatcat cctttgttct atggtttacc agatcatatg agcagttgta	480
ataataaatc ttccaatgat cccaagccgt ttcagtgatt cttcaaagac ttgttcatca	540
agtggtttag agagtgaagt tctctcatct ggktttagca gtcttagtgc b	

(2) INFORMATION FOR SEQ ID NO:1044:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 144 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..144
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499487

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1044:

Met Gln Ser Lys Asn Met Ile Val Ala Ser Ser His Gln Gln Gln Gln
1 5 10 15
Gln Gln Gln Pro Gln Gln Pro Gln Pro Gln Leu Lys Cys Pro Arg Cys
20 25 30
Asp Ser Ser Asn Thr Lys Phe Cys Tyr Tyr Asn Asn Tyr Ser Leu Ser
35 40 45
Gln Pro Arg His Phe Cys Lys Ala Cys Lys Arg Tyr Trp Thr Arg Gly
50 55 60
Gly Thr Leu Arg Asn Val Pro Val Xaa Xaa Ser Tyr Arg Lys Asn Lys
65 70 75 80
Arg Val Lys Arg Pro Ser Thr Ala Thr Thr Thr Thr Ala Ser Thr Val

				85					90					95					
Ser	Thr	Thr	Asn	Ser	Ser	Ser	Pro	Asn	Asn	Pro	His	Gln	Ile	Ser	His				
			100					105					110						
Phe	Ser	Ser	Met	Asn	His	His	Pro	Leu	Phe	Tyr	Gly	Leu	Ser	Asp	His				
			115				120					125							
Met	Ser	Ser	Cys	Asn	Asn	Lys	Ser	Ser	Asn	Asp	Pro	Lys	Pro	Phe	Gln				
			130			135					140								

(2) INFORMATION FOR SEQ ID NO:1045:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 139 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..139

(D) OTHER INFORMATION: / Ceres Seq. ID 1499488

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1045:

Met	Ile	Val	Ala	Ser	Ser	His	Gln	Gln	Gln	Gln	Gln	Gln	Pro	Gln					
1				5			10						15						
Gln	Pro	Gln	Pro	Gln	Leu	Lys	Cys	Pro	Arg	Cys	Asp	Ser	Ser	Asn	Thr				
			20				25					30							
Lys	Phe	Cys	Tyr	Tyr	Asn	Asn	Tyr	Ser	Leu	Ser	Gln	Pro	Arg	His	Phe				
		35			40						45								
Cys	Lys	Ala	Cys	Lys	Arg	Tyr	Trp	Thr	Arg	Gly	Gly	Thr	Leu	Arg	Asn				
	50				55					60									
Val	Pro	Val	Xaa	Xaa	Ser	Tyr	Arg	Lys	Asn	Lys	Arg	Val	Lys	Arg	Pro				
65				70					75					80					
Ser	Thr	Ala	Thr	Thr	Thr	Thr	Ala	Ser	Thr	Val	Ser	Thr	Thr	Asn	Ser				
			85				90							95					
Ser	Ser	Pro	Asn	Asn	Pro	His	Gln	Ile	Ser	His	Phe	Ser	Ser	Met	Asn				
		100			105							110							
His	His	Pro	Leu	Phe	Tyr	Gly	Leu	Ser	Asp	His	Met	Ser	Ser	Cys	Asn				
		115			120						125								
Asn	Lys	Ser	Ser	Asn	Asp	Pro	Lys	Pro	Phe	Gln									
			130		135														

(2) INFORMATION FOR SEQ ID NO:1046:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1762 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1762

(D) OTHER INFORMATION: / Ceres Seq. ID 1499501

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1046:

agaccgctag	tttttttttg	ccactctctt	cgtctctctc	ttgtagcaat	gccgcttctt	60
catccacagt	cgttgcggca	tccttctttc	gagattcaga	cccaaagaag	aagcaattcc	120
acaacaagat	tgcttctttc	tcacaagttt	ctccattctc	aagcttccat	tatctcaatc	180
tccaggacaa	gaatcctcaa	acgggtctct	cagaatctct	ctgtagctaa	agctgcttca	240
gctcaagcta	gtagtagtgt	tggtgagagt	gttgctcaaa	catcagaaaa	agatgtgttg	300
aaggtcttgt	ctcagattat	tgatcctgat	tttgggacag	atattgtttc	ttgtggtttt	360
gtgaaagatt	tggggattaa	tgaagctttg	ggtgaggttt	cgttccggtt	ggagctgaca	420
acaccgcat	gtccagtcaa	agacatgttt	gagaacaagg	caaatgaggt	agttgcagcc	480
cttccatggg	tgaagaaggt	aaatctgaca	atgtcagcac	aaccagccaa	gcccattttt	540
gcagggcagc	ttcccttttg	attatcaaga	atttcgaaca	tcatcgctgt	ttctagttgc	600

aaggggtggtg	ttgggaaatc	aacagtagct	gtaaatcttg	cttatacatt	agctggtatg	660
ggtgctagag	ttggtatctt	tgatgctgat	gtctatggtc	caagtctacc	aaccatggtc	720
aatcctgaga	gccgtatatt	ggaaatgaac	ccggagaaga	agaccatcat	tccaacagaa	780
tacatgggcg	tcaagctagt	ctcatattgga	tttgcaggac	aagggcgtgc	cattatgaga	840
ggtcctatgg	tgtctggtgt	tataaaccac	ctccttacaa	caactgaatg	gggagagctg	900
gactatcttg	ttatcgacat	gcctcctgga	actggtgata	tacaactgac	cttatgccag	960
gttgcgccat	tgacagcagc	ggtaattgtc	accaccctc	aaaagttggc	gtttattgat	1020
gttgcaaaag	gtgtaaggat	gtttcctaaa	cttaaggtgc	cttgcggtgc	tggtgtggag	1080
aatatgtgcc	actttgacgc	tgatgggaaa	cgttattacc	cttttgggaa	aggttcaggt	1140
tctgaggtgg	tcaagcaatt	cggcatacct	cacctctttg	acctcccat	tagaccaacg	1200
ttatctgctt	cgggggatag	cgggaactcct	gaagtagtgt	cggatcctct	aagtgcggtt	1260
gccagaacgt	tccaggatct	tggtgtatgt	gtagtgcaac	aatgcgcaa	gatacgccag	1320
caagtatcaa	cggccgtgac	atcgcacaag	tatctcaagg	caattagagt	gaaggtacca	1380
aactcagacg	aagagttctt	actgcacct	gcaaccgtca	gaagaaatga	tagatctgca	1440
caaagtgtgg	atgaatggac	tggagagcaa	aaagttctat	atggcgatgt	agcgggaagt	1500
atcgaacctg	aggacatacg	accaatggga	aactacgctg	tctcgataac	ctggcccgac	1560
gggtttagcc	agattgctcc	atatgaccag	ttggaagaaa	ttgaaaggct	agtagatgtt	1620
cctccattgt	ctccagtcga	agtctagtgc	ttgaacaata	tgttttcgct	ttacgatatc	1680
tcttgaaaat	gaaatttgta	tattcatatt	aagagcattg	ttatgaatct	tacaatgatg	1740
aaaagagggt	tactgtaagc	tg				

(2) INFORMATION FOR SEQ ID NO:1047:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 548 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..548

(D) OTHER INFORMATION: / Ceres Seq. ID 1499502

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1047:

Arg	Pro	Leu	Val	Phe	Phe	Cys	His	Ser	Leu	Arg	Leu	Ser	Leu	Val	Ala
1				5				10						15	
Met	Pro	Leu	Leu	His	Pro	Gln	Ser	Leu	Arg	His	Pro	Ser	Phe	Glu	Ile
			20					25					30		
Gln	Thr	Gln	Arg	Arg	Ser	Asn	Ser	Thr	Thr	Arg	Leu	Leu	Leu	Ser	His
		35				40					45				
Lys	Phe	Leu	His	Ser	Gln	Ala	Ser	Ile	Ile	Ser	Ile	Ser	Arg	Thr	Arg
	50					55				60					
Ile	Leu	Lys	Arg	Val	Ser	Gln	Asn	Leu	Ser	Val	Ala	Lys	Ala	Ala	Ser
65				70					75					80	
Ala	Gln	Ala	Ser	Ser	Val	Gly	Glu	Ser	Val	Ala	Gln	Thr	Ser	Glu	
			85					90					95		
Lys	Asp	Val	Leu	Lys	Ala	Leu	Ser	Gln	Ile	Ile	Asp	Pro	Asp	Phe	Gly
		100						105					110		
Thr	Asp	Ile	Val	Ser	Cys	Gly	Phe	Val	Lys	Asp	Leu	Gly	Ile	Asn	Glu
	115					120						125			
Ala	Leu	Gly	Glu	Val	Ser	Phe	Arg	Leu	Glu	Leu	Thr	Thr	Pro	Ala	Cys
	130					135					140				
Pro	Val	Lys	Asp	Met	Phe	Glu	Asn	Lys	Ala	Asn	Glu	Val	Val	Ala	Ala
145				150					155					160	
Leu	Pro	Trp	Val	Lys	Lys	Val	Asn	Leu	Thr	Met	Ser	Ala	Gln	Pro	Ala
			165					170						175	
Lys	Pro	Ile	Phe	Ala	Gly	Gln	Leu	Pro	Phe	Gly	Leu	Ser	Arg	Ile	Ser
		180						185					190		
Asn	Ile	Ile	Ala	Val	Ser	Ser	Cys	Lys	Gly	Gly	Val	Gly	Lys	Ser	Thr
	195						200					205			
Val	Ala	Val	Asn	Leu	Ala	Tyr	Thr	Leu	Ala	Gly	Met	Gly	Ala	Arg	Val
	210					215					220				
Gly	Ile	Phe	Asp	Ala	Asp	Val	Tyr	Gly	Pro	Ser	Leu	Pro	Thr	Met	Val


```

225          230          235          240
Asn Pro Glu Ser Arg Ile Leu Glu Met Asn Pro Glu Lys Lys Thr Ile
          245          250          255
Ile Pro Thr Glu Tyr Met Gly Val Lys Leu Val Ser Phe Gly Phe Ala
          260          265          270
Gly Gln Gly Arg Ala Ile Met Arg Gly Pro Met Val Ser Gly Val Ile
          275          280          285
Asn Gln Leu Leu Thr Thr Thr Glu Trp Gly Glu Leu Asp Tyr Leu Val
          290          295          300
Ile Asp Met Pro Pro Gly Thr Gly Asp Ile Gln Leu Thr Leu Cys Gln
305          310          315          320
Val Ala Pro Leu Thr Ala Ala Val Ile Val Thr Thr Pro Gln Lys Leu
          325          330          335
Ala Phe Ile Asp Val Ala Lys Gly Val Arg Met Phe Ser Lys Leu Lys
          340          345          350
Val Pro Cys Val Ala Val Val Glu Asn Met Cys His Phe Asp Ala Asp
          355          360          365
Gly Lys Arg Tyr Tyr Pro Phe Gly Lys Gly Ser Gly Ser Glu Val Val
          370          375          380
Lys Gln Phe Gly Ile Pro His Leu Phe Asp Leu Pro Ile Arg Pro Thr
385          390          395          400
Leu Ser Ala Ser Gly Asp Ser Gly Thr Pro Glu Val Val Ser Asp Pro
          405          410          415
Leu Ser Asp Val Ala Arg Thr Phe Gln Asp Leu Gly Val Cys Val Val
          420          425          430
Gln Gln Cys Ala Lys Ile Arg Gln Gln Val Ser Thr Ala Val Thr Tyr
          435          440          445
Asp Lys Tyr Leu Lys Ala Ile Arg Val Lys Val Pro Asn Ser Asp Glu
          450          455          460
Glu Phe Leu Leu His Pro Ala Thr Val Arg Arg Asn Asp Arg Ser Ala
465          470          475          480
Gln Ser Val Asp Glu Trp Thr Gly Glu Gln Lys Val Leu Tyr Gly Asp
          485          490          495
Val Ala Glu Asp Ile Glu Pro Glu Asp Ile Arg Pro Met Gly Asn Tyr
          500          505          510
Ala Val Ser Ile Thr Trp Pro Asp Gly Phe Ser Gln Ile Ala Pro Tyr
          515          520          525
Asp Gln Leu Glu Glu Ile Glu Arg Leu Val Asp Val Pro Pro Leu Ser
530          535          540
Pro Val Glu Val
545

```

(2) INFORMATION FOR SEQ ID NO:1048:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 532 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..532
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499503

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1048:

```

Met Pro Leu Leu His Pro Gln Ser Leu Arg His Pro Ser Phe Glu Ile
1          5          10          15
Gln Thr Gln Arg Ser Asn Ser Thr Thr Arg Leu Leu Leu Ser His
          20          25          30
Lys Phe Leu His Ser Gln Ala Ser Ile Ile Ser Ile Ser Arg Thr Arg
          35          40          45
Ile Leu Lys Arg Val Ser Gln Asn Leu Ser Val Ala Lys Ala Ala Ser
50          55          60

```

Ala	Gln	Ala	Ser	Ser	Ser	Val	Gly	Glu	Ser	Val	Ala	Gln	Thr	Ser	Glu
65					70					75					80
Lys	Asp	Val	Leu	Lys	Ala	Leu	Ser	Gln	Ile	Ile	Asp	Pro	Asp	Phe	Gly
				85					90					95	
Thr	Asp	Ile	Val	Ser	Cys	Gly	Phe	Val	Lys	Asp	Leu	Gly	Ile	Asn	Glu
			100					105					110		
Ala	Leu	Gly	Glu	Val	Ser	Phe	Arg	Leu	Glu	Leu	Thr	Thr	Pro	Ala	Cys
		115					120					125			
Pro	Val	Lys	Asp	Met	Phe	Glu	Asn	Lys	Ala	Asn	Glu	Val	Val	Ala	Ala
	130					135					140				
Leu	Pro	Trp	Val	Lys	Lys	Val	Asn	Leu	Thr	Met	Ser	Ala	Gln	Pro	Ala
145				150						155					160
Lys	Pro	Ile	Phe	Ala	Gly	Gln	Leu	Pro	Phe	Gly	Leu	Ser	Arg	Ile	Ser
				165					170					175	
Asn	Ile	Ile	Ala	Val	Ser	Ser	Cys	Lys	Gly	Gly	Val	Gly	Lys	Ser	Thr
			180					185					190		
Val	Ala	Val	Asn	Leu	Ala	Tyr	Thr	Leu	Ala	Gly	Met	Gly	Ala	Arg	Val
		195					200					205			
Gly	Ile	Phe	Asp	Ala	Asp	Val	Tyr	Gly	Pro	Ser	Leu	Pro	Thr	Met	Val
	210					215						220			
Asn	Pro	Glu	Ser	Arg	Ile	Leu	Glu	Met	Asn	Pro	Glu	Lys	Lys	Thr	Ile
225				230						235					240
Ile	Pro	Thr	Glu	Tyr	Met	Gly	Val	Lys	Leu	Val	Ser	Phe	Gly	Phe	Ala
				245					250					255	
Gly	Gln	Gly	Arg	Ala	Ile	Met	Arg	Gly	Pro	Met	Val	Ser	Gly	Val	Ile
			260					265					270		
Asn	Gln	Leu	Thr	Thr	Thr	Glu	Trp	Gly	Glu	Leu	Asp	Tyr	Leu	Val	
		275				280					285				
Ile	Asp	Met	Pro	Pro	Gly	Thr	Gly	Asp	Ile	Gln	Leu	Thr	Leu	Cys	Gln
	290					295				300					
Val	Ala	Pro	Leu	Thr	Ala	Ala	Val	Ile	Val	Thr	Thr	Pro	Gln	Lys	Leu
305					310					315					320
Ala	Phe	Ile	Asp	Val	Ala	Lys	Gly	Val	Arg	Met	Phe	Ser	Lys	Leu	Lys
				325					330					335	
Val	Pro	Cys	Val	Ala	Val	Val	Glu	Asn	Met	Cys	His	Phe	Asp	Ala	Asp
			340					345					350		
Gly	Lys	Arg	Tyr	Tyr	Pro	Phe	Gly	Lys	Gly	Ser	Gly	Ser	Glu	Val	Val
		355					360					365			
Lys	Gln	Phe	Gly	Ile	Pro	His	Leu	Phe	Asp	Leu	Pro	Ile	Arg	Pro	Thr
	370					375					380				
Leu	Ser	Ala	Ser	Gly	Asp	Ser	Gly	Thr	Pro	Glu	Val	Val	Ser	Asp	Pro
385					390					395					400
Leu	Ser	Asp	Val	Ala	Arg	Thr	Phe	Gln	Asp	Leu	Gly	Val	Cys	Val	Val
				405					410					415	
Gln	Gln	Cys	Ala	Lys	Ile	Arg	Gln	Gln	Val	Ser	Thr	Ala	Val	Thr	Tyr
			420					425					430		
Asp	Lys	Tyr	Leu	Lys	Ala	Ile	Arg	Val	Lys	Val	Pro	Asn	Ser	Asp	Glu
		435					440					445			
Glu	Phe	Leu	Leu	His	Pro	Ala	Thr	Val	Arg	Arg	Asn	Asp	Arg	Ser	Ala
	450					455					460				
Gln	Ser	Val	Asp	Glu	Trp	Thr	Gly	Glu	Gln	Lys	Val	Leu	Tyr	Gly	Asp
465					470					475					480
Val	Ala	Glu	Asp	Ile	Glu	Pro	Glu	Asp	Ile	Arg	Pro	Met	Gly	Asn	Tyr
				485					490					495	
Ala	Val	Ser	Ile	Thr	Trp	Pro	Asp	Gly	Phe	Ser	Gln	Ile	Ala	Pro	Tyr
			500					505					510		
Asp	Gln	Leu	Glu	Glu	Ile	Glu	Arg	Leu	Val	Asp	Val	Pro	Pro	Leu	Ser
		515					520					525			
Pro	Val	Glu	Val												
			530												

(2) INFORMATION FOR SEQ ID NO:1049:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..400
 (D) OTHER INFORMATION: / Ceres Seq. ID 1499504
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1049:

Met	Phe	Glu	Asn	Lys	Ala	Asn	Glu	Val	Val	Ala	Ala	Leu	Pro	Trp	Val
1			5					10						15	
Lys	Lys	Val	Asn	Leu	Thr	Met	Ser	Ala	Gln	Pro	Ala	Lys	Pro	Ile	Phe
			20					25					30		
Ala	Gly	Gln	Leu	Pro	Phe	Gly	Leu	Ser	Arg	Ile	Ser	Asn	Ile	Ile	Ala
		35					40					45			
Val	Ser	Ser	Cys	Lys	Gly	Gly	Val	Gly	Lys	Ser	Thr	Val	Ala	Val	Asn
	50				55					60					
Leu	Ala	Tyr	Thr	Leu	Ala	Gly	Met	Gly	Ala	Arg	Val	Gly	Ile	Phe	Asp
65				70					75						80
Ala	Asp	Val	Tyr	Gly	Pro	Ser	Leu	Pro	Thr	Met	Val	Asn	Pro	Glu	Ser
			85						90					95	
Arg	Ile	Leu	Glu	Met	Asn	Pro	Glu	Lys	Lys	Thr	Ile	Ile	Pro	Thr	Glu
		100						105					110		
Tyr	Met	Gly	Val	Lys	Leu	Val	Ser	Phe	Gly	Phe	Ala	Gly	Gln	Gly	Arg
	115					120						125			
Ala	Ile	Met	Arg	Gly	Pro	Met	Val	Ser	Gly	Val	Ile	Asn	Gln	Leu	Leu
	130					135					140				
Thr	Thr	Thr	Glu	Trp	Gly	Glu	Leu	Asp	Tyr	Leu	Val	Ile	Asp	Met	Pro
145					150					155					160
Pro	Gly	Thr	Gly	Asp	Ile	Gln	Leu	Thr	Leu	Cys	Gln	Val	Ala	Pro	Leu
			165						170						175
Thr	Ala	Ala	Val	Ile	Val	Thr	Thr	Pro	Gln	Lys	Leu	Ala	Phe	Ile	Asp
		180						185					190		
Val	Ala	Lys	Gly	Val	Arg	Met	Phe	Ser	Lys	Leu	Lys	Val	Pro	Cys	Val
	195					200						205			
Ala	Val	Val	Glu	Asn	Met	Cys	His	Phe	Asp	Ala	Asp	Gly	Lys	Arg	Tyr
	210				215					220					
Tyr	Pro	Phe	Gly	Lys	Gly	Ser	Gly	Ser	Glu	Val	Val	Lys	Gln	Phe	Gly
225				230					235						240
Ile	Pro	His	Leu	Phe	Asp	Leu	Pro	Ile	Arg	Pro	Thr	Leu	Ser	Ala	Ser
			245						250					255	
Gly	Asp	Ser	Gly	Thr	Pro	Glu	Val	Val	Ser	Asp	Pro	Leu	Ser	Asp	Val
		260						265					270		
Ala	Arg	Thr	Phe	Gln	Asp	Leu	Gly	Val	Cys	Val	Val	Gln	Gln	Cys	Ala
		275					280					285			
Lys	Ile	Arg	Gln	Gln	Val	Ser	Thr	Ala	Val	Thr	Tyr	Asp	Lys	Tyr	Leu
	290				295						300				
Lys	Ala	Ile	Arg	Val	Lys	Val	Pro	Asn	Ser	Asp	Glu	Glu	Phe	Leu	Leu
305				310						315					320
His	Pro	Ala	Thr	Val	Arg	Arg	Asn	Asp	Arg	Ser	Ala	Gln	Ser	Val	Asp
			325					330						335	
Glu	Trp	Thr	Gly	Glu	Gln	Lys	Val	Leu	Tyr	Gly	Asp	Val	Ala	Glu	Asp
		340						345					350		
Ile	Glu	Pro	Glu	Asp	Ile	Arg	Pro	Met	Gly	Asn	Tyr	Ala	Val	Ser	Ile
	355					360					365				
Thr	Trp	Pro	Asp	Gly	Phe	Ser	Gln	Ile	Ala	Pro	Tyr	Asp	Gln	Leu	Glu
	370					375					380				
Glu	Ile	Glu	Arg	Leu	Val	Asp	Val	Pro	Pro	Leu	Ser	Pro	Val	Glu	Val
385				390						395					400

(2) INFORMATION FOR SEQ ID NO:1050:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1211 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1211
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499509

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1050:

```
aagcatctct ccctcatatt cacctaaaaa tcagggttaat aaaaaagaat aatgatgttt      60
tcggtgacgg ttgcgatcct tgtttgtctt attgggtaca ttaccgatc atttaagcct      120
ccaccaccgc gaatctgctg ccatacctaac ggtcctccgg ttacttctcc gagaatcaag      180
ctcagtgatg gaagatatct tgcttataga gaatctgggg ttgatagaga caatgctaac      240
tacaagatca ttgtcgttca tggcttcaac agctccaaag acactgaatt ttccatccct      300
aaggatgtaa ttgaggagct tgggatatac tttgtgttct acgatagagc aggatatgga      360
gaaagtgatc cacacccatc acgcactggt aagagtgaag cacacgacat tcaagaactc      420
gccgataaac tcaagatcgg accaaagttc tacgttcttg gtatatcact cgggtgcttac      480
tcggtttata gttgcctcaa atacattccc cacagactag ctggagcagt cttaatgggt      540
ccatttgtga actattgggt gactaaagtg cctcaagaaa aattgagtaa agcgttggag      600
ctaattgccaa agaaagacca atggacgttt aaagtggctc attatgttcc gtggttggtta      660
tattggtggt tgacccaaaa actatttccg tcttcgagta tgatcacggg gaacaatgcg      720
ttatgcagcg acaaagattt ggtcgtcata aagaagaaaa tggagaatcc acgccctggc      780
ttggaaaaag ttagacaaca aggtgaccat gaatgtcttc accgggacat gatagccgga      840
ttcgcgacat gggaattcga cccgactgaa ttagaaaatc cgtttgcgga aggcgaagga      900
tcggtccacg tttggcaagg gatggaagac agaatcattc catacgaaat taatcgatat      960
atatcagaga agcttccatg gattaagtac catgaggctt taggttatgg acatcttcta     1020
aacgccgagg aggagaaatg caaagacatt atcaaggcac ttcttgtaaa ctgatgatca     1080
tctctacaca agatgccaca aaaaatatag catatttaat agattttatt ttttatttat     1140
ggattataat attatagcat attataagtt tgtaagtaag atgaaaacca cttgaaaqtc     1200
attaatttac t
```

(2) INFORMATION FOR SEQ ID NO:1051:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 340 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..340
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499510

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1051:

```
Met Met Phe Ser Val Thr Val Ala Ile Leu Val Cys Leu Ile Gly Tyr
1          5          10          15
Ile Tyr Arg Ser Phe Lys Pro Pro Pro Arg Ile Cys Gly His Pro
20          25          30
Asn Gly Pro Pro Val Thr Ser Pro Arg Ile Lys Leu Ser Asp Gly Arg
35          40          45
Tyr Leu Ala Tyr Arg Glu Ser Gly Val Asp Arg Asp Asn Ala Asn Tyr
50          55          60
Lys Ile Ile Val Val His Gly Phe Asn Ser Ser Lys Asp Thr Glu Phe
65          70          75          80
Ser Ile Pro Lys Asp Val Ile Glu Glu Leu Gly Ile Tyr Phe Val Phe
85          90          95
Tyr Asp Arg Ala Gly Tyr Gly Glu Ser Asp Pro His Pro Ser Arg Thr
100          105          110
```

Val Lys Ser Glu Ala His Asp Ile Gln Glu Leu Ala Asp Lys Leu Lys
115 120 125
Ile Gly Pro Lys Phe Tyr Val Leu Gly Ile Ser Leu Gly Ala Tyr Ser
130 135 140
Val Tyr Ser Cys Leu Lys Tyr Ile Pro His Arg Leu Ala Gly Ala Val
145 150 155 160
Leu Met Val Pro Phe Val Asn Tyr Trp Trp Thr Lys Val Pro Gln Glu
165 170 175
Lys Leu Ser Lys Ala Leu Glu Leu Met Pro Lys Lys Asp Gln Trp Thr
180 185 190
Phe Lys Val Ala His Tyr Val Pro Trp Leu Leu Tyr Trp Trp Leu Thr
195 200 205
Gln Lys Leu Phe Pro Ser Ser Ser Met Ile Thr Gly Asn Asn Ala Leu
210 215 220
Cys Ser Asp Lys Asp Leu Val Val Ile Lys Lys Lys Met Glu Asn Pro
225 230 235 240
Arg Pro Gly Leu Glu Lys Val Arg Gln Gln Gly Asp His Glu Cys Leu
245 250 255
His Arg Asp Met Ile Ala Gly Phe Ala Thr Trp Glu Phe Asp Pro Thr
260 265 270
Glu Leu Glu Asn Pro Phe Ala Glu Gly Glu Gly Ser Val His Val Trp
275 280 285
Gln Gly Met Glu Asp Arg Ile Ile Pro Tyr Glu Ile Asn Arg Tyr Ile
290 295 300
Ser Glu Lys Leu Pro Trp Ile Lys Tyr His Glu Val Leu Gly Tyr Gly
305 310 315 320
His Leu Leu Asn Ala Glu Glu Glu Lys Cys Lys Asp Ile Ile Lys Ala
325 330 335
Leu Leu Val Asn
340

(2) INFORMATION FOR SEQ ID NO:1052:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 339 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..339

(D) OTHER INFORMATION: / Ceres Seq. ID 1499511

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1052:

Met Phe Ser Val Thr Val Ala Ile Leu Val Cys Leu Ile Gly Tyr Ile
1 5 10 15
Tyr Arg Ser Phe Lys Pro Pro Pro Pro Arg Ile Cys Gly His Pro Asn
20 25 30
Gly Pro Pro Val Thr Ser Pro Arg Ile Lys Leu Ser Asp Gly Arg Tyr
35 40 45
Leu Ala Tyr Arg Glu Ser Gly Val Asp Arg Asp Asn Ala Asn Tyr Lys
50 55 60
Ile Ile Val Val His Gly Phe Asn Ser Ser Lys Asp Thr Glu Phe Ser
65 70 75 80
Ile Pro Lys Asp Val Ile Glu Glu Leu Gly Ile Tyr Phe Val Phe Tyr
85 90 95
Asp Arg Ala Gly Tyr Gly Glu Ser Asp Pro His Pro Ser Arg Thr Val
100 105 110
Lys Ser Glu Ala His Asp Ile Gln Glu Leu Ala Asp Lys Leu Lys Ile
115 120 125
Gly Pro Lys Phe Tyr Val Leu Gly Ile Ser Leu Gly Ala Tyr Ser Val
130 135 140
Tyr Ser Cys Leu Lys Tyr Ile Pro His Arg Leu Ala Gly Ala Val Leu

(2) INFORMATION FOR SEQ ID NO:1053:

(A) LENGTH: 179 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..179

(D) OTHER INFORMATION: / Ceres Seq. ID 1499512

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1053:

[illegible]

(2) INFORMATION FOR SEQ ID NO:1054:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1192 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1192
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499513

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1054:

```
atctacgcat gaaaatatga ttctgtcttt tttttgtttg tctatctttc aatacttttaa      60
aaagtgtatt tctagaggcg atttgtcatt tcccgaatag gaatttgagt aaaaaaaaca      120
ctctgttttt tatttccact aatatcaaat cggcgaatat agttcccacc attcttatct      180
ccttgctcgtc actcggaatt ttttaaataa taggatcgct ttaataatat aatctctata      240
atztatagtt ctttttccaa tattggcgtc tccgttgaag ctttccacaa atctcaaatt      300
tgtttgagga ctctcaaatt tctcttctc tcgacaatga tttcgtctct gatttgtttt      360
gcttcgatca aagcaatgga gcagaacttg atgattacac acagtttggt gtaaatttgc      420
agactgatca agaggatacc tttccagatt ttgtgtcata tgggtgtgaat ttgcagcagg      480
agccagatga agtcttttagt attggagctt ctcaattgga tttgtcctcg tataatggag      540
ttttgtcgct agagccagaa caggtggggc aacaagattg tgaagttgtg caggaagaag      600
aagtagagat caattctggt tcatctggtg gagctggtta gagctggtta ggaagaacag      660
atgacgattg ctccagaaag cgggcaagga ctggatcggt tagcagagga ggaggaacta      720
aagcgtgtcg tgaaagggtg aggagggaga agctaaatga gaggtttatg gatttgagct      780
cgggttttga gcctgggagg actcctaaga ctgataaacc ggctatactc gatgatgcaa      840
tccgtatatt gaatcaactt agagatgaag ctcttaagct tgaagaaact aaccagaagc      900
ttttagagga gatcaagagt ctcaaggcgg agaagaacga gctgagggag gaaaagctgg      960
tgttgaaggc ggataaagag aagacagaac aacagtttaa gtctatgacg gctccatctt     1020
cagggttcat acctcatatt ccagctgcat ttaaccacaa caaatgggt gtttatccaa     1080
gttacggtta catgccaatg tggcattata tgccatcaatc cgttcgtgac acatctcgtg     1140
atcaagaact caggcctcct gctgcttaaa ctctcaattg tttttttttg gt
```

(2) INFORMATION FOR SEQ ID NO:1055:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 283 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..283
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499514

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1055:

```
Met Tyr Pro Ser Leu Asp Asn Asp Phe Val Ser Asp Leu Phe Cys Phe
1           5           10           15
Asp Gln Ser Asn Gly Ala Glu Leu Asp Asp Tyr Thr Gln Phe Gly Val
          20          25          30
Asn Leu Gln Thr Asp Gln Glu Asp Thr Phe Pro Asp Phe Val Ser Tyr
          35          40          45
Gly Val Asn Leu Gln Gln Glu Pro Asp Glu Val Phe Ser Ile Gly Ala
          50          55          60
Ser Gln Leu Asp Leu Ser Ser Tyr Asn Gly Val Leu Ser Leu Glu Pro
65          70          75          80
Glu Gln Val Gly Gln Gln Asp Cys Glu Val Val Gln Glu Glu Glu Val
          85          90          95
Glu Ile Asn Ser Gly Ser Ser Gly Gly Ala Val Lys Glu Glu Gln Glu
          100         105         110
His Leu Asp Asp Asp Cys Ser Arg Lys Arg Ala Arg Thr Gly Ser Cys
          115         120         125
Ser Arg Gly Gly Gly Thr Lys Ala Cys Arg Glu Arg Leu Arg Arg Glu
```

130	135	140
Lys Leu Asn Glu Arg Phe Met Asp Leu Ser Ser Val Leu Glu Pro Gly		
145	150	155
Arg Thr Pro Lys Thr Asp Lys Pro Ala Ile Leu Asp Asp Ala Ile Arg		160
	165	170
Ile Leu Asn Gln Leu Arg Asp Glu Ala Leu Lys Leu Glu Glu Thr Asn		175
	180	185
Gln Lys Leu Leu Glu Glu Ile Lys Ser Leu Lys Ala Glu Lys Asn Glu		190
	195	200
Leu Arg Glu Glu Lys Leu Val Leu Lys Ala Asp Lys Glu Lys Thr Glu		205
	210	215
Gln Gln Leu Lys Ser Met Thr Ala Pro Ser Ser Gly Phe Ile Pro His		220
225	230	235
Ile Pro Ala Ala Phe Asn His Asn Lys Met Ala Val Tyr Pro Ser Tyr		240
	245	250
Gly Tyr Met Pro Met Trp His Tyr Met Pro Gln Ser Val Arg Asp Thr		255
	260	265
Ser Arg Asp Gln Glu Leu Arg Pro Pro Ala Ala		270
	275	280

(2) INFORMATION FOR SEQ ID NO:1056:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1191 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1191
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499519

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1056:

attctaaacc	acacaggcaa	gcatgtgggc	tgtgcctttg	tagagtttgg	ttctgctaac	60
gaagcaaaga	tgtcgttgga	aacgaaaaac	ggcgaatatt	tgaacgattg	caagattttt	120
cttgaagtgg	ctaagatggc	tccataccct	ccacccaagt	attgcattga	tcacaaggtt	180
tggtacgaag	actaccttcg	acgagaaatc	cttctgatag	aagaaaatga	ggcagaggaa	240
ggacttgatg	acactcccg	tcttggtgag	gaatttgccg	taagaaaaaa	gacgctcttt	300
gttgccaatc	tctcaccag	aactaaaata	tcacatatca	tcaagttttt	taaagatggt	360
gcagaagttg	ttcgtgttcg	acttattgta	aaccacaggg	gtgagcatgt	gggctgtggc	420
tttggttgag	ttgcttctgt	taacgaagca	cagaaggcgc	tgcaaaagaa	gaatggtgaa	480
aatttgcgca	gtcgtgagat	ttttcttgac	gtggctgagt	tagctccata	ccctctccga	540
cccaagtaca	accatgcaga	gaaacttttg	cacgaacgag	aaagtcttct	gaagaaacag	600
aaggaatatg	agatgttgag	cgagaggacc	gaattctgcg	gtccttttag	gttttcggat	660
tcgagcaaaa	acaaaatctc	cgcaatcgag	agaaactctg	agatcggaat	caatggagtc	720
cacaatatcg	ttgaagggtca	acaaaggaaa	aggcaaagg	tcaaagggag	cttcctcttc	780
cgatgacaaa	tccaagtttg	atgtcgttaa	ggaatggacc	aattgggtcat	tgaagaaggc	840
taaagtcgtc	actcactatg	gcttcattcc	tctggtcatc	ttcgtcggca	tgaactccga	900
tcccaaacct	catctcttcc	agctccttag	ccctgtctga	tccatccaat	ttcatcatca	960
acctaaatca	atcgaatcgg	tcttctctct	gttttggttc	ttcatatctt	tacgcgtggt	1020
cttagattcg	ccgaatcttc	ttttatgctt	ttttcattag	ctagtttttg	aatactttct	1080
ctatggtact	gtattgaata	actttagatt	atgatataat	gtgaaatcga	attttatggt	1140
ttgaaaatct	gggaattgct	ttaaagattg	aagtttggtg	gaatgtcttg	t	

(2) INFORMATION FOR SEQ ID NO:1057:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 261 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..261

(D) OTHER INFORMATION: / Ceres Seq. ID 1499520

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1057:

Ile	Leu	Asn	His	Thr	Gly	Lys	His	Val	Gly	Cys	Ala	Phe	Val	Glu	Phe
1				5					10					15	
Gly	Ser	Ala	Asn	Glu	Ala	Lys	Met	Ser	Leu	Glu	Thr	Lys	Asn	Gly	Glu
			20					25					30		
Tyr	Leu	Asn	Asp	Cys	Lys	Ile	Phe	Leu	Glu	Val	Ala	Lys	Met	Ala	Pro
			35				40					45			
Tyr	Pro	Pro	Pro	Lys	Tyr	Cys	Ile	Asp	His	Lys	Val	Trp	Tyr	Glu	Asp
			50			55					60				
Tyr	Leu	Arg	Arg	Glu	Ile	Leu	Leu	Ile	Glu	Glu	Asn	Glu	Ala	Glu	Glu
65				70					75					80	
Gly	Leu	Asp	Asp	Thr	Pro	Ala	Leu	Val	Glu	Glu	Phe	Ala	Val	Arg	Lys
				85					90					95	
Lys	Thr	Leu	Phe	Val	Ala	Asn	Leu	Ser	Pro	Arg	Thr	Lys	Ile	Ser	His
			100					105					110		
Ile	Ile	Lys	Phe	Phe	Lys	Asp	Val	Ala	Glu	Val	Val	Arg	Val	Arg	Leu
			115				120					125			
Ile	Val	Asn	His	Arg	Gly	Glu	His	Val	Gly	Cys	Gly	Phe	Val	Glu	Phe
			130			135					140				
Ala	Ser	Val	Asn	Glu	Ala	Gln	Lys	Ala	Leu	Gln	Lys	Lys	Asn	Gly	Glu
145					150					155					160
Asn	Leu	Arg	Ser	Arg	Glu	Ile	Phe	Leu	Asp	Val	Ala	Glu	Leu	Ala	Pro
				165					170					175	
Tyr	Pro	Leu	Arg	Pro	Lys	Tyr	Asn	His	Ala	Glu	Lys	Leu	Trp	His	Glu
			180					185					190		
Arg	Glu	Ser	Leu	Leu	Lys	Lys	Gln	Lys	Glu	Tyr	Glu	Met	Leu	Ser	Glu
			195				200					205			
Arg	Thr	Glu	Phe	Cys	Gly	Pro	Leu	Gly	Phe	Ser	Asp	Ser	Ser	Lys	Asn
			210				215				220				
Lys	Ile	Ser	Ala	Ile	Glu	Arg	Asn	Ser	Glu	Ile	Gly	Ile	Asn	Gly	Val
225				230						235					240
His	Asn	Ile	Val	Glu	Gly	Gln	Gln	Arg	Lys	Arg	Gln	Arg	Ile	Lys	Gly
			245						250					255	
Ser	Phe	Leu	Phe	Arg											
			260												

(2) INFORMATION FOR SEQ ID NO:1058:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 238 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..238

(D) OTHER INFORMATION: / Ceres Seq. ID 1499521

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1058:

Met	Ser	Leu	Glu	Thr	Lys	Asn	Gly	Glu	Tyr	Leu	Asn	Asp	Cys	Lys	Ile
1				5					10					15	
Phe	Leu	Glu	Val	Ala	Lys	Met	Ala	Pro	Tyr	Pro	Pro	Pro	Lys	Tyr	Cys
			20					25					30		
Ile	Asp	His	Lys	Val	Trp	Tyr	Glu	Asp	Tyr	Leu	Arg	Arg	Glu	Ile	Leu
			35				40					45			
Leu	Ile	Glu	Glu	Asn	Glu	Ala	Glu	Glu	Gly	Leu	Asp	Asp	Thr	Pro	Ala
			50			55					60				
Leu	Val	Glu	Glu	Phe	Ala	Val	Arg	Lys	Lys	Thr	Leu	Phe	Val	Ala	Asn
65				70					75					80	
Leu	Ser	Pro	Arg	Thr	Lys	Ile	Ser	His	Ile	Ile	Lys	Phe	Phe	Lys	Asp
			85						90					95	
Val	Ala	Glu	Val	Val	Arg	Val	Arg	Leu	Ile	Val	Asn	His	Arg	Gly	Glu

(2) INFORMATION FOR SEQ ID NO:1059:

(A) LENGTH: 216 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..216

(D) OTHER INFORMATION: / Ceres Seq. ID 1499522

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1059:

Met	Ala	Pro	Tyr		Pro	Pro	Lys	Tyr	Cys	Ile	Asp	His	Lys	Val	Trp
1				5					10					15	
Tyr	Glu	Asp	Tyr	Leu	Arg	Arg	Glu	Ile	Leu	Leu	Ile	Glu	Glu	Asn	Glu
			20					25					30		
Ala	Glu	Glu	Gly	Leu	Asp	Asp	Thr	Pro	Ala	Leu	Val	Glu	Glu	Phe	Ala
			35				40					45			
Val	Arg	Lys	Lys	Thr	Leu	Phe	Val	Ala	Asn	Leu	Ser	Pro	Arg	Thr	Lys
			50			55					60				
Ile	Ser	His	Ile	Ile	Lys	Phe	Phe	Lys	Asp	Val	Ala	Glu	Val	Val	Arg
65					70					75					80
Val	Arg	Leu	Ile	Val	Asn	His	Arg	Gly	Glu	His	Val	Gly	Cys	Gly	Phe
				85					90					95	
Val	Glu	Phe	Ala	Ser	Val	Asn	Glu	Ala	Gln	Lys	Ala	Leu	Gln	Lys	Lys
			100					105					110		
Asn	Gly	Glu	Asn	Leu	Arg	Ser	Arg	Glu	Ile	Phe	Leu	Asp	Val	Ala	Glu
			115				120					125			
Leu	Ala	Pro	Tyr	Pro	Leu	Arg	Pro	Lys	Tyr	Asn	His	Ala	Glu	Lys	Leu
			130			135					140				
Trp	His	Glu	Arg	Glu	Ser	Leu	Leu	Lys	Lys	Gln	Lys	Glu	Tyr	Glu	Met
145					150					155					160
Leu	Ser	Glu	Arg	Thr	Glu	Phe	Cys	Gly	Pro	Leu	Gly	Phe	Ser	Asp	Ser
				165					170					175	
Ser	Lys	Asn	Lys	Ile	Ser	Ala	Ile	Glu	Arg	Asn	Ser	Glu	Ile	Gly	Ile
			180					185					190		
Asn	Gly	Val	His	Asn	Ile	Val	Glu	Gly	Gln	Gln	Arg	Lys	Arg	Gln	Arg
			195				200					205			
Ile	Lys	Gly	Ser	Phe	Leu	Phe	Arg								
			210			215									

(2) INFORMATION FOR SEQ ID NO:1060:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1673 base pairs

(B) TYPE: nucleic acid

- (C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
(A) NAME/KEY: -
(B) LOCATION: 1..1673
(D) OTHER INFORMATION: / Ceres Seq. ID 1499523
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1060:

```
ataatttgtc attgttcttg ggcggaccaa taaaagcctc tcttttgaat cccccacaca      60
gatctatcgc ctcttcttcc ctctgtctctg ccagaatttt tgtttcccgt tgataaaggg      120
tttatctttg gtggatgatt agtgaaactt ttttaaggaga tattagttca catgttttag      180
ttaaaaaatg cagcttcaag cggctctggt ttggaagctg aggaggggga aataagtata      240
gacatggaag aagacatgga tctaacagaa gatgatttca gaaatgtgtc tggccagttt      300
tcaggacaag catcgatcgt ggaggttggt gatgctgttg atgtgagagt cgaaaccgtg      360
aaagtagatg ttagttctaa atctggtggt aaaagagcca gaacaatctc tctggaacag      420
caaccttcag tccatgttac ttataaacac ttaacaagag atagtaagca gaagctggaa      480
agttttattac agcaatggtc agaatgggag gcagaacaaa attccttgtc cgaggatcaa      540
gaacaagtac tagaagctgg tgatgagaca tactttcctg ctttgcggtg gggattgcag      600
aagacatcat ctgtatcatt ttggtttgac taccaaactg gtcacagttc ttcgaagaag      660
tctgttccag tggaaagtag cactactcct ctttataacc gtggatttac aattggttta      720
gattcaggtt caaataacgt ggaaggaggc ttggagatta ttgatgatcc tccacgttgc      780
ttcaactgtg gcgcatacag tcattctatt agagaatgtc caaggccttt tgatcgatca      840
gcagttagta atgctcggag gcaacataaa agaaaaagaa atcagactcc tggatcccgt      900
ctaccatcca gatattatca gagccttcaa cgtggaaaat atgatggctt gaagcctggc      960
tcacttgatg cagagacgcg taagcttctc ggtctaaagg aactcgatcc tctccatgg      1020
cttaacagaa tgcgagagat tggatatcca ccaggatatt ttgctgtaga agaagacgat      1080
gatgatcact cgagaataac tatatttggt gaggaagaga ctaaagaaga ggaagaagtt      1140
aagactgaag aaggtgaaat cttggaaaaa gcaagccctc aagagccaag aaagataatg      1200
acagttggat ttcccgggat taacgcaccc attccagaaa acgcagattc gtggctatgg      1260
gaacagagga atagtaacac aggacatact aattatcata atcaccttcg accacaatat      1320
gagatgggcc ctctaggtat tcaactgtct tcaagctttc ctccaatgca tggcattaga      1380
tatgatcata ggttcgggtt atgaccaata agcccgggat ccgaaagagt taagatccat      1440
tttagtttta gcagcagaag atagattcat tagtgaatgt gggatgtatg ataaccatta      1500
gttaaagagt taaccacaag ccaactacgg ttaaaacatt caggcctaag ccaaagtagt      1560
ctatgcttaa ggcagaatcg aacttttacg tctttggtcg taaaactgga atcgtgatta      1620
tacacgtttg gtgttgtaac atgtccatca atgtacaaga tttttgtttt gtt
```

(2) INFORMATION FOR SEQ ID NO:1061:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 405 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..405
(D) OTHER INFORMATION: / Ceres Seq. ID 1499524

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1061:

```
Met Ala Ala Ser Ser Gly Ser Gly Leu Glu Ala Glu Glu Gly Glu Ile
1          5          10          15
Ser Ile Asp Met Glu Glu Asp Met Asp Leu Thr Glu Asp Asp Phe Arg
20        25        30
Asn Val Ser Gly Gln Phe Ser Gly Gln Ala Ser Ile Val Glu Val Gly
35        40        45
Asp Ala Val Asp Val Arg Val Glu Thr Val Lys Val Asp Val Ser Ser
50        55        60
Lys Ser Gly Val Lys Arg Ala Arg Thr Ile Ser Leu Glu Gln Gln Pro
65        70        75        80
Ser Val His Val Thr Tyr Lys His Leu Thr Arg Asp Ser Lys Gln Lys
85        90        95
Leu Glu Ser Leu Leu Gln Gln Trp Ser Glu Trp Glu Ala Glu Gln Asn
```

Met	Glu	Glu	Asp	Met	Asp	Leu	Thr	Glu	Asp	Asp	Phe	Arg	Asn	Val	Ser
1				5					10					15	
Gly	Gln	Phe	Ser	Gly	Gln	Ala	Ser	Ile	Val	Glu	Val	Gly	Asp	Ala	Val
			20					25					30		
Asp	Val	Arg	Val	Glu	Thr	Val	Lys	Val	Asp	Val	Ser	Ser	Lys	Ser	Gly
		35					40					45			
Val	Lys	Arg	Ala	Arg	Thr	Ile	Ser	Leu	Glu	Gln	Gln	Pro	Ser	Val	His
	50					55					60				
Val	Thr	Tyr	Lys	His	Leu	Thr	Arg	Asp	Ser	Lys	Gln	Lys	Leu	Glu	Ser
65					70					75					80

Leu Leu Gln Gln Trp Ser Glu Trp Glu Ala Glu Gln Asn Ser Leu Ser
85 90 95
Glu Asp Gln Glu Gln Val Leu Glu Ala Gly Asp Glu Thr Tyr Phe Pro
100 105 110
Ala Leu Arg Val Gly Leu Gln Lys Thr Ser Ser Val Ser Phe Trp Phe
115 120 125
Asp Tyr Gln Thr Gly His Ser Ser Ser Lys Lys Ser Val Pro Val Glu
130 135 140
Ser Ser Thr Thr Pro Leu Tyr Asn Arg Gly Phe Thr Ile Gly Leu Asp
145 150 155 160
Ser Gly Ser Asn Asn Val Glu Gly Gly Leu Glu Ile Ile Asp Asp Pro
165 170 175
Pro Arg Cys Phe Asn Cys Gly Ala Tyr Ser His Ser Ile Arg Glu Cys
180 185 190
Pro Arg Pro Phe Asp Arg Ser Ala Val Ser Asn Ala Arg Arg Gln His
195 200 205
Lys Arg Lys Arg Asn Gln Thr Pro Gly Ser Arg Leu Pro Ser Arg Tyr
210 215 220
Tyr Gln Ser Leu Gln Arg Gly Lys Tyr Asp Gly Leu Lys Pro Gly Ser
225 230 235 240
Leu Asp Ala Glu Thr Arg Lys Leu Leu Gly Leu Lys Glu Leu Asp Pro
245 250 255
Pro Pro Trp Leu Asn Arg Met Arg Glu Ile Gly Tyr Pro Pro Gly Tyr
260 265 270
Phe Ala Val Glu Glu Asp Asp Asp Asp His Ser Arg Ile Thr Ile Phe
275 280 285
Gly Glu Glu Glu Thr Lys Glu Glu Glu Glu Val Lys Thr Glu Glu Gly
290 295 300
Glu Ile Leu Glu Lys Ala Ser Pro Gln Glu Pro Arg Lys Ile Met Thr
305 310 315 320
Val Gly Phe Pro Gly Ile Asn Ala Pro Ile Pro Glu Asn Ala Asp Ser
325 330 335
Trp Leu Trp Glu Gln Arg Asn Ser Asn Thr Gly His Thr Asn Tyr His
340 345 350
Asn His Leu Arg Pro Gln Tyr Glu Met Gly Pro Leu Gly Ile Gln Leu
355 360 365
Ser Ser Ser Phe Pro Pro Met His Gly Ile Arg Tyr Asp His Arg Phe
370 375 380
Gly Leu
385

(2) INFORMATION FOR SEQ ID NO:1063:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 382 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..382

(D) OTHER INFORMATION: / Ceres Seq. ID 1499526

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1063:

Met Asp Leu Thr Glu Asp Asp Phe Arg Asn Val Ser Gly Gln Phe Ser
1 5 10 15
Gly Gln Ala Ser Ile Val Glu Val Gly Asp Ala Val Asp Val Arg Val
20 25 30
Glu Thr Val Lys Val Asp Val Ser Ser Lys Ser Gly Val Lys Arg Ala
35 40 45
Arg Thr Ile Ser Leu Glu Gln Gln Pro Ser Val His Val Thr Tyr Lys
50 55 60
His Leu Thr Arg Asp Ser Lys Gln Lys Leu Glu Ser Leu Leu Gln Gln

65	70	75	80
Trp Ser Glu Trp	Glu Ala Glu Gln Asn Ser Leu Ser Glu Asp Gln Glu		
	85	90	95
Gln Val Leu Glu	Ala Gly Asp Glu Thr Tyr Phe Pro Ala Leu Arg Val		
	100	105	110
Gly Leu Gln Lys	Thr Ser Ser Val Ser Phe Trp Phe Asp Tyr Gln Thr		
	115	120	125
Gly His Ser Ser	Ser Lys Lys Ser Val Pro Val Glu Ser Ser Thr Thr		
	130	135	140
Pro Leu Tyr Asn	Arg Gly Phe Thr Ile Gly Leu Asp Ser Gly Ser Asn		
	145	150	155
Asn Val Glu Gly	Gly Leu Glu Ile Ile Asp Asp Pro Pro Arg Cys Phe		
	165	170	175
Asn Cys Gly Ala	Tyr Ser His Ser Ile Arg Glu Cys Pro Arg Pro Phe		
	180	185	190
Asp Arg Ser Ala	Val Ser Asn Ala Arg Arg Gln His Lys Arg Lys Arg		
	195	200	205
Asn Gln Thr Pro	Gly Ser Arg Leu Pro Ser Arg Tyr Tyr Gln Ser Leu		
	210	215	220
Gln Arg Gly Lys	Tyr Asp Gly Leu Lys Pro Gly Ser Leu Asp Ala Glu		
	225	230	235
Thr Arg Lys Leu	Leu Gly Leu Lys Glu Leu Asp Pro Pro Pro Trp Leu		
	245	250	255
Asn Arg Met Arg	Glu Ile Gly Tyr Pro Pro Gly Tyr Phe Ala Val Glu		
	260	265	270
Glu Asp Asp Asp	Asp His Ser Arg Ile Thr Ile Phe Gly Glu Glu Glu		
	275	280	285
Thr Lys Glu Glu	Glu Glu Val Lys Thr Glu Glu Gly Glu Ile Leu Glu		
	290	295	300
Lys Ala Ser Pro	Gln Glu Pro Arg Lys Ile Met Thr Val Gly Phe Pro		
	305	310	315
Gly Ile Asn Ala	Pro Ile Pro Glu Asn Ala Asp Ser Trp Leu Trp Glu		
	325	330	335
Gln Arg Asn Ser	Asn Thr Gly His Thr Asn Tyr His Asn His Leu Arg		
	340	345	350
Pro Gln Tyr Glu	Met Gly Pro Leu Gly Ile Gln Leu Ser Ser Ser Phe		
	355	360	365
Pro Pro Met His	Gly Ile Arg Tyr Asp His Arg Phe Gly Leu		
	370	375	380

(2) INFORMATION FOR SEQ ID NO:1064:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1043 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1043
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499527

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1064:

gaaatttcct	ctcttcttct	tttgcttgag	cttttaggttt	tgagagcaaa	gaaaaacgaa	60
gacgcgtcaa	agagcttttg	tgagagaggtt	ctgcttgctt	gctacaatgg	gttacgccca	120
gctagttatt	ggtccagcag	gcagtggaaa	gtcaacttat	tgctcgtctt	tgtatgaaca	180
ttgtgaaact	atcgggtcgaa	caatgcatgt	tgttaacctt	gacccgtctg	cggagatcct	240
caactatcct	gtggctatgg	atatcagaga	acttatttct	ttggaagatg	tgatggagga	300
tctaaagctt	ggtccctaag	gtgcccttat	gtattgcatg	gagtatcttg	aggatagctt	360
acatgattgg	gtggatgaag	aattggagaa	ctacagggat	gacgattacc	ttatctttga	420
ttgtccaggc	cagatagagc	tgtttacaca	tgttcctgtg	ctcaagaact	ttgtggagca	480
tttgaagcag	aagaacttca	acgtctgtgt	tgtttatctg	cttgattcac	agttcatcac	540
agatgtaacc	aagtttatca	gtggttgcat	gtcatctctc	gctgcaatga	tccagcttga	600

```
attaccacat gtcaacatcc tctcaaaaat ggacctcttg caggacaaaa gcaacattga      660
tgattacttg aatccggagc ctgcacacatt gctagcagag ttaaacaaaa ggatgggtcc      720
tcaatatgca aaactaaaca aggccttgat tgagatggtg ggagagtatg ggatggtgaa      780
tttcataccc attaacttga ggaaagaaaa gagcattcaa tatgttctgt cacaaatcga      840
cgtctgtatt cagtttggag aagatgctga tgtgaacatc aaagatgatg acgattttag      900
tgacgatggg cctgacctat aattgttata ttcggtttct acaacttttg ttaaaagtct      960
aaacaagctt ggtctcattg ttcttgtcag ttaccaatgg cgtttgtgag aacttttgtt     1020
gaatatcaaa agccttcaat gtg
```

(2) INFORMATION FOR SEQ ID NO:1065:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 271 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..271
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499528

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1065:

```
Met Gly Tyr Ala Gln Leu Val Ile Gly Pro Ala Gly Ser Gly Lys Ser
1      5      10      15
Thr Tyr Cys Ser Ser Leu Tyr Glu His Cys Glu Thr Ile Gly Arg Thr
20     25     30
Met His Val Val Asn Leu Asp Pro Ala Ala Glu Ile Phe Asn Tyr Pro
35     40     45
Val Ala Met Asp Ile Arg Glu Leu Ile Ser Leu Glu Asp Val Met Glu
50     55     60
Asp Leu Lys Leu Gly Pro Asn Gly Ala Leu Met Tyr Cys Met Glu Tyr
65     70     75     80
Leu Glu Asp Ser Leu His Asp Trp Val Asp Glu Glu Leu Glu Asn Tyr
85     90     95
Arg Asp Asp Asp Tyr Leu Ile Phe Asp Cys Pro Gly Gln Ile Glu Leu
100    105    110
Phe Thr His Val Pro Val Leu Lys Asn Phe Val Glu His Leu Lys Gln
115    120    125
Lys Asn Phe Asn Val Cys Val Val Tyr Leu Leu Asp Ser Gln Phe Ile
130    135    140
Thr Asp Val Thr Lys Phe Ile Ser Gly Cys Met Ser Ser Leu Ala Ala
145    150    155    160
Met Ile Gln Leu Glu Leu Pro His Val Asn Ile Leu Ser Lys Met Asp
165    170    175
Leu Leu Gln Asp Lys Ser Asn Ile Asp Asp Tyr Leu Asn Pro Glu Pro
180    185    190
Arg Thr Leu Leu Ala Glu Leu Asn Lys Arg Met Gly Pro Gln Tyr Ala
195    200    205
Lys Leu Asn Lys Ala Leu Ile Glu Met Val Gly Glu Tyr Gly Met Val
210    215    220
Asn Phe Ile Pro Ile Asn Leu Arg Lys Glu Lys Ser Ile Gln Tyr Val
225    230    235    240
Leu Ser Gln Ile Asp Val Cys Ile Gln Phe Gly Glu Asp Ala Asp Val
245    250    255
Asn Ile Lys Asp Asp Asp Asp Phe Ser Asp Asp Gly Pro Asp Leu
260    265    270
```

(2) INFORMATION FOR SEQ ID NO:1066:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 239 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

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(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..239

(D) OTHER INFORMATION: / Ceres Seq. ID 1499529

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1066:

Met His Val Val Asn Leu Asp Pro Ala Ala Glu Ile Phe Asn Tyr Pro
1 5 10 15
Val Ala Met Asp Ile Arg Glu Leu Ile Ser Leu Glu Asp Val Met Glu
20 25 30
Asp Leu Lys Leu Gly Pro Asn Gly Ala Leu Met Tyr Cys Met Glu Tyr
35 40 45
Leu Glu Asp Ser Leu His Asp Trp Val Asp Glu Glu Leu Glu Asn Tyr
50 55 60
Arg Asp Asp Asp Tyr Leu Ile Phe Asp Cys Pro Gly Gln Ile Glu Leu
65 70 75 80
Phe Thr His Val Pro Val Leu Lys Asn Phe Val Glu His Leu Lys Gln
85 90 95
Lys Asn Phe Asn Val Cys Val Val Tyr Leu Leu Asp Ser Gln Phe Ile
100 105 110
Thr Asp Val Thr Lys Phe Ile Ser Gly Cys Met Ser Ser Leu Ala Ala
115 120 125
Met Ile Gln Leu Glu Leu Pro His Val Asn Ile Leu Ser Lys Met Asp
130 135 140
Leu Leu Gln Asp Lys Ser Asn Ile Asp Asp Tyr Leu Asn Pro Glu Pro
145 150 155 160
Arg Thr Leu Leu Ala Glu Leu Asn Lys Arg Met Gly Pro Gln Tyr Ala
165 170 175
Lys Leu Asn Lys Ala Leu Ile Glu Met Val Gly Glu Tyr Gly Met Val
180 185 190
Asn Phe Ile Pro Ile Asn Leu Arg Lys Glu Lys Ser Ile Gln Tyr Val
195 200 205
Leu Ser Gln Ile Asp Val Cys Ile Gln Phe Gly Glu Asp Ala Asp Val
210 215 220
Asn Ile Lys Asp Asp Asp Phe Ser Asp Asp Gly Pro Asp Leu
225 230 235

(2) INFORMATION FOR SEQ ID NO:1067:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 221 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..221

(D) OTHER INFORMATION: / Ceres Seq. ID 1499530

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1067:

Met Asp Ile Arg Glu Leu Ile Ser Leu Glu Asp Val Met Glu Asp Leu
1 5 10 15
Lys Leu Gly Pro Asn Gly Ala Leu Met Tyr Cys Met Glu Tyr Leu Glu
20 25 30
Asp Ser Leu His Asp Trp Val Asp Glu Glu Leu Glu Asn Tyr Arg Asp
35 40 45
Asp Asp Tyr Leu Ile Phe Asp Cys Pro Gly Gln Ile Glu Leu Phe Thr
50 55 60
His Val Pro Val Leu Lys Asn Phe Val Glu His Leu Lys Gln Lys Asn
65 70 75 80
Phe Asn Val Cys Val Val Tyr Leu Leu Asp Ser Gln Phe Ile Thr Asp
85 90 95
Val Thr Lys Phe Ile Ser Gly Cys Met Ser Ser Leu Ala Ala Met Ile
100 105 110

Gln Leu Glu Leu Pro His Val Asn Ile Leu Ser Lys Met Asp Leu Leu
115 120 125
Gln Asp Lys Ser Asn Ile Asp Asp Tyr Leu Asn Pro Glu Pro Arg Thr
130 135 140
Leu Leu Ala Glu Leu Asn Lys Arg Met Gly Pro Gln Tyr Ala Lys Leu
145 150 155 160
Asn Lys Ala Leu Ile Glu Met Val Gly Glu Tyr Gly Met Val Asn Phe
165 170 175
Ile Pro Ile Asn Leu Arg Lys Glu Lys Ser Ile Gln Tyr Val Leu Ser
180 185 190
Gln Ile Asp Val Cys Ile Gln Phe Gly Glu Asp Ala Asp Val Asn Ile
195 200 205
Lys Asp Asp Asp Asp Phe Ser Asp Asp Gly Pro Asp Leu
210 215 220

(2) INFORMATION FOR SEQ ID NO:1068:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 444 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..444
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499538

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1068:

aaaatttagt	tcctttctca	tttatccact	gctcttaatc	caacttcaat	atctctctat	60
cctcacaata	tttgttctgt	ttctmcttca	actttcaact	gataaagttt	aaacctttat	120
gctctttact	ctctgatctc	aaaagggttt	tgttttagttc	nmctcaaaac	catggrgatt	180
tgcttaagtg	ctmagattaa	agctgtgagt	ccaggtaagc	caggtgcaag	tccgaagtat	240
atgagctcag	aggctaata	gttactggga	agtaaaagct	cttctgtgtc	aatcagaaca	300
aaccaagaa	ctgaaggaga	gatcttgcaa	tctcctaata	tcaaaagttt	cacttttgct	360
gagcttaaag	cagcanctag	gnattttaga	ccagatagtg	ttcttggtga	agggtggttt	420
ggttctgttt	tcaaaggttg	gatt				

(2) INFORMATION FOR SEQ ID NO:1069:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 91 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..91
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499539

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1069:

Met Xaa Ile Cys Leu Ser Ala Xaa Ile Lys Ala Val Ser Pro Gly Lys	
1 5 10 15	
Pro Gly Ala Ser Pro Lys Tyr Met Ser Glu Ala Asn Asp Ser Leu	
20 25 30	
Gly Ser Lys Ser Ser Ser Val Ser Ile Arg Thr Asn Pro Arg Thr Glu	
35 40 45	
Gly Glu Ile Leu Gln Ser Pro Asn Leu Lys Ser Phe Thr Phe Ala Glu	
50 55 60	
Leu Lys Ala Ala Xaa Arg Xaa Phe Arg Pro Asp Ser Val Leu Gly Glu	
65 70 75 80	
Gly Gly Phe Gly Ser Val Phe Lys Gly Trp Ile	
85 90	

(2) INFORMATION FOR SEQ ID NO:1070:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 68 amino acids

(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..68
(D) OTHER INFORMATION: / Ceres Seq. ID 1499540
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1070:
Met Ser Ser Glu Ala Asn Asp Ser Leu Gly Ser Lys Ser Ser Ser Val
1 5 10 15
Ser Ile Arg Thr Asn Pro Arg Thr Glu Gly Glu Ile Leu Gln Ser Pro
20 25 30
Asn Leu Lys Ser Phe Thr Phe Ala Glu Leu Lys Ala Ala Xaa Arg Xaa
35 40 45
Phe Arg Pro Asp Ser Val Leu Gly Glu Gly Gly Phe Gly Ser Val Phe
50 55 60
Lys Gly Trp Ile
65

(2) INFORMATION FOR SEQ ID NO:1071:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 62 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..62
(D) OTHER INFORMATION: / Ceres Seq. ID 1499541
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1071:
Met Ile His Trp Glu Val Lys Ala Leu Leu Cys Gln Ser Glu Gln Thr
1 5 10 15
Gln Glu Leu Lys Glu Arg Ser Cys Asn Leu Leu Ile Ser Lys Val Ser
20 25 30
Leu Leu Leu Ser Leu Lys Gln Xaa Leu Xaa Ile Leu Asp Gln Ile Val
35 40 45
Phe Leu Val Lys Val Val Leu Val Leu Phe Ser Lys Val Gly
50 55 60

(2) INFORMATION FOR SEQ ID NO:1072:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1396 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
(A) NAME/KEY: -
(B) LOCATION: 1..1396
(D) OTHER INFORMATION: / Ceres Seq. ID 1499542
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1072:
agaaccaaatt cctcggcggc gattgaagaa acctttccga tggatctgct caggggaagag 60
attctgaaga aacgtaagag tctagctgag gaatctggtg gtaagaagtt cttcaagcgg 120
tctgagatcg agcagaagaa aatccagaag cttcgagagg aagaacgacg cgagcacgag 180
cttaaggctc agcggagagc cgccgccgcc gcttccggtg gagatggaaa atcatccggc 240
tctgctcctg gttcttctaa cgcagctacg tctgcgtctt ccaaattcctc tgcacgcgac 300
gctgctgcta tcgccgattc aaaagcccta accgacgaaa acctaattct cccgaggcag 360
gaagtgattc gtcggttgag attccttaag cagccgatga ctctcttcgg agaagatgat 420
caatcgcggc tcgatcgact caagtacggt ttgaagggaag gattgttcga gggtgatagt 480
gatatgactg aaggacagac gaatgatattc ttgcgtgaca tcgcagagct taagaagagg 540
cagaagagtg gtatgatggg agataggaag aggaagagta gagatgagag aggaagaagac 600

gaaggtgata	gaggtgaaac	aagggaatat	gaacttagtg	gtggtgaatc	gagtgatggt	660
gatgctgata	aagatatgaa	acgtttgaaa	gctaactttg	aggatctatg	cgatgaggat	720
aagatccttg	tgttttataa	gaagctgttg	attgaatgga	aacaggagct	tgatgcgatg	780
gagaacactg	agaggagaac	tgcaaaaagg	aaacagatgg	tagccacttt	taagcagtgt	840
gctaggtatc	tagttcctct	cttcaactta	tgcaggaaga	agggtttacc	agctgacatt	900
cgtcaagctt	taatggtgat	ggtaaccac	tgcataaagc	gagactacct	tgctgcaatg	960
gaccactaca	tcaaactagc	tatcgggaac	gcgccatggc	ctattggagt	gactatgggt	1020
ggtattcacg	aacgttcagc	tcgagagaag	atttacacca	acagtgttgc	tcacatcatg	1080
aacgatgaaa	ccactcgcaa	gtatcttcag	tcagttaaaa	gactgatgac	tttctgtcaa	1140
agacgttatc	caactatgcc	ttctaaagcc	gttgagttca	atagcttagc	caacggaagc	1200
gacttacagt	ctttgctagc	cgaagagaga	ttctttggtg	gtaatcgtga	acaggtctca	1260
gaggagagac	tccggctcat	gccttctcag	agcgaaagct	agtcttactg	tgttttctgc	1320
tttggtgtgt	ttttattttt	gtatcaaaaac	gttgactctg	tattatcgtc	tatttaaaaac	1380
gttgacctga	ttgtcg					

(2) INFORMATION FOR SEQ ID NO:1073:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 433 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..433

(D) OTHER INFORMATION: / Ceres Seq. ID 1499543

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1073:

Arg	Thr	Lys	Ser	Ser	Ala	Ala	Ile	Glu	Glu	Thr	Phe	Pro	Met	Asp	Leu
1			5					10					15		
Leu	Arg	Glu	Glu	Ile	Leu	Lys	Lys	Arg	Lys	Ser	Leu	Ala	Glu	Ser	
			20					25					30		
Gly	Gly	Lys	Lys	Phe	Phe	Lys	Arg	Ser	Glu	Ile	Glu	Gln	Lys	Lys	Ile
			35				40					45			
Gln	Lys	Leu	Arg	Glu	Glu	Glu	Arg	Arg	Glu	His	Glu	Leu	Lys	Ala	Gln
			50			55					60				
Arg	Arg	Ala	Ala	Ala	Ala	Ala	Ser	Gly	Gly	Asp	Gly	Lys	Ser	Ser	Gly
65					70					75				80	
Ser	Ala	Pro	Gly	Ser	Ser	Asn	Ala	Ala	Thr	Ser	Ala	Ser	Ser	Lys	Ser
			85						90					95	
Ser	Ala	Ser	Asp	Ala	Ala	Ala	Ile	Ala	Asp	Ser	Lys	Ala	Leu	Thr	Asp
			100					105					110		
Glu	Asn	Leu	Ile	Leu	Pro	Arg	Gln	Glu	Val	Ile	Arg	Arg	Leu	Arg	Phe
			115				120					125			
Leu	Lys	Gln	Pro	Met	Thr	Leu	Phe	Gly	Glu	Asp	Asp	Gln	Ser	Arg	Leu
			130			135					140				
Asp	Arg	Leu	Lys	Tyr	Val	Leu	Lys	Glu	Gly	Leu	Phe	Glu	Val	Asp	Ser
145					150					155				160	
Asp	Met	Thr	Glu	Gly	Gln	Thr	Asn	Asp	Phe	Leu	Arg	Asp	Ile	Ala	Glu
			165						170					175	
Leu	Lys	Lys	Arg	Gln	Lys	Ser	Gly	Met	Met	Gly	Asp	Arg	Lys	Arg	Lys
			180					185					190		
Ser	Arg	Asp	Glu	Arg	Gly	Arg	Asp	Glu	Gly	Asp	Arg	Gly	Glu	Thr	Arg
			195				200					205			
Glu	Tyr	Glu	Leu	Ser	Gly	Gly	Glu	Ser	Ser	Asp	Val	Asp	Ala	Asp	Lys
			210			215					220				
Asp	Met	Lys	Arg	Leu	Lys	Ala	Asn	Phe	Glu	Asp	Leu	Cys	Asp	Glu	Asp
225					230					235				240	
Lys	Ile	Leu	Val	Phe	Tyr	Lys	Lys	Leu	Leu	Ile	Glu	Trp	Lys	Gln	Glu
			245						250					255	
Leu	Asp	Ala	Met	Glu	Asn	Thr	Glu	Arg	Arg	Thr	Ala	Lys	Gly	Lys	Gln
			260					265					270		
Met	Val	Ala	Thr	Phe	Lys	Gln	Cys	Ala	Arg	Tyr	Leu	Val	Pro	Leu	Phe

	275					280					285				
Asn	Leu	Cys	Arg	Lys	Lys	Gly	Leu	Pro	Ala	Asp	Ile	Arg	Gln	Ala	Leu
290						295					300				
Met	Val	Met	Val	Asn	His	Cys	Ile	Lys	Arg	Asp	Tyr	Leu	Ala	Ala	Met
305					310					315					320
Asp	His	Tyr	Ile	Lys	Leu	Ala	Ile	Gly	Asn	Ala	Pro	Trp	Pro	Ile	Gly
				325					330					335	
Val	Thr	Met	Val	Gly	Ile	His	Glu	Arg	Ser	Ala	Arg	Glu	Lys	Ile	Tyr
			340					345					350		
Thr	Asn	Ser	Val	Ala	His	Ile	Met	Asn	Asp	Glu	Thr	Thr	Arg	Lys	Tyr
		355				360						365			
Leu	Gln	Ser	Val	Lys	Arg	Leu	Met	Thr	Phe	Cys	Gln	Arg	Arg	Tyr	Pro
370						375					380				
Thr	Met	Pro	Ser	Lys	Ala	Val	Glu	Phe	Asn	Ser	Leu	Ala	Asn	Gly	Ser
385					390					395					400
Asp	Leu	Gln	Ser	Leu	Leu	Ala	Glu	Glu	Arg	Phe	Phe	Gly	Gly	Asn	Arg
				405					410					415	
Glu	Gln	Val	Ser	Glu	Glu	Arg	Leu	Arg	Leu	Met	Pro	Ser	Gln	Ser	Glu
			420					425					430		

Ser

(2) INFORMATION FOR SEQ ID NO:1074:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 420 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..420

(D) OTHER INFORMATION: / Ceres Seq. ID 1499544

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1074:

Met	Asp	Leu	Leu	Arg	Glu	Glu	Ile	Leu	Lys	Arg	Lys	Ser	Leu	Ala
1			5					10					15	
Glu	Glu	Ser	Gly	Gly	Lys	Lys	Phe	Phe	Lys	Arg	Ser	Glu	Ile	Glu
			20				25					30		Gln
Lys	Lys	Ile	Gln	Lys	Leu	Arg	Glu	Glu	Glu	Arg	Arg	Glu	His	Glu
		35				40					45			Leu
Lys	Ala	Gln	Arg	Arg	Ala	Ala	Ala	Ala	Ser	Gly	Gly	Asp	Gly	Lys
	50				55				60					
Ser	Ser	Gly	Ser	Ala	Pro	Gly	Ser	Ser	Asn	Ala	Ala	Thr	Ser	Ala
65				70					75					80
Ser	Lys	Ser	Ser	Ala	Ser	Asp	Ala	Ala	Ala	Ile	Ala	Asp	Ser	Lys
			85				90						95	Ala
Leu	Thr	Asp	Glu	Asn	Leu	Ile	Leu	Pro	Arg	Gln	Glu	Val	Ile	Arg
		100					105					110		Arg
Leu	Arg	Phe	Leu	Lys	Gln	Pro	Met	Thr	Leu	Phe	Gly	Glu	Asp	Gln
		115				120						125		
Ser	Arg	Leu	Asp	Arg	Leu	Lys	Tyr	Val	Leu	Lys	Glu	Gly	Leu	Phe
	130				135						140			Glu
Val	Asp	Ser	Asp	Met	Thr	Glu	Gly	Gln	Thr	Asn	Asp	Phe	Leu	Arg
145				150						155				160
Ile	Ala	Glu	Leu	Lys	Lys	Arg	Gln	Lys	Ser	Gly	Met	Met	Gly	Asp
			165					170					175	Arg
Lys	Arg	Lys	Ser	Arg	Asp	Glu	Arg	Gly	Arg	Asp	Glu	Gly	Asp	Arg
			180					185				190		Gly
Glu	Thr	Arg	Glu	Tyr	Glu	Leu	Ser	Gly	Gly	Glu	Ser	Ser	Asp	Val
		195				200						205		Asp
Ala	Asp	Lys	Asp	Met	Lys	Arg	Leu	Lys	Ala	Asn	Phe	Glu	Asp	Leu
210						215								Cys

Asp Glu Asp Lys Ile Leu Val Phe Tyr Lys Lys Leu Leu Ile Glu Trp
225 230 235 240
Lys Gln Glu Leu Asp Ala Met Glu Asn Thr Glu Arg Arg Thr Ala Lys
245 250 255
Gly Lys Gln Met Val Ala Thr Phe Lys Lys Glu Cys Ala Arg Tyr Leu Val
260 265 270
Pro Leu Phe Asn Leu Cys Arg Lys Lys Gly Leu Pro Ala Asp Ile Arg
275 280 285
Gln Ala Leu Met Val Met Val Asn His Cys Ile Lys Arg Asp Tyr Leu
290 295 300
Ala Ala Met Asp His Tyr Ile Lys Leu Ala Ile Gly Asn Ala Pro Trp
305 310 315 320
Pro Ile Gly Val Thr Met Val Gly Ile His Glu Arg Ser Ala Arg Glu
325 330 335
Lys Ile Tyr Thr Asn Ser Val Ala His Ile Met Asn Asp Glu Thr Thr
340 345 350
Arg Lys Tyr Leu Gln Ser Val Lys Arg Leu Met Thr Phe Cys Gln Arg
355 360 365
Arg Tyr Pro Thr Met Pro Ser Lys Ala Val Glu Phe Asn Ser Leu Ala
370 375 380
Asn Gly Ser Asp Leu Gln Ser Leu Leu Ala Glu Glu Arg Phe Phe Gly
385 390 395 400
Gly Asn Arg Glu Gln Val Ser Glu Glu Arg Leu Arg Leu Met Pro Ser
405 410 415
Gln Ser Glu Ser
420

(2) INFORMATION FOR SEQ ID NO:1075:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 301 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..301

(D) OTHER INFORMATION: / Ceres Seq. ID 1499545

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1075:

Met Thr Leu Phe Gly Glu Asp Asp Gln Ser Arg Leu Asp Arg Leu Lys
1 5 10 15
Tyr Val Leu Lys Glu Gly Leu Phe Glu Val Asp Ser Asp Met Thr Glu
20 25 30
Gly Gln Thr Asn Asp Phe Leu Arg Asp Ile Ala Glu Leu Lys Lys Arg
35 40 45
Gln Lys Ser Gly Met Met Gly Asp Arg Lys Arg Lys Ser Arg Asp Glu
50 55 60
Arg Gly Arg Asp Glu Gly Asp Arg Gly Glu Thr Arg Glu Tyr Glu Leu
65 70 75 80
Ser Gly Gly Glu Ser Ser Asp Val Asp Ala Asp Lys Asp Met Lys Arg
85 90 95
Leu Lys Ala Asn Phe Glu Asp Leu Cys Asp Glu Asp Lys Ile Leu Val
100 105 110
Phe Tyr Lys Lys Leu Leu Ile Glu Trp Lys Gln Glu Leu Asp Ala Met
115 120 125
Glu Asn Thr Glu Arg Arg Thr Ala Lys Gly Lys Gln Met Val Ala Thr
130 135 140
Phe Lys Gln Cys Ala Arg Tyr Leu Val Pro Leu Phe Asn Leu Cys Arg
145 150 155 160
Lys Lys Gly Leu Pro Ala Asp Ile Arg Gln Ala Leu Met Val Met Val
165 170 175
Asn His Cys Ile Lys Arg Asp Tyr Leu Ala Ala Met Asp His Tyr Ile

(2) INFORMATION FOR SEQ ID NO:1076:

(A) LENGTH: 527 base pairs

(C) STRANDEDNESS: single

MOLECULE TYPE: DNA (α)

(ix) FEATURE:

(B) LOCATION: 1..527

(D) OTHER INFORMATION: / Ceres Seq. ID 1499547

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1076:

acagaacang	nagggaggta	gagaggacta	gaggagtctg	agcctcggag	gagggagag	60
gcgaagagta	gggggaacca	aatcttggag	gggaaacgta	gagttctttc	gtggaggaag	120
cgggtgcaac	tggaggaggg	tagaggtagc	tcaatagatc	tactgctgtc	gggggagtta	180
atgcaaagct	gagttgctgc	acgttggtct	tcttcagaga	tggcttcagc	tgggtgtagcc	240
ccatctgggt	acaaaaacag	cagcagcact	agcattgggt	ccgagaagtt	gcaagatcag	300
atgaacgagc	taaagattat	agatgataag	gaagttgaag	caaccataat	taatgggaaa	360
gggactgaaa	ctgggcacat	aattgtcacc	actactggtg	gcaagaattg	tcaacccaaa	420
cagacagtga	ctgtacatggc	tgagcgcatt	gtaggtcaag	gttcttttgg	gattgtcttc	480
caggctaagt	gtttggagac	gggtgagact	gttgccataa	agaaggt		

(2) INFORMATION FOR SEQ ID NO:1077:

(A) LENGTH: 102 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..102

(D) OTHER INFORMATION: / Ceres Seq. ID 1499548

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1077:

[illegible]

100

(2) INFORMATION FOR SEQ ID NO:1078:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 75 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..75

(D) OTHER INFORMATION: / Ceres Seq. ID 1499549

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1078:

Met Asn Glu Leu Lys Ile Arg Asp Asp Lys Glu Val Glu Ala Thr Ile
1 5 10 15
Ile Asn Gly Lys Gly Thr Glu Thr Gly His Ile Ile Val Thr Thr Thr
20 25 30
Gly Gly Lys Asn Gly Gln Pro Lys Gln Thr Val Ser Tyr Met Ala Glu
35 40 45
Arg Ile Val Gly Gln Gly Ser Phe Gly Ile Val Phe Gln Ala Lys Cys
50 55 60
Leu Glu Thr Gly Glu Thr Val Ala Ile Lys Lys
65 70 75

(2) INFORMATION FOR SEQ ID NO:1079:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 398 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..398

(D) OTHER INFORMATION: / Ceres Seq. ID 1499558

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1079:

aaagctcccg cacaccctgc ctgatccctc ccaataagct cccagctcc acgccggacg 60
cagcagcagc agcagtagag atggccgccc tcgccgcctc ctccacggcc gccttcgccc 120
ccaagccgcg cctccacgcg gcgcgcctca ccgtggcctg ctccgccacc ggcgncgacg 180
gcaacggcag cagcagcagt gtgtcgctcg cctcctccgt gaagacgttc tcggccgcgc 240
tggctctgtc gtcggtgctt ctctcctcgg ccgcsacctc cmctscctcc gcggccgctg 300
acatcgccgg gctgaccccg tgcaaggagt ccaaggcgtt cgccaagcgc gagaagaact 360
cgatcaagaa gstcaccgcg tcgctcaaga agtacgcg

(2) INFORMATION FOR SEQ ID NO:1080:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 132 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..132

(D) OTHER INFORMATION: / Ceres Seq. ID 1499559

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1080:

Ser Ser Arg Thr Pro Cys Leu Ile Pro Pro Asn Lys Leu Pro Ser Ser
1 5 10 15
Thr Pro Asp Ala Ala Ala Ala Val Glu Met Ala Ala Leu Ala Ala
20 25 30
Ser Ser Thr Ala Ala Phe Ala Ala Lys Pro Arg Leu Pro Arg Ala Arg
35 40 45
Leu Thr Val Ala Cys Ser Ala Thr Gly Xaa Asp Gly Asn Gly Ser Ser

50 55 60
Ser Ser Val Ser Leu Ala Ser Ser Val Lys Thr Phe Ser Ala Ala Leu
65 70 75 80
Ala Leu Ser Ser Val Leu Leu Ser Ser Ala Xaa Thr Ser Xaa Xaa Pro
85 90 95
Ala Ala Ala Asp Ile Ala Gly Leu Thr Pro Cys Lys Glu Ser Lys Ala
100 105 110
Phe Ala Lys Arg Glu Lys Asn Ser Ile Lys Lys Xaa Thr Ala Ser Leu
115 120 125
Lys Lys Tyr Ala
130

(2) INFORMATION FOR SEQ ID NO:1081:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 106 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..106
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499560

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1081:

Met Ala Ala Leu Ala Ala Ser Ser Thr Ala Ala Phe Ala Ala Lys Pro
1 5 10 15
Arg Leu Pro Arg Ala Arg Leu Thr Val Ala Cys Ser Ala Thr Gly Xaa
20 25 30
Asp Gly Asn Gly Ser Ser Ser Ser Val Ser Leu Ala Ser Ser Val Lys
35 40 45
Thr Phe Ser Ala Ala Leu Ala Leu Ser Ser Val Leu Leu Ser Ser Ala
50 55 60
Xaa Thr Ser Xaa Xaa Pro Ala Ala Ala Asp Ile Ala Gly Leu Thr Pro
65 70 75 80
Cys Lys Glu Ser Lys Ala Phe Ala Lys Arg Glu Lys Asn Ser Ile Lys
85 90 95
Lys Xaa Thr Ala Ser Leu Lys Lys Tyr Ala
100 105

(2) INFORMATION FOR SEQ ID NO:1082:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 439 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..439
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499567

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1082:

atcctcaagt catcagctag ctagccttcc ctacagcaac tgcatacata caacacttcc 60
atctgcccg ctcgtcttcga tcaattccca agtcaaataa tataacagca atggtggttc 120
ccgtgatcga cttctccaag ctggacggcg ctgagagggc cgaaaccctg gcgcagatcg 180
ccaatggctg cgaggagtgg ggattcttcc agctcgtgaa ccacggcatc ccgctggagc 240
tgctcgagcg cgtcaagaag gtgtgctccg acagctaccg cctccgggag gccgggttca 300
aggcgctcga gccgggtgcg acgctggagg cgctcgtcga cgcggasrcg ccggtttgaa 360
gtgggtggcg cggtggacga cctggactgg gaggacatct tctacattca tgacgggatgc 420
cagtdgccgt ccgaccgc

(2) INFORMATION FOR SEQ ID NO:1083:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 82 amino acids
- (B) TYPE: amino acid

- (C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..82
(D) OTHER INFORMATION: / Ceres Seq. ID 1499568
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1083:

Met Val Val Pro Val Ile Asp Phe Ser Lys Leu Asp Gly Ala Glu Arg
1 5 10 15
Ala Glu Thr Leu Ala Gln Ile Ala Asn Gly Cys Glu Glu Trp Gly Phe
20 25 30
Phe Gln Leu Val Asn His Gly Ile Pro Leu Glu Leu Leu Glu Arg Val
35 40 45
Lys Lys Val Cys Ser Asp Ser Tyr Arg Leu Arg Glu Ala Gly Phe Lys
50 55 60
Ala Ser Glu Pro Val Arg Thr Leu Glu Ala Leu Val Asp Ala Xaa Xaa
65 70 75 80
Pro Xaa

(2) INFORMATION FOR SEQ ID NO:1084:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 471 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
(A) NAME/KEY: -
(B) LOCATION: 1..471
(D) OTHER INFORMATION: / Ceres Seq. ID 1499576
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1084:

accaaacaga tcaaatacaga gatggcaagt cgtagtagct ctgcagaagg tgcaggcagg 60
acgttgacctg tcaatctcaa gttgatcacc gtgctgagca tcgatggcgg cggcatcaga 120
gggatcatcc cggccaccat cctgccttc ctggaagcga actccaggaa ctggacgggc 180
cagacgctcg tatcgcgac tacttcgacg tcgtcgccgg cagcagcacc ggcggtctcc 240
tgacggcgat gctcacggcc ccggacacga acgaacggcc gctgttcgcc gccaaaggacc 300
tggcgcggtt ctacatccag cactcgccca aaatcttccg gcagaagaat gctatggggt 360
ccaagctcgt cggcaagctg aggatggctt gtgggcccaa gtacgacggc aagtacctcc 420
atgcgcavtc cgacggcttc ttgtaatat gaggctggac aggacactga c

(2) INFORMATION FOR SEQ ID NO:1085:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 80 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..80
(D) OTHER INFORMATION: / Ceres Seq. ID 1499577
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1085:

Thr Lys Gln Ile Lys Ser Glu Met Ala Ser Arg Ser Ser Ser Ala Glu
1 5 10 15
Gly Ala Gly Arg Thr Leu Pro Val Asn Leu Lys Leu Ile Thr Val Leu
20 25 30
Ser Ile Asp Gly Gly Gly Ile Arg Gly Ile Ile Pro Ala Thr Ile Leu
35 40 45
Ala Phe Leu Glu Ala Asn Ser Arg Asn Trp Thr Gly Gln Thr Leu Val
50 55 60
Ser Arg Thr Thr Ser Thr Ser Ser Pro Ala Arg Ala Pro Ala Val Ser

65

70

75

80

(2) INFORMATION FOR SEQ ID NO:1086:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 73 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..73
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499578

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1086:

Met Ala Ser Arg Ser Ser Ser Ala Glu Gly Ala Gly Arg Thr Leu Pro
1 5 10 15
Val Asn Leu Lys Leu Ile Thr Val Leu Ser Ile Asp Gly Gly Gly Ile
20 25 30
Arg Gly Ile Ile Pro Ala Thr Ile Leu Ala Phe Leu Glu Ala Asn Ser
35 40 45
Arg Asn Trp Thr Gly Gln Thr Leu Val Ser Arg Thr Thr Ser Thr Ser
50 55 60
Ser Pro Ala Arg Ala Pro Ala Val Ser
65 70

(2) INFORMATION FOR SEQ ID NO:1087:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 122 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..122
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499579

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1087:

Met Ala Ala Ala Ser Glu Gly Ser Ser Arg Pro Pro Ser Ser Pro Ser
1 5 10 15
Trp Lys Arg Thr Pro Gly Thr Gly Arg Ala Arg Arg Ser Tyr Arg Gly
20 25 30
Leu Leu Arg Arg Arg Arg His Glu His Arg Arg Ser Pro Asp Gly
35 40 45
Asp Ala His Gly Pro Gly His Glu Arg Thr Ala Ala Val Arg Arg Gln
50 55 60
Gly Pro Gly Ala Val Leu His Pro Ala Leu Ala Gln Asn Leu Pro Ala
65 70 75 80
Glu Glu Cys Tyr Gly Val Gln Ala Arg Arg Gln Ala Glu Asp Gly Leu
85 90 95
Trp Ala Gln Val Arg Arg Gln Val Pro Cys Ala Xaa Arg Arg Leu
100 105 110
Leu Gly Asn Met Arg Leu Asp Arg Thr Leu
115 120

(2) INFORMATION FOR SEQ ID NO:1088:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 477 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..477

(D) OTHER INFORMATION: / Ceres Seq. ID 1499591

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1088:

aactcgggtgc	gaaaccacac	cacccatcgc	caccaccaat	caatccatca	cgtttagctgc	60
acctgcgcct	ctccttgavg	tcgcgcasca	gcaatggcgt	gctocaaagc	ngtgctgctc	120
gcmgcgctcc	tagccgtcgc	aggagcgctc	tcctccgctg	cggtgtggga	ggactacgac	180
caccacatgt	accacaagtg	ctacaggctc	tgcatgagga	agtgcgacga	cgacgatgcc	240
gatgatgcct	tgaagaatag	catcagcccc	gttgtcacct	ctgtgtccga	tgatcacgac	300
catgacgacg	atcacgacca	ccacgatgat	cacaaccacg	accacgacga	ccaccatgat	360
gatcacgacc	acgaccacca	tcacgatgat	cacgaccacg	accatgatga	tcacgaccac	420
gaccataatg	acaaccacgg	cgaacaccat	gacgacgacg	atgaggatga	cgattac	

(2) INFORMATION FOR SEQ ID NO:1089:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 128 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..128

(D) OTHER INFORMATION: / Ceres Seq. ID 1499592

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1089:

Met	Ala	Cys	Ser	Lys	Xaa	Val	Leu	Leu	Xaa	Ala	Leu	Leu	Ala	Val	Ala	
1				5					10					15		
Gly	Ala	Leu	Ser	Ser	Ala	Ala	Val	Trp	Glu	Asp	Tyr	Asp	His	His	Met	
			20					25					30			
Tyr	His	Lys	Cys	Tyr	Arg	Ser	Cys	Met	Arg	Lys	Cys	Asp	Asp	Asp	Asp	
		35					40					45				
Ala	Asp	Asp	Ala	Leu	Lys	Asn	Ser	Ile	Ser	Pro	Val	Val	Thr	Ser	Val	
		50				55					60					
Ser	Asp	Asp	His	Asp	His	Asp	Asp	Asp	His	Asp	His	His	Asp	Asp	His	
65					70				75					80		
Asn	His	Asp	His	Asp	Asp	His	His	Asp	Asp	His	Asp	His	Asp	His	His	
			85					90					95			
His	Asp	Asp	His	Asp	His	Asp	His	Asp	His	Asp	His	Asp	His	Asp	His	Asn
		100					105					110				
Asp	Asn	His	Gly	Glu	His	His	Asp	Asp	Asp	Asp	Glu	Asp	Asp	Asp	Tyr	
		115					120					125				

(2) INFORMATION FOR SEQ ID NO:1090:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 97 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..97

(D) OTHER INFORMATION: / Ceres Seq. ID 1499593

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1090:

Met	Tyr	His	Lys	Cys	Tyr	Arg	Ser	Cys	Met	Arg	Lys	Cys	Asp	Asp	Asp	
1				5					10					15		
Asp	Ala	Asp	Asp	Ala	Leu	Lys	Asn	Ser	Ile	Ser	Pro	Val	Val	Thr	Ser	
			20					25					30			
Val	Ser	Asp	Asp	His	Asp	His	Asp	Asp	His	Asp	His	His	Asp	Asp		
		35					40					45				
His	Asn	His	Asp	His	Asp	Asp	His	His	Asp	Asp	His	Asp	His	Asp	His	

```

      50              55              60
His His Asp Asp His Asp His Asp His Asp Asp His Asp His Asp His
65              70              75              80
Asn Asp Asn His Gly Glu His His Asp Asp Asp Asp Glu Asp Asp Asp
      85              90              95
Tyr

```

(2) INFORMATION FOR SEQ ID NO:1091:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 88 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..88
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499594

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1091:

```

Met Arg Lys Cys Asp Asp Asp Asp Ala Asp Asp Ala Leu Lys Asn Ser
1              5              10              15
Ile Ser Pro Val Val Thr Ser Val Ser Asp Asp His Asp His Asp Asp
      20              25              30
Asp His Asp His His Asp Asp His Asn His Asp His Asp Asp His His
      35              40              45
Asp Asp His Asp His Asp His His His Asp Asp His Asp His Asp His
      50              55              60
Asp Asp His Asp His Asp His Asn Asp Asn His Gly Glu His His Asp
65              70              75              80
Asp Asp Asp Glu Asp Asp Asp Tyr
      85

```

(2) INFORMATION FOR SEQ ID NO:1092:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 347 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..347
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499605

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1092:

```

tctcctttcg gargargcgg accargtaag cagcagcagg aaccctagca ccgccgcacgc      60
cccagccatg ggtatcgacc tcgttgccgg tgggaggaac aagaagacca agcgcacagc      120
gccgaagtcc gacgatgttt atctcaccgg gatggargtc gccgagatcg acggcgcccc      180
gaggatgggc ccgacgttcg gcgccatgat gatctccggc cagaaggcgg cgcacctrgc      240
gctgaaggca ctgngncagg cccaacgccg tggacgggac catccccgar gtgtcgccgg      300
cgctrckmga rgagttcgtg attdcracca aggacgacga ggtcgtg

```

(2) INFORMATION FOR SEQ ID NO:1093:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 115 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..115
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499606

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1093:

Leu Leu Ser Xaa Xaa Ala Asp Xaa Val Ser Ser Ser Arg Asn Pro Ser
1 5 10 15
Thr Ala Ala Ser Pro Ala Met Gly Ile Asp Leu Val Ala Gly Gly Arg
20 25 30
Asn Lys Lys Thr Lys Arg Thr Ala Pro Lys Ser Asp Asp Val Tyr Leu
35 40 45
Thr Gly Met Xaa Val Ala Glu Ile Asp Gly Ala Pro Arg Met Gly Pro
50 55 60
Thr Phe Gly Ala Met Met Ile Ser Gly Gln Lys Ala Ala His Xaa Ala
65 70 75 80
Leu Lys Ala Leu Xaa Gln Ala Gln Arg Arg Gly Arg Asp His Pro Arg
85 90 95
Xaa Val Ala Gly Ala Xaa Xaa Xaa Val Arg Asp Xaa Xaa Gln Gly Arg
100 105 110
Arg Gly Arg
115

(2) INFORMATION FOR SEQ ID NO:1094:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 93 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..93
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499607

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1094:

Met Gly Ile Asp Leu Val Ala Gly Gly Arg Asn Lys Lys Thr Lys Arg
1 5 10 15
Thr Ala Pro Lys Ser Asp Asp Val Tyr Leu Thr Gly Met Xaa Val Ala
20 25 30
Glu Ile Asp Gly Ala Pro Arg Met Gly Pro Thr Phe Gly Ala Met Met
35 40 45
Ile Ser Gly Gln Lys Ala Ala His Xaa Ala Leu Lys Ala Leu Xaa Gln
50 55 60
Ala Gln Arg Arg Gly Arg Asp His Pro Arg Xaa Val Ala Gly Ala Xaa
65 70 75 80
Xaa Xaa Val Arg Asp Xaa Xaa Gln Gly Arg Arg Gly Arg
85 90

(2) INFORMATION FOR SEQ ID NO:1095:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 65 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..65
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499608

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1095:

Met Xaa Val Ala Glu Ile Asp Gly Ala Pro Arg Met Gly Pro Thr Phe
1 5 10 15
Gly Ala Met Met Ile Ser Gly Gln Lys Ala Ala His Xaa Ala Leu Lys
20 25 30
Ala Leu Xaa Gln Ala Gln Arg Arg Gly Arg Asp His Pro Arg Xaa Val
35 40 45
Ala Gly Ala Xaa Xaa Xaa Val Arg Asp Xaa Xaa Gln Gly Arg Arg Gly
50 55 60
Arg

65

(2) INFORMATION FOR SEQ ID NO:1096:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 503 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..503
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499627

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1096:

ctctaaaagt ggtctgttct gcaggttact ccctgtgact aagtaaccga ggcttccagt	60
ggtcgatagc tcaggcaaac tggttgggat cattacaaga gggaacgtcg tccaagccgc	120
cctcgaaatc aagaaaaagg ttgaaggac actctgagat gactacctcc aggtatcctt	180
tttgctgcca catggggggc ttaggacttg gacacatctc tagttggcaa ctgatcaatc	240
aaagcgactg tcagagttag cgatgaaagt cgctatgttt atgaagattt gcccggagaa	300
gcacaggtgt atgtgtagt tttgttatat atgctgatgc agtccttgct ggccaaaaca	360
caggttaccg attgttctgg ttccctgggc ttctttggac accaaattct taacctaggt	420
cttgtttggg tgcacacgta tctagttcaa cttacttgta ttgaggttca ttgaagtgga	480
aaatcaacta gttttcgcac ttc	

(2) INFORMATION FOR SEQ ID NO:1097:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 51 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..51
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499628

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1097:

Ser	Lys	Ser	Gly	Leu	Phe	Cys	Arg	Leu	Pro	Val	Thr	Lys	Tyr	Arg	
1				5				10					15		
Arg	Leu	Pro	Val	Val	Asp	Ser	Ser	Gly	Lys	Leu	Val	Gly	Ile	Ile	Thr
			20					25					30		
Arg	Gly	Asn	Val	Val	Gln	Ala	Ala	Leu	Glu	Ile	Lys	Lys	Lys	Val	Glu
		35					40					45			
Gly	Thr	Leu													
		50													

(2) INFORMATION FOR SEQ ID NO:1098:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 47 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..47
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499629

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1098:

Met	Leu	Met	Gln	Ser	Leu	Leu	Ala	Lys	Thr	Gln	Val	Thr	Asp	Cys	Ser
1				5				10					15		
Gly	Phe	Leu	Gly	Phe	Phe	Gly	His	Gln	Ile	Leu	Asn	Leu	Gly	Leu	Val
			20					25					30		
Trp	Val	His	Thr	Tyr	Leu	Val	Gln	Leu	Thr	Cys	Ile	Glu	Val	His	
		35					40					45			

(2) INFORMATION FOR SEQ ID NO:1099:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 45 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..45
 (D) OTHER INFORMATION: / Ceres Seq. ID 1499630
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1099:
Met Gln Ser Leu Leu Ala Lys Thr Gln Val Thr Asp Cys Ser Gly Phe
1 5 10 15
Leu Gly Phe Phe Gly His Gln Ile Leu Asn Leu Gly Leu Val Trp Val
 20 25 30
His Thr Tyr Leu Val Gln Leu Thr Cys Ile Glu Val His
 35 40 45
(2) INFORMATION FOR SEQ ID NO:1100:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 476 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: DNA (genomic)
 (ix) FEATURE:
 (A) NAME/KEY: -
 (B) LOCATION: 1..476
 (D) OTHER INFORMATION: / Ceres Seq. ID 1499649
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1100:
aattactgtg cttttatctt caacccaaac catccattac catattccta agctatcatg 60
gtgcaccgga cttccatagc cgatgtgcat gtgatgtgca tggatctaag cccaaagaaa 120
cccaacaagg ccagcgccas sancggcgga gctactacga ctgggtcccc gccgatctgc 180
ccatgctcgg cgttgcctcc attggtgccg ccaagctctg cctcaccgcc ggaggtcttg 240
ccctaccagc ctactccgac tctgccaaga tcgcctacgt cctccaaggc aaaggatat 300
tcggcggtgt tctcccgagg gcgaccaagg agaaggtcat ctccgtcaag gaaggcgacg 360
cgctggcgct ccccttcggc gtcgtcacct ggtggcaca caacgccgac gccgctatct 420
ccgacctcgt ggtgctcttc ctcggcgaca cctccacggg ccacaagccg ggccag
(2) INFORMATION FOR SEQ ID NO:1101:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 158 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: peptide
 (ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..158
 (D) OTHER INFORMATION: / Ceres Seq. ID 1499650
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1101:
Leu Leu Cys Leu Tyr Leu Gln Pro Lys Pro Ser Ile Thr Ile Phe Leu
1 5 10 15
Ser Tyr His Gly Ala Pro Asp Phe His Ser Arg Cys Ala Cys Asp Val
 20 25 30
His Gly Ser Lys Pro Lys Glu Thr Gln Gln Gly Gln Arg Xaa Xaa Arg
 35 40 45
Arg Ser Tyr Tyr Asp Trp Ser Pro Ala Asp Leu Pro Met Leu Gly Val
 50 55 60
Ala Ser Ile Gly Ala Ala Lys Leu Cys Leu Thr Ala Gly Gly Leu Ala
65 70 75 80
Leu Pro Ser Tyr Ser Asp Ser Ala Lys Ile Ala Tyr Val Leu Gln Gly
 85 90 95

Lys Gly Ile Phe Gly Val Val Leu Pro Glu Ala Thr Lys Glu Lys Val
100 105 110
Ile Ser Val Lys Glu Gly Asp Ala Leu Ala Leu Pro Phe Gly Val Val
115 120 125
Thr Trp Trp His Asn Asn Ala Asp Ala Ala Ile Ser Asp Leu Val Val
130 135 140
Leu Phe Leu Gly Asp Thr Ser Thr Gly His Lys Pro Gly Gln
145 150 155

(2) INFORMATION FOR SEQ ID NO:1102:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 139 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..139
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499651

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1102:

Met Val His Arg Thr Ser Ile Ala Asp Val His Val Met Cys Met Asp
1 5 10 15
Leu Ser Pro Lys Lys Pro Asn Lys Ala Ser Ala Xaa Xaa Gly Gly Ala
20 25 30
Thr Thr Thr Gly Pro Pro Pro Ile Cys Pro Cys Ser Ala Leu Pro Pro
35 40 45
Leu Val Pro Pro Ser Ser Ala Ser Pro Pro Glu Val Leu Pro Tyr Pro
50 55 60
Ala Thr Pro Thr Leu Pro Arg Ser Pro Thr Ser Ser Lys Ala Lys Val
65 70 75 80
Tyr Ser Ala Trp Phe Ser Arg Arg Arg Pro Arg Arg Arg Ser Ser Pro
85 90 95
Ser Arg Lys Ala Thr Arg Trp Arg Ser Pro Ser Ala Ser Ser Pro Gly
100 105 110
Gly Thr Thr Thr Pro Thr Pro Leu Ser Pro Thr Ser Trp Cys Ser Ser
115 120 125
Ser Ala Thr Pro Pro Arg Ala Thr Ser Arg Ala
130 135

(2) INFORMATION FOR SEQ ID NO:1103:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 127 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..127
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499652

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1103:

Met Cys Met Asp Leu Ser Pro Lys Lys Pro Asn Lys Ala Ser Ala Xaa
1 5 10 15
Xaa Gly Gly Ala Thr Thr Thr Gly Pro Pro Pro Ile Cys Pro Cys Ser
20 25 30
Ala Leu Pro Pro Leu Val Pro Pro Ser Ser Ala Ser Pro Glu Val
35 40 45
Leu Pro Tyr Pro Ala Thr Pro Thr Leu Pro Arg Ser Pro Thr Ser Ser
50 55 60
Lys Ala Lys Val Tyr Ser Ala Trp Phe Ser Arg Arg Arg Pro Arg Arg
65 70 75 80
Arg Ser Ser Pro Ser Arg Lys Ala Thr Arg Trp Arg Ser Pro Ser Ala

(2) INFORMATION FOR SEO ID NO:1104:

(A) LENGTH: 476 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -
(B) LOCATION: 1..476
(D) OTHER INFORMATION: / Ceres Seq. ID 1499655

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1104:

ctactaacgc	cgtctcctct	ccagcgcccc	ccgtcgccgc	cgcctcctc	ttggtcccgc	60
cgcccgctcg	ggtcatcatg	gtgaggggtca	gtgtgctcaa	cgatgcgctc	aagtccatgt	120
acaatgcaga	gaagaggggc	aagaggcagg	tcatgatcag	gccgtcgtcc	aaggtgatca	180
tcaagttcct	gacggtcaag	acctgggctt	ctttgccaat	ttcctgggca	tcttcatctt	240
tgtcttggtt	attgcttacc	acttcgtgat	ggcagacccg	aagtacgaag	gaaactgatg	300
tctcttagtg	caaagatcct	attatctgca	ggccgaataa	gggctatact	gttagctaat	360
cgtagtgaga	tcgcttgaca	ctttgagtgc	atatcatgga	agctggacat	gcagttcctg	420
gcatttttgg	tttgcccatg	ttttaatctg	ctgaattagt	aaatccctgga	gaatcc	

(2) INFORMATION FOR SEQ ID NO:1105:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 88 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide
(B) LOCATION: 1..88
(D) OTHER INFORMATION: / Ceres Seq. ID 1499656

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1105:

Thr 1	Asn	Arg	Val	Ser 5	Ser	Pro	Ala	Pro	Ala 10	Val	Ala	Ala	Ala	Leu 15	Leu
Leu	Val	Pro	Pro 20	Ser	Val	Glu	Val	Ile 25	Met	Val	Arg	Val	Ser 30	Val	Leu
Asn	Asp	Ala 35	Leu	Lys	Ser	Met	Tyr 40	Asn	Ala	Glu	Lys	Arg 45	Gly	Lys	Arg
Gln	Val 50	Met	Ile	Arg	Pro	Ser 55	Ser	Lys	Val	Ile 60	Ile	Lys	Phe	Leu	Thr
Val 65	Lys	Thr	Trp	Ala 70	Ser	Leu	Pro	Ile	Ser	Trp 75	Ala	Ser	Ser	Ser	Leu 80
Ser	Trp	Leu	Leu	Arg 85	Thr	Thr	Ser								

(2) INFORMATION FOR SEQ ID NO:1106:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 63 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide
(B) LOCATION: 1..63
(D) OTHER INFORMATION: / Ceres Seq. ID 1499657

(xi) SEQUENCE DESCRIPTION: SEO ID NO:1106:

Met Val Arg Val Ser Val Leu Asn Asp Ala Leu Lys Ser Met Tyr Asn
1 5 10 15
Ala Glu Lys Arg Gly Lys Arg Gln Val Met Ile Arg Pro Ser Ser Lys
20 25 30
Val Ile Ile Lys Phe Leu Thr Val Lys Thr Trp Ala Ser Leu Pro Ile
35 40 45
Ser Trp Ala Ser Ser Ser Leu Ser Trp Leu Leu Arg Thr Thr Ser
50 55 60

(2) INFORMATION FOR SEQ ID NO:1107:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..50
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499658

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1107:

Met Tyr Asn Ala Glu Lys Arg Gly Lys Arg Gln Val Met Ile Arg Pro
1 5 10 15
Ser Ser Lys Val Ile Ile Lys Phe Leu Thr Val Lys Thr Trp Ala Ser
20 25 30
Leu Pro Ile Ser Trp Ala Ser Ser Ser Leu Ser Trp Leu Leu Arg Thr
35 40 45
Thr Ser
50

(2) INFORMATION FOR SEQ ID NO:1108:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 514 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..514
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499667

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1108:

agaggatttc tattgtagaa atgcagttag gccattagg ttttgcctct ttttttttca	60
gactcggatt ggtctgccgt ccttgtgctc cgccggcaat ggcgtccacc gccgtcaagc	120
tcatcgacat cgcagtcacac ttacagatg gcatgttcaa gggcatctac cacggcaagc	180
agtgccacgc cgccgacatc ccggccgtac ttgcgcgcgc gtgggctgca ggcgtcgacc	240
gcatcattgt caccggaggc tccctgaaag agtccagaga ggcattgcag atcgccgaga	300
ccgacgggag actgttctgc actgtgggag tgcacccaac aagatgcggg gaattcgagg	360
agagtggaga tcccgarggt cattttcagg cactgctggc tctagcgaag gagggtttag	420
ataaaggcaa ggatgtrct gttggtgaat gtgggttggg ttatgacaga cttcagttct	480
gtccsggcag atatgcaaaa gaagtacttc gagg	

(2) INFORMATION FOR SEQ ID NO:1109:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 140 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..140
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499668

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1109:

Glu Asp Phe Tyr Cys Arg Asn Ala Val Arg Pro Ile Arg Phe Cys Leu
1 5 10 15
Phe Phe Phe Gln Thr Arg Ile Gly Leu Pro Ser Leu Cys Ser Ala Gly
20 25 30
Asn Gly Val His Arg Arg Gln Ala His Arg His Arg Ser Gln Leu His
35 40 45
Arg Trp His Val Gln Gly His Leu Pro Arg Gln Ala Val Pro Arg Arg
50 55 60
Arg His Pro Gly Arg Thr Cys Ala Arg Val Gly Cys Arg Arg Arg Pro
65 70 75 80
His His Cys His Arg Arg Leu Pro Glu Arg Val Gln Arg Gly Ile Ala
85 90 95
Asp Arg Arg Asp Arg Arg Glu Thr Val Leu His Cys Gly Ser Ala Pro
100 105 110
Asn Lys Met Arg Gly Ile Arg Gly Glu Trp Arg Ser Arg Xaa Ser Phe
115 120 125
Ser Gly Thr Ala Gly Ser Ser Glu Gly Gly Phe Arg
130 135 140

(2) INFORMATION FOR SEQ ID NO:1110:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 170 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..170
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499669

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1110:

Arg Ile Ser Ile Val Glu Met Gln Leu Gly Pro Leu Gly Phe Ala Ser
1 5 10 15
Phe Phe Phe Arg Leu Gly Leu Val Cys Arg Pro Cys Ala Pro Pro Ala
20 25 30
Met Ala Ser Thr Ala Val Lys Leu Ile Asp Ile Ala Val Asn Phe Thr
35 40 45
Asp Gly Met Phe Lys Gly Ile Tyr His Gly Lys Gln Cys His Ala Ala
50 55 60
Asp Ile Pro Ala Val Leu Ala Arg Ala Trp Ala Ala Gly Val Asp Arg
65 70 75 80
Ile Ile Val Thr Gly Ser Leu Lys Glu Ser Arg Glu Ala Leu Gln
85 90 95
Ile Ala Glu Thr Asp Gly Arg Leu Phe Cys Thr Val Gly Val His Pro
100 105 110
Thr Arg Cys Gly Glu Phe Glu Glu Ser Gly Asp Pro Xaa Gly His Phe
115 120 125
Gln Ala Leu Leu Ala Leu Ala Lys Glu Gly Leu Asp Lys Gly Lys Val
130 135 140
Val Xaa Val Gly Glu Cys Gly Leu Asp Tyr Asp Arg Leu Gln Phe Cys
145 150 155 160
Xaa Gly Arg Tyr Ala Lys Glu Val Leu Arg
165 170

(2) INFORMATION FOR SEQ ID NO:1111:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 164 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide

(B) LOCATION: 1..164

(D) OTHER INFORMATION: / Ceres Seq. ID 1499670

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1111:

Met	Gln	Leu	Gly	Pro	Leu	Gly	Phe	Ala	Ser	Phe	Phe	Phe	Arg	Leu	Gly
1				5					10					15	
Leu	Val	Cys	Arg	Pro	Cys	Ala	Pro	Pro	Ala	Met	Ala	Ser	Thr	Ala	Val
			20					25					30		
Lys	Leu	Ile	Asp	Ile	Ala	Val	Asn	Phe	Thr	Asp	Gly	Met	Phe	Lys	Gly
	35						40					45			
Ile	Tyr	His	Gly	Lys	Gln	Cys	His	Ala	Ala	Asp	Ile	Pro	Ala	Val	Leu
	50					55					60				
Ala	Arg	Ala	Trp	Ala	Ala	Gly	Val	Asp	Arg	Ile	Ile	Val	Thr	Gly	Gly
65					70				75					80	
Ser	Leu	Lys	Glu	Ser	Arg	Glu	Ala	Leu	Gln	Ile	Ala	Glu	Thr	Asp	Gly
			85						90					95	
Arg	Leu	Phe	Cys	Thr	Val	Gly	Val	His	Pro	Thr	Arg	Cys	Gly	Glu	Phe
			100					105					110		
Glu	Glu	Ser	Gly	Asp	Pro	Xaa	Gly	His	Phe	Gln	Ala	Leu	Leu	Ala	Leu
	115						120					125			
Ala	Lys	Glu	Gly	Leu	Asp	Lys	Gly	Lys	Val	Val	Xaa	Val	Gly	Glu	Cys
	130					135					140				
Gly	Leu	Asp	Tyr	Asp	Arg	Leu	Gln	Phe	Cys	Xaa	Gly	Arg	Tyr	Ala	Lys
145					150					155					160
Glu	Val	Leu	Arg												

(2) INFORMATION FOR SEQ ID NO:1112:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 540 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..540

(D) OTHER INFORMATION: / Ceres Seq. ID 1499671

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1112:

atagaagaag	agcaggcag	agctataagt	accccgcccc	cttccaccct	ctccttcac	60
ctccctccct	tgctgctca	tccattccag	agctgcgaag	acagacagac	agagagaaag	120
agggatcgac	ggagcaaggc	ggggccgtgt	ccggtcacac	acgagcgagc	cctctcggcc	180
gcgcgtttgt	gaatggtgaa	cvgcgagcgg	cgggcggacg	cggagtgcac	gcgggcgtcg	240
ctgctgggga	ggtatgagat	cgggcggacc	ctcggcgagg	gcaacttcgg	caaggtgaag	300
tacgcgcgcc	acatcgccag	cgggnccac	ttcgccatca	agatcctcga	ccgcagcaag	360
atcctctccc	tccgcatcga	cgaccagatc	aggagggaga	tcgggacgct	caagctgctc	420
aagcaccgga	atgtcgtccg	cttgacagag	gttgctgcca	gtaaaacgaa	gatctacatg	480
gtgcttgagt	ttgtcaacgg	cggcgagctc	ttcgacaaga	tcgctatcaa	ggggaaactg	540

(2) INFORMATION FOR SEQ ID NO:1113:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 63 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..63

(D) OTHER INFORMATION: / Ceres Seq. ID 1499672

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1113:

Ile	Glu	Glu	Glu	Gln	Ala	Gly	Ala	Ile	Ser	Thr	Pro	Pro	Pro	Ser	Thr
1				5					10					15	

Leu Ser Phe His Leu Pro Pro Leu Leu Pro His Pro Phe Gln Ser Cys
20 25 30
Glu Asp Arg Gln Thr Glu Arg Lys Arg Asp Arg Arg Ser Lys Ala Gly
35 40 45
Pro Cys Pro Val Thr His Glu Arg Ala Leu Ser Ala Ala Arg Leu
50 55 60

(2) INFORMATION FOR SEQ ID NO:1114:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 84 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..84

(D) OTHER INFORMATION: / Ceres Seq. ID 1499673

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1114:

Arg Arg Arg Ala Gly Arg Ser Tyr Lys Tyr Pro Ala Pro Phe His Pro
1 5 10 15
Leu Leu Pro Pro Ser Leu Ala Ala Ser Ser Ile Pro Glu Leu Arg
20 25 30
Arg Gln Thr Asp Arg Glu Lys Glu Gly Ser Thr Glu Gln Gly Gly Ala
35 40 45
Val Ser Gly His Thr Arg Ala Ser Pro Leu Gly Arg Ala Phe Val Asn
50 55 60
Gly Glu Xaa Arg Ala Ala Gly Gly Arg Gly Val His Ala Gly Val Ala
65 70 75 80
Ala Gly Glu Val

(2) INFORMATION FOR SEQ ID NO:1115:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 116 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..116

(D) OTHER INFORMATION: / Ceres Seq. ID 1499674

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1115:

Met Val Asn Xaa Glu Arg Arg Ala Asp Ala Glu Cys Thr Arg Ala Ser
1 5 10 15
Leu Leu Gly Arg Tyr Glu Ile Gly Arg Thr Leu Gly Glu Gly Asn Phe
20 25 30
Gly Lys Val Lys Tyr Ala Arg His Ile Ala Ser Gly Xaa His Phe Ala
35 40 45
Ile Lys Ile Leu Asp Arg Ser Lys Ile Leu Ser Leu Arg Ile Asp Asp
50 55 60
Gln Ile Arg Arg Glu Ile Gly Thr Leu Lys Leu Leu Lys His Pro Asn
65 70 75 80
Val Val Arg Leu His Glu Val Ala Ala Ser Lys Thr Lys Ile Tyr Met
85 90 95
Val Leu Glu Phe Val Asn Gly Gly Glu Leu Phe Asp Lys Ile Ala Ile
100 105 110
Lys Gly Lys Leu
115

(2) INFORMATION FOR SEQ ID NO:1116:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 478 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..478
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1499675

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1116:

aaaaaccaca acacaagaac gggaagcgtg catgcacacg caccgagcacg aacctgagct	60
gtagcgccct ctcgctcgtc ccccgcgcgc aatggccagc gtascccagg tcccatgcaa	120
accagccatg cctcacggcg gccgatccct acagctacag gccccgtgcc cgtggccgtg	180
cttctcgccg ccgcgcgcgt cggcctcctc gcgctgctgc cgtcgtggtg cgaggccgtg	240
tgggaggtgc cgcacctctt cctcctcggc gccgtcatct ccttcggcgt cttcacgcag	300
aggaacacgc acgccgacgg ccgcgccaag gacagctcac aggcgtggag cgcggtgtgc	360
caccccgatg cccccctcgt cgtgatcgcg gatcacacg cgccgagcga cgacgacgac	420
aacgacgact acgggctgga actggaagaa ggcgacacg agacgccgct ttcgttgc	

(2) INFORMATION FOR SEQ ID NO:1117:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 158 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..158
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1499676

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1117:

Lys	Pro	Gln	His	Lys	Asn	Gly	Lys	Arg	Ala	Cys	Thr	Arg	Thr	Ser	Thr
1			5						10					15	
Asn	Leu	Ser	Cys	Ser	Ala	Leu	Ser	Leu	Ala	Pro	Arg	Ala	Gln	Trp	Pro
			20						25				30		
Ala	Xaa	Pro	Arg	Ser	His	Ala	Asn	Gln	Pro	Cys	Leu	Thr	Ala	Ala	Asp
			35				40					45			
Pro	Tyr	Ser	Tyr	Arg	Pro	Arg	Ala	Arg	Gly	Arg	Ala	Ser	Arg	Arg	Arg
			50				55				60				
Arg	Arg	Arg	Pro	Pro	Arg	Ala	Ala	Ala	Val	Ala	Gly	Arg	Gly	Arg	Val
65					70				75					80	
Gly	Gly	Ala	Ala	Pro	Leu	Pro	Pro	Arg	Arg	Arg	His	Leu	Leu	Arg	Arg
				85					90					95	
Leu	His	Ala	Glu	Glu	Gln	Arg	Arg	Arg	Arg	Pro	Arg	Gln	Gly	Gln	Leu
			100						105					110	
Thr	Gly	Val	Glu	Arg	Gly	Val	Pro	Pro	Arg	Cys	Pro	Pro	Arg	Arg	Asp
			115				120					125			
Arg	Gly	Ser	His	Gly	Ala	Glu	Arg	Arg	Arg	Arg	Gln	Arg	Arg	Leu	Arg
			130				135				140				
Ala	Gly	Thr	Gly	Arg	Arg	Arg	Thr	Arg	Asp	Ala	Ala	Phe	Val		
145					150					155					

(2) INFORMATION FOR SEQ ID NO:1118:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 97 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..97
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1499677
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1118:

Met Ala Ser Val Xaa Gln Val Pro Cys Lys Pro Ala Met Pro His Gly
1 5 10 15
Gly Arg Ser Leu Gln Leu Gln Ala Pro Cys Pro Trp Pro Cys Phe Ser
20 25 30
Pro Pro Pro Pro Ser Ala Ser Ser Arg Cys Cys Arg Arg Trp Pro Arg
35 40 45
Pro Cys Gly Arg Cys Arg Thr Ser Ser Ser Ser Ala Pro Ser Ser Pro
50 55 60
Ser Ala Ser Ser Arg Arg Gly Thr Ala Thr Pro Thr Ala Ala Pro Arg
65 70 75 80
Thr Ala His Arg Arg Gly Ala Arg Cys Ala Thr Pro Met Pro Pro Ser
85 90 95
Ser

(2) INFORMATION FOR SEQ ID NO:1119:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 121 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..121
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499678

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1119:

Met Gln Thr Ser His Ala Ser Arg Arg Pro Ile Pro Thr Ala Thr Gly
1 5 10 15
Pro Val Pro Val Ala Val Leu Leu Ala Ala Ala Val Gly Leu Leu
20 25 30
Ala Leu Leu Pro Ser Leu Ala Glu Ala Val Trp Glu Val Pro His Leu
35 40 45
Phe Leu Leu Gly Ala Val Ile Ser Phe Gly Val Phe Thr Gln Arg Asn
50 55 60
Ser Asp Ala Asp Gly Arg Ala Lys Asp Ser Ser Gln Ala Trp Ser Ala
65 70 75 80
Val Cys His Pro Asp Ala Pro Leu Val Val Ile Ala Asp His Thr Ala
85 90 95
Pro Ser Asp Asp Asp Asp Asn Asp Asp Tyr Gly Leu Glu Leu Glu Glu
100 105 110
Gly Ala Arg Glu Thr Pro Leu Ser Leu
115 120

(2) INFORMATION FOR SEQ ID NO:1120:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 518 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..518
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499686

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1120:

aggcagagca	ctgcacgcca	ccttatctct	aaccggagat	caaagaagta	gccgttaacg	60
atggcttccg	acgagctcgc	aaaggccgtc	gagcccagga	agaagggcaa	cgtcaagtat	120
gcctccatat	gtgccatcct	ggcctccatg	gcctctgtca	tccttggtta	tgacattggg	180
gtgatgagt	gagcggccat	gtacatcaag	aaggacctga	atatcacgga	cgtkcagctg	240
gagatcctga	tcgggatcct	cagtctctac	tcgctgttcg	gatccttcgc	tggcgcgcgg	300
acgtccgaca	ggatcggggc	ccgcttgacc	gtcgtgttcg	ccgctgtcat	cttcttcgtg	360
ggctcgttgc	tcatggggtt	cgccgtcaac	tacggcatgc	tcatggcggg	ccgcttcgtg	420

gccggagtcg gtgtgggcta cgggggcatg atcgcrcccg tgtacacggc cgagatctcg 480
cctgcrgstc ccgtggcttc ctgaccacct tcccggag

(2) INFORMATION FOR SEQ ID NO:1121:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 147 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..147
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499687

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1121:

Met Ala Ser Asp Glu Leu Ala Lys Ala Val Glu Pro Arg Lys Lys Gly
1 5 10 15
Asn Val Lys Tyr Ala Ser Ile Cys Ala Ile Leu Ala Ser Met Ala Ser
20 25 30
Val Ile Leu Gly Tyr Asp Ile Gly Val Met Ser Gly Ala Ala Met Tyr
35 40 45
Ile Lys Lys Asp Leu Asn Ile Thr Asp Xaa Gln Leu Glu Ile Leu Ile
50 55 60
Gly Ile Leu Ser Leu Tyr Ser Leu Phe Gly Ser Phe Ala Gly Ala Arg
65 70 75 80
Thr Ser Asp Arg Ile Gly Arg Arg Leu Thr Val Val Phe Ala Ala Val
85 90 95
Ile Phe Phe Val Gly Ser Leu Leu Met Gly Phe Ala Val Asn Tyr Gly
100 105 110
Met Leu Met Ala Gly Arg Phe Val Ala Gly Val Gly Val Gly Tyr Gly
115 120 125
Gly Met Ile Xaa Pro Val Tyr Thr Ala Glu Ile Ser Pro Xaa Xaa Pro
130 135 140
Val Ala Ser
145

(2) INFORMATION FOR SEQ ID NO:1122:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 118 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..118
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499688

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1122:

Met Ala Ser Val Ile Leu Gly Tyr Asp Ile Gly Val Met Ser Gly Ala
1 5 10 15
Ala Met Tyr Ile Lys Lys Asp Leu Asn Ile Thr Asp Xaa Gln Leu Glu
20 25 30
Ile Leu Ile Gly Ile Leu Ser Leu Tyr Ser Leu Phe Gly Ser Phe Ala
35 40 45
Gly Ala Arg Thr Ser Asp Arg Ile Gly Arg Arg Leu Thr Val Val Phe
50 55 60
Ala Ala Val Ile Phe Phe Val Gly Ser Leu Leu Met Gly Phe Ala Val
65 70 75 80
Asn Tyr Gly Met Leu Met Ala Gly Arg Phe Val Ala Gly Val Gly Val
85 90 95
Gly Tyr Gly Gly Met Ile Xaa Pro Val Tyr Thr Ala Glu Ile Ser Pro
100 105 110
Xaa Xaa Pro Val Ala Ser

115

(2) INFORMATION FOR SEQ ID NO:1123:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 106 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..106

(D) OTHER INFORMATION: / Ceres Seq. ID 1499689

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1123:

Met Ser Gly Ala Ala Met Tyr Ile Lys Asp Leu Asn Ile Thr Asp
1 5 10 15
Xaa Gln Leu Glu Ile Leu Ile Gly Ile Leu Ser Leu Tyr Ser Leu Phe
20 25 30
Gly Ser Phe Ala Gly Ala Arg Thr Ser Asp Arg Ile Gly Arg Arg Leu
35 40 45
Thr Val Val Phe Ala Ala Val Ile Phe Phe Val Gly Ser Leu Leu Met
50 55 60
Gly Phe Ala Val Asn Tyr Gly Met Leu Met Ala Gly Arg Phe Val Ala
65 70 75 80
Gly Val Gly Val Gly Tyr Gly Gly Met Ile Xaa Pro Val Tyr Thr Ala
85 90 95
Glu Ile Ser Pro Xaa Xaa Pro Val Ala Ser
100 105

(2) INFORMATION FOR SEQ ID NO:1124:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 861 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..861

(D) OTHER INFORMATION: / Ceres Seq. ID 1499690

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1124:

aagcaagcga asatcgccag attggtatat cgatcgattg awcrghnnnn gavgaangrg 60
aggacggrgg gcagatggcg gcggtgccgg gcttcttcga gtgcctgctc aggctgctca 120
acttcaccc caccgtcgcc ggcctcgcta tggttgggta cgggatctac ctgctcgctc 180
agtggatgaa gatattccgan gacggcator gcggggcttc gacggcgbag gtgctcgtct 240
ctdgccggcc gttgttgggg gctgtcattc tcggtgacag ctctcctgac aatctaccca 300
aagcatggtt tatttatttg tttattggtg ttggcaccat cgtcattctt gtgtctctgt 360
ttggctgcat tggagcaggg acaagaaaca cctgctgttt gtgtttctat gctttcttgg 420
tcatattggt gatccttgct gaagctgcag ctgctgcatt cattttcttt gaccatggct 480
ggaaagatgt aattccagtg gacaaaacac ataactttga tgttatgtat gactttctga 540
aggaaaactg ggagattgca agatgggtcg ctctgggcgt tggtgttttt gaggcagtgc 600
tcttgctgtt agctctggct gtcagggcaa tgaacaaacc tgctgagtat gacagtgatg 660
acgaaattat agcaattggc cgaagcccta ccatccggca gccactgatc catacccaaa 720
atgttcctgc cactggtgtt cctgtcccaa cacttgatca acgtgcaagt agaaatgatg 780
cctggagcca aaggatgcga gagaagtatg gtctggacac gagccagttc acatacaacc 840
cttcagaccc aagcaggtac c

(2) INFORMATION FOR SEQ ID NO:1125:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 262 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..262

(D) OTHER INFORMATION: / Ceres Seq. ID 1499691

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1125:

Met Ala Ala Cys Arg Gly Phe Phe Glu Cys Leu Leu Arg Leu Leu Asn
1 5 10 15
Phe Ile Leu Thr Val Ala Gly Leu Ala Met Val Gly Tyr Gly Ile Tyr
20 25 30
Leu Leu Val Glu Trp Met Lys Ile Ser Xaa Asp Gly Ile Xaa Gly Ala
35 40 45
Ser Thr Ala Xaa Val Leu Val Ser Xaa Arg Pro Leu Leu Gly Ala Val
50 55 60
Ile Leu Gly Asp Ser Phe Leu Asp Asn Leu Pro Lys Ala Trp Phe Ile
65 70 75 80
Tyr Leu Phe Ile Gly Val Gly Thr Ile Val Ile Leu Val Ser Leu Phe
85 90 95
Gly Cys Ile Gly Ala Gly Thr Arg Asn Thr Cys Cys Leu Cys Phe Tyr
100 105 110
Ala Phe Leu Val Ile Leu Leu Ile Leu Ala Glu Ala Ala Ala Ala
115 120 125
Phe Ile Phe Phe Asp His Gly Trp Lys Asp Val Ile Pro Val Asp Lys
130 135 140
Thr His Asn Phe Asp Val Met Tyr Asp Phe Leu Lys Glu Asn Trp Glu
145 150 155 160
Ile Ala Arg Trp Val Ala Leu Gly Val Val Val Phe Glu Ala Val Leu
165 170 175
Leu Leu Leu Ala Leu Ala Val Arg Ala Met Asn Lys Pro Ala Glu Tyr
180 185 190
Asp Ser Asp Asp Glu Ile Ile Ala Ile Gly Arg Ser Pro Thr Ile Arg
195 200 205
Gln Pro Leu Ile His Thr Gln Asn Val Pro Ala Thr Gly Val Pro Val
210 215 220
Pro Thr Leu Asp Gln Arg Ala Ser Arg Asn Asp Ala Trp Ser Gln Arg
225 230 235 240
Met Arg Glu Lys Tyr Gly Leu Asp Thr Ser Gln Phe Thr Tyr Asn Pro
245 250 255
Ser Asp Pro Ser Arg Tyr
260

(2) INFORMATION FOR SEQ ID NO:1126:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 237 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..237

(D) OTHER INFORMATION: / Ceres Seq. ID 1499692

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1126:

Met Val Gly Tyr Gly Ile Tyr Leu Leu Val Glu Trp Met Lys Ile Ser
1 5 10 15
Xaa Asp Gly Ile Xaa Gly Ala Ser Thr Ala Xaa Val Leu Val Ser Xaa
20 25 30
Arg Pro Leu Leu Gly Ala Val Ile Leu Gly Asp Ser Phe Leu Asp Asn
35 40 45
Leu Pro Lys Ala Trp Phe Ile Tyr Leu Phe Ile Gly Val Gly Thr Ile
50 55 60
Val Ile Leu Val Ser Leu Phe Gly Cys Ile Gly Ala Gly Thr Arg Asn
65 70 75 80

Thr Cys Cys Leu Cys Phe Tyr Ala Phe Leu Val Ile Leu Leu Ile Leu
85 90 95
Ala Glu Ala Ala Ala Ala Phe Ile Phe Phe Asp His Gly Trp Lys
100 105 110
Asp Val Ile Pro Val Asp Lys Thr His Asn Phe Asp Val Met Tyr Asp
115 120 125
Phe Leu Lys Glu Asn Trp Glu Ile Ala Arg Trp Val Ala Leu Gly Val
130 135 140
Val Val Phe Glu Ala Val Leu Leu Leu Leu Ala Leu Ala Val Arg Ala
145 150 155 160
Met Asn Lys Pro Ala Glu Tyr Asp Ser Asp Asp Glu Ile Ile Ala Ile
165 170 175
Gly Arg Ser Pro Thr Ile Arg Gln Pro Leu Ile His Thr Gln Asn Val
180 185 190
Pro Ala Thr Gly Val Pro Val Pro Thr Leu Asp Gln Arg Ala Ser Arg
195 200 205
Asn Asp Ala Trp Ser Gln Arg Met Arg Glu Lys Tyr Gly Leu Asp Thr
210 215 220
Ser Gln Phe Thr Tyr Asn Pro Ser Asp Pro Ser Arg Tyr
225 230 235

(2) INFORMATION FOR SEQ ID NO:1127:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 225 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..225

(D) OTHER INFORMATION: / Ceres Seq. ID 1499693

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1127:

Met Lys Ile Ser Xaa Asp Gly Ile Xaa Gly Ala Ser Thr Ala Xaa Val
1 5 10 15
Leu Val Ser Xaa Arg Pro Leu Leu Gly Ala Val Ile Leu Gly Asp Ser
20 25 30
Phe Leu Asp Asn Leu Pro Lys Ala Trp Phe Ile Tyr Leu Phe Ile Gly
35 40 45
Val Gly Thr Ile Val Ile Leu Val Ser Leu Phe Gly Cys Ile Gly Ala
50 55 60
Gly Thr Arg Asn Thr Cys Cys Leu Cys Phe Tyr Ala Phe Leu Val Ile
65 70 75 80
Leu Leu Ile Leu Ala Glu Ala Ala Ala Ala Ala Phe Ile Phe Phe Asp
85 90 95
His Gly Trp Lys Asp Val Ile Pro Val Asp Lys Thr His Asn Phe Asp
100 105 110
Val Met Tyr Asp Phe Leu Lys Glu Asn Trp Glu Ile Ala Arg Trp Val
115 120 125
Ala Leu Gly Val Val Val Phe Glu Ala Val Leu Leu Leu Leu Ala Leu
130 135 140
Ala Val Arg Ala Met Asn Lys Pro Ala Glu Tyr Asp Ser Asp Asp Glu
145 150 155 160
Ile Ile Ala Ile Gly Arg Ser Pro Thr Ile Arg Gln Pro Leu Ile His
165 170 175
Thr Gln Asn Val Pro Ala Thr Gly Val Pro Val Pro Thr Leu Asp Gln
180 185 190
Arg Ala Ser Arg Asn Asp Ala Trp Ser Gln Arg Met Arg Glu Lys Tyr
195 200 205
Gly Leu Asp Thr Ser Gln Phe Thr Tyr Asn Pro Ser Asp Pro Ser Arg
210 215 220
Tyr

225

(2) INFORMATION FOR SEQ ID NO:1128:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 435 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..435
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499694

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1128:

aatatcatgc	gcaggggctg	aaagctgaaa	ctgctcaaga	cgccaccgtc	ttcctccgcg	60
atcttcagtt	ctctgtctct	ccctctctct	ttcctctagc	tcccaaccaa	gccaagagta	120
cgctgtcaag	cgcgccgcs	gtgtgtgtgt	cagtaggcta	cagggctcgg	aggaacgccg	180
tcatgagctt	gatcagcatg	atggaggcgc	ggctgccgcc	ggggttccgg	ttccaccgca	240
gggacgacga	gctcgtgctc	gactacctct	gccgcaagct	ctccggcaaa	ggcggcgccg	300
gasgtacggc	ggcatcgcat	ggtcgacgtc	gacctcaaca	agtgcgagcc	gtgggatctt	360
ccagacgagg	cgtrcrtggg	cggccgcgag	tggtacttct	tcagcctgca	cgaccgcaag	420
tacgccacgg	ggcag					

(2) INFORMATION FOR SEQ ID NO:1129:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 144 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..144
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499695

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1129:

Tyr	His	Ala	Gln	Gly	Leu	Lys	Ala	Glu	Thr	Ala	Gln	Asp	Ala	Thr	Val	
1				5				10						15		
Phe	Leu	Arg	Asp	Leu	Gln	Phe	Ser	Val	Ser	Pro	Ser	Leu	Phe	Pro	Leu	
				20				25						30		
Ala	Pro	Asn	Gln	Ala	Lys	Ser	Thr	Ser	Ser	Ser	Ala	Pro	Xaa	Xaa	Cys	
				35				40						45		
Val	Ser	Val	Gly	Tyr	Arg	Ala	Arg	Arg	Asn	Ala	Val	Met	Ser	Leu	Ile	
				50				55						60		
Ser	Met	Met	Glu	Ala	Arg	Leu	Pro	Pro	Gly	Phe	Arg	Phe	His	Pro	Arg	
65				70						75				80		
Asp	Asp	Glu	Leu	Val	Leu	Asp	Tyr	Leu	Cys	Arg	Lys	Leu	Ser	Gly	Lys	
				85						90				95		
Gly	Gly	Gly	Gly	Xaa	Thr	Ala	Ala	Ser	His	Gly	Arg	Arg	Arg	Pro	Gln	
				100				105						110		
Gln	Val	Arg	Ala	Val	Gly	Ser	Ser	Arg	Arg	Gly	Xaa	Xaa	Gly	Arg	Pro	
				115				120						125		
Arg	Val	Val	Leu	Leu	Gln	Pro	Ala	Arg	Pro	Gln	Val	Arg	His	Gly	Ala	
				130				135						140		

(2) INFORMATION FOR SEQ ID NO:1130:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 84 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide
(B) LOCATION: 1..84
(D) OTHER INFORMATION: / Ceres Seq. ID 1499696

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1130:

Met	Ser	Leu	Ile	Ser	Met	Met	Glu	Ala	Arg	Leu	Pro	Pro	Gly	Phe	Arg
1				5					10					15	
Phe	His	Pro	Arg	Asp	Asp	Glu	Leu	Val	Leu	Asp	Tyr	Leu	Cys	Arg	Lys
			20					25					30		
Leu	Ser	Gly	Lys	Gly	Gly	Gly	Gly	Xaa	Thr	Ala	Ala	Ser	His	Gly	Arg
		35					40					45			
Arg	Arg	Pro	Gln	Gln	Val	Arg	Ala	Val	Gly	Ser	Ser	Arg	Arg	Gly	Xaa
	50					55					60				
Xaa	Gly	Arg	Pro	Arg	Val	Val	Leu	Leu	Gln	Pro	Ala	Arg	Pro	Gln	Val
65					70				75					80	
Arg	His	Gly	Ala												

(2) INFORMATION FOR SEQ ID NO:1131:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 79 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide
(B) LOCATION: 1..79
(D) OTHER INFORMATION: / Ceres Seq. ID 1499697

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1131:

Met	Met	Glu	Ala	Arg	Leu	Pro	Pro	Gly	Phe	Arg	Phe	His	Pro	Arg	Asp
1				5					10					15	
Asp	Glu	Leu	Val	Leu	Asp	Tyr	Leu	Cys	Arg	Lys	Leu	Ser	Gly	Lys	Gly
			20					25				30			
Gly	Gly	Gly	Xaa	Thr	Ala	Ala	Ser	His	Gly	Arg	Arg	Arg	Pro	Gln	Gln
		35					40					45			
Val	Arg	Ala	Val	Gly	Ser	Ser	Arg	Arg	Gly	Xaa	Xaa	Gly	Arg	Pro	Arg
	50					55					60				
Val	Val	Leu	Leu	Gln	Pro	Ala	Arg	Pro	Gln	Val	Arg	His	Gly	Ala	
65				70					75						

(2) INFORMATION FOR SEQ ID NO:1132:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1156 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -
(B) LOCATION: 1..1156
(D) OTHER INFORMATION: / Ceres Seq. ID 1499720

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1132:

atttttcgctc	aaaagaatca	gtaaaaacta	aacattttga	ctatatccta	cttgaatcaa	60
ttcttcggct	gattttgaag	ttttgtgaca	ttcagatatt	ctagggtttt	gtggtaaagt	120
gaatcgaatc	acgaaggcaa	cgcgatacaa	gtgattgacc	aagtaacaac	catgacccat	180
ctgtctgacc	cgaatccgaa	aaccaaaccg	ggtatgatgc	tcatgaaaca	agaagacggg	240
tatttgcagc	cggatgaagac	taaaccgggt	ccgaagagac	cgacttctaa	agaccgtcac	300
acgaaagtag	aaggacgagg	tcggaggagt	cgaatgccgg	cgggttgccg	tgctcgggtc	360
tttcaattga	cccgtgaact	tggtcacaaa	tccgacggag	aaacgatacg	gtggttattg	420
gaacgagctg	aaccggcgat	aattgaagca	accggaaccg	gaactgtacc	ggctattgct	480
gtatcgggta	acggaacttt	aaaaatcccg	acgagctctc	cagtgttgaa	tgacggcggc	540
cgtgacggtg	acggtgacct	aatgaagaaa	cggaggaaga	gaaactgtac	gagcgatttc	600
gtagacgtta	atgacagctg	tcatagctcc	gttacttctg	ggtagctcc	gataacggcg	660

tcaaaactacg	gcgtaaatat	cctgaacgtt	aatacacagg	ggtttgtgcc	gttttggcct	720
atgggtatgg	gtactgcgta	tgttactggt	gggccggatc	aaatggggcca	aatgtgggct	780
attcctaccg	ttgctacagc	tccgtttctc	aatgttggtg	ctagaccggt	gtctagttat	840
gtctcaaacg	cttcagacgc	tgaggcggag	atggaaacga	gcggtggcgg	aacgacgcaa	900
ccgctgaggg	atttttcgtt	ggagatttat	gataagagag	agcttcagtt	tttgggtggc	960
tcagggaact	catctccgtc	ttcatgtcat	gagacttaag	gaattttaac	tcttagttct	1020
agtttctttt	tagtttttag	taagtttgat	tcctgattta	ggttaagtaa	gatttgtaaa	1080
agaattggga	gcacaatttc	aattttatgt	ttctgtcaaa	cattttggta	attaatgaaa	1140
ctatcctatc	attttt					

(2) INFORMATION FOR SEQ ID NO:1133:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 293 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..293

(D) OTHER INFORMATION: / Ceres Seq. ID 1499721

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1133:

Met	Glu	Ser	Asn	His	Glu	Gly	Asn	Ala	Ile	Gln	Val	Ile	Asp	Gln	Val
1			5						10					15	
Thr	Thr	Met	Thr	His	Leu	Ser	Asp	Pro	Asn	Pro	Lys	Thr	Lys	Pro	Gly
			20					25					30		
Met	Met	Leu	Met	Lys	Gln	Glu	Asp	Gly	Tyr	Leu	Gln	Pro	Val	Lys	Thr
			35				40					45			
Lys	Pro	Ala	Pro	Lys	Arg	Pro	Thr	Ser	Lys	Asp	Arg	His	Thr	Lys	Val
			50			55					60				
Glu	Gly	Arg	Gly	Arg	Arg	Ile	Arg	Met	Pro	Ala	Gly	Cys	Ala	Ala	Arg
65					70					75					80
Val	Phe	Gln	Leu	Thr	Arg	Glu	Leu	Gly	His	Lys	Ser	Asp	Gly	Glu	Thr
				85					90					95	
Ile	Arg	Trp	Leu	Leu	Glu	Arg	Ala	Glu	Pro	Ala	Ile	Ile	Glu	Ala	Thr
			100					105					110		
Gly	Thr	Gly	Thr	Val	Pro	Ala	Ile	Ala	Val	Ser	Val	Asn	Gly	Thr	Leu
			115				120						125		
Lys	Ile	Pro	Thr	Ser	Ser	Pro	Val	Leu	Asn	Asp	Gly	Gly	Arg	Asp	Gly
			130				135					140			
Asp	Gly	Asp	Leu	Met	Lys	Lys	Arg	Arg	Lys	Arg	Asn	Cys	Thr	Ser	Asp
145					150					155				160	
Phe	Val	Asp	Val	Asn	Asp	Ser	Cys	His	Ser	Ser	Val	Thr	Ser	Gly	Leu
				165					170					175	
Ala	Pro	Ile	Thr	Ala	Ser	Asn	Tyr	Gly	Val	Asn	Ile	Leu	Asn	Val	Asn
			180					185					190		
Thr	Gln	Gly	Phe	Val	Pro	Phe	Trp	Pro	Met	Gly	Met	Gly	Thr	Ala	Tyr
			195				200					205			
Val	Thr	Gly	Gly	Pro	Asp	Gln	Met	Gly	Gln	Met	Trp	Ala	Ile	Pro	Thr
			210			215					220				
Val	Ala	Thr	Ala	Pro	Phe	Leu	Asn	Val	Gly	Ala	Arg	Pro	Val	Ser	Ser
225					230					235				240	
Tyr	Val	Ser	Asn	Ala	Ser	Asp	Ala	Glu	Ala	Glu	Met	Glu	Thr	Ser	Gly
				245					250					255	
Gly	Gly	Thr	Thr	Gln	Pro	Leu	Arg	Asp	Phe	Ser	Leu	Glu	Ile	Tyr	Asp
			260				265						270		
Lys	Arg	Glu	Leu	Gln	Phe	Leu	Gly	Ser	Gly	Asn	Ser	Ser	Pro	Ser	
			275				280					285			
Ser	Cys	His	Glu	Thr											
			290												

(2) INFORMATION FOR SEQ ID NO:1134:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 275 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..275
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1499722
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1134:

Met Thr His Leu Ser Asp Pro Asn Pro Lys Thr Lys Pro Gly Met Met
1 5 10 15
Leu Met Lys Gln Glu Asp Gly Tyr Leu Gln Pro Val Lys Thr Lys Pro
20 25 30
Ala Pro Lys Arg Pro Thr Ser Lys Asp Arg His Thr Lys Val Glu Gly
35 40 45
Arg Gly Arg Arg Ile Arg Met Pro Ala Gly Cys Ala Ala Arg Val Phe
50 55 60
Gln Leu Thr Arg Glu Leu Gly His Lys Ser Asp Gly Glu Thr Ile Arg
65 70 75 80
Trp Leu Leu Glu Arg Ala Glu Pro Ala Ile Ile Glu Ala Thr Gly Thr
85 90 95
Gly Thr Val Pro Ala Ile Ala Val Ser Val Asn Gly Thr Leu Lys Ile
100 105 110
Pro Thr Ser Ser Pro Val Leu Asn Asp Gly Gly Arg Asp Gly Asp Gly
115 120 125
Asp Leu Met Lys Lys Arg Arg Lys Arg Asn Cys Thr Ser Asp Phe Val
130 135 140
Asp Val Asn Asp Ser Cys His Ser Ser Val Thr Ser Gly Leu Ala Pro
145 150 155 160
Ile Thr Ala Ser Asn Tyr Gly Val Asn Ile Leu Asn Val Asn Thr Gln
165 170 175
Gly Phe Val Pro Phe Trp Pro Met Gly Met Gly Thr Ala Tyr Val Thr
180 185 190
Gly Gly Pro Asp Gln Met Gly Gln Met Trp Ala Ile Pro Thr Val Ala
195 200 205
Thr Ala Pro Phe Leu Asn Val Gly Ala Arg Pro Val Ser Ser Tyr Val
210 215 220
Ser Asn Ala Ser Asp Ala Glu Ala Glu Met Glu Thr Ser Gly Gly Gly
225 230 235 240
Thr Thr Gln Pro Leu Arg Asp Phe Ser Leu Glu Ile Tyr Asp Lys Arg
245 250 255
Glu Leu Gln Phe Leu Gly Gly Ser Gly Asn Ser Ser Pro Ser Ser Cys
260 265 270
His Glu Thr
275

(2) INFORMATION FOR SEQ ID NO:1135:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 261 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..261
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1499723
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1135:

Met Met Leu Met Lys Gln Glu Asp Gly Tyr Leu Gln Pro Val Lys Thr
1 5 10 15
Lys Pro Ala Pro Lys Arg Pro Thr Ser Lys Asp Arg His Thr Lys Val

	20		25		30
Glu Gly Arg Gly Arg Arg Ile Arg Met Pro Ala Gly Cys Ala Ala Arg					
Val Phe Gln Leu Thr Arg Glu Leu Gly His Lys Ser Asp Gly Glu Thr	35	40	45		
Ile Arg Trp Leu Leu Glu Arg Ala Glu Pro Ala Ile Ile Glu Ala Thr	50	55	60		
Gly Thr Gly Thr Val Pro Ala Ile Ala Val Ser Val Asn Gly Thr Leu	65	70	75	80	
Lys Ile Pro Thr Ser Ser Pro Val Leu Asn Asp Gly Gly Arg Asp Gly	85	90	95		
Asp Gly Asp Leu Met Lys Lys Arg Arg Lys Arg Asn Cys Thr Ser Asp	100	105	110		
Phe Val Asp Val Asn Asp Ser Cys His Ser Ser Val Thr Ser Gly Leu	115	120	125		
Ala Pro Ile Thr Ala Ser Asn Tyr Gly Val Asn Ile Leu Asn Val Asn	130	135	140		
Thr Gln Gly Phe Val Pro Phe Trp Pro Met Gly Met Gly Thr Ala Tyr	145	150	155	160	
Val Thr Gly Gly Pro Asp Gln Met Gly Gln Met Trp Ala Ile Pro Thr	165	170	175		
Val Ala Thr Ala Pro Phe Leu Asn Val Gly Ala Arg Pro Val Ser Ser	180	185	190		
Tyr Val Ser Asn Ala Ser Asp Ala Glu Ala Glu Met Glu Thr Ser Gly	195	200	205		
Gly Gly Thr Thr Gln Pro Leu Arg Asp Phe Ser Leu Glu Ile Tyr Asp	210	215	220		
Lys Arg Glu Leu Gln Phe Leu Gly Gly Ser Gly Asn Ser Ser Pro Ser	225	230	235	240	
Ser Cys His Glu Thr	245	250	255		
	260				

(2) INFORMATION FOR SEQ ID NO:1136:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1680 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1680
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499728

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1136:

cattaacggtt gttgcagagg aaagctggaa aatagagagt tcgatgaact cttgttacta	60
taatggaggc tcaggagttt gaaaaccgag agatttcccc cggttcgagg ttcctgattg	120
agaatcagat cagaagtagc tcaatatgtt gacaactacc accgatgagg aaatagactt	180
gtcctgcgac ggaggtgtca cggagcctca aaaagttgct ataatcttcg cgttttgtgg	240
tgtaggatac caaggaatgc aaaagaatcc cggcgcgaaa accattgaag gcgagctcga	300
agaagctttg tttcatgccg gagctgtacc ggagtcatt agaggcaagc caaaactata	360
cgatttcgca cgatctgcac ggacagataa aggagttagt gctggtggac aagtagtttc	420
aggctcgctt atcgttgatc cacttggatt cgtgaatcgt ctcaattcaa atctccctaa	480
tcagattaga atcttcgggtt acaagcatgt aacgccgctg tttagctcca agaagttttg	540
cgatcgaaga aggtatgtgt atctgcttcc agtgtttgct cttgatccaa tctcgcatcg	600
tgatagagaa acagtaattg ctagtttggg tccgggagag gaatatgtta agtgctttga	660
gtgctcagag agaggtcgta agattcctcc aggtcttgtg ggtaaattga aaggtaccaa	720
ctttgggact aaatcattgg attttcagtc agacatttcg tcgaacaact ctagtgcatt	780
aagaagtgac atcaagattg aagctttgag ttctaattta gctggcttat gctcagtaga	840
tgttgaagta ggtaggatac aagaagacag ttgtaaattg aatacaaaatt catcagagac	900
taaggtaaag agcaagtttt gttatggtga aaaggaaaag gaaaggttca gtagaatact	960
aagttgttat gttggatcat ataatttcca taacttcact acaagaacaa aagcagatga	1020
tccgactgcg aatcgtcaaa tcattctcct cactgctaact actgtgatta atcttgatgg	1080

gattgacttt	atcaagtgtg	aagtcttagg	caaaagcttt	atgottcatc	agattcggaa	1140
gatgatgggt	cttgctgttg	caatcatgcg	gaattgtgct	tctgaatcac	ttatccaaag	1200
tgctttcagc	aaggatgtga	atataactgt	accaatggcg	ccagaagttg	gactttatct	1260
ggacgaatgc	ttcttcacat	cttataacag	aaactttgaa	gacagtcacg	aagaagtgtc	1320
catggaagca	tacaaagaag	aagctgaagc	attcaaattg	aagcatatct	attctcatat	1380
cggcgctaca	gagcgaaaat	acggaaatat	ggctctttgg	ttacattcct	tgaactatag	1440
aaactatcca	gacctaaact	ttggcagctg	tggaacaaaac	acagaccaag	ttcttggtca	1500
taagaaaatt	gatgaaagag	caagtcacag	tctctaagca	aaatgatgga	agcttagttt	1560
gaagattttg	acattgtttt	tgttattgtt	ggttaatccc	accatttttg	taacttttta	1620
atcaaattag	tatatttttg	tgttgtaagg	tgacactaat	gaattgattt	gttatcctcc	1680

(2) INFORMATION FOR SEQ ID NO:1137:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 463 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..463

(D) OTHER INFORMATION: / Ceres Seq. ID 1499729

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1137:

Met	Leu	Thr	Thr	Thr	Thr	Asp	Glu	Glu	Ile	Asp	Leu	Ser	Cys	Asp	Gly	
1				5					10					15		
Gly	Val	Thr	Glu	Pro	Gln	Lys	Val	Ala	Ile	Ile	Phe	Ala	Phe	Cys	Gly	
			20					25					30			
Val	Gly	Tyr	Gln	Gly	Met	Gln	Lys	Asn	Pro	Gly	Ala	Lys	Thr	Ile	Glu	
		35					40					45				
Gly	Glu	Leu	Glu	Glu	Ala	Leu	Phe	His	Ala	Gly	Ala	Val	Pro	Glu	Ser	
	50					55					60					
Ile	Arg	Gly	Lys	Pro	Lys	Leu	Tyr	Asp	Phe	Ala	Arg	Ser	Ala	Arg	Thr	
65					70				75					80		
Asp	Lys	Gly	Val	Ser	Ala	Val	Gly	Gln	Val	Val	Ser	Gly	Arg	Phe	Ile	
			85						90					95		
Val	Asp	Pro	Leu	Gly	Phe	Val	Asn	Arg	Leu	Asn	Ser	Asn	Leu	Pro	Asn	
			100					105					110			
Gln	Ile	Arg	Ile	Phe	Gly	Tyr	Lys	His	Val	Thr	Pro	Ser	Phe	Ser	Ser	
		115					120					125				
Lys	Lys	Phe	Cys	Asp	Arg	Arg	Arg	Tyr	Val	Tyr	Leu	Leu	Pro	Val	Phe	
	130					135					140					
Ala	Leu	Asp	Pro	Ile	Ser	His	Arg	Asp	Arg	Glu	Thr	Val	Met	Ala	Ser	
145					150					155				160		
Leu	Gly	Pro	Gly	Glu	Glu	Tyr	Val	Lys	Cys	Phe	Glu	Cys	Ser	Glu	Arg	
			165						170					175		
Gly	Arg	Lys	Ile	Pro	Pro	Gly	Leu	Val	Gly	Lys	Trp	Lys	Gly	Thr	Asn	
		180					185						190			
Phe	Gly	Thr	Lys	Ser	Leu	Asp	Phe	Gln	Ser	Asp	Ile	Ser	Ser	Asn	Asn	
	195						200					205				
Ser	Ser	Ala	Leu	Arg	Ser	Asp	Ile	Lys	Ile	Glu	Ala	Leu	Ser	Ser	Asn	
	210					215					220					
Leu	Ala	Gly	Leu	Cys	Ser	Val	Asp	Val	Glu	Val	Gly	Arg	Ile	Gln	Glu	
225					230					235				240		
Asp	Ser	Cys	Lys	Leu	Asn	Thr	Asn	Ser	Ser	Glu	Thr	Lys	Val	Lys	Ser	
			245						250					255		
Lys	Phe	Cys	Tyr	Gly	Glu	Lys	Glu	Lys	Glu	Arg	Phe	Ser	Arg	Ile	Leu	
		260					265						270			
Ser	Cys	Tyr	Val	Gly	Ser	Tyr	Asn	Phe	His	Asn	Phe	Thr	Thr	Arg	Thr	
		275					280					285				
Lys	Ala	Asp	Asp	Pro	Thr	Ala	Asn	Arg	Gln	Ile	Ile	Ser	Phe	Thr	Ala	
	290					295					300					

Asn Thr Val Ile Asn Leu Asp Gly Ile Asp Phe Ile Lys Cys Glu Val
305 310 315 320
Leu Gly Lys Ser Phe Met Leu His Gln Ile Arg Lys Met Met Gly Leu
325 330 335
Ala Val Ala Ile Met Arg Asn Cys Ala Ser Glu Ser Leu Ile Gln Ser
340 345 350
Ala Phe Ser Lys Asp Val Asn Ile Thr Val Pro Met Ala Pro Glu Val
355 360 365
Gly Leu Tyr Leu Asp Glu Cys Phe Phe Thr Ser Tyr Asn Arg Asn Phe
370 375 380
Glu Asp Ser His Glu Glu Val Ser Met Glu Ala Tyr Lys Glu Glu Ala
385 390 395 400
Glu Ala Phe Lys Leu Lys His Ile Tyr Ser His Ile Gly Ala Thr Glu
405 410 415
Arg Lys Tyr Gly Asn Met Ala Leu Trp Leu His Ser Leu Asn Tyr Arg
420 425 430
Asn Tyr Pro Asp Leu Asn Phe Gly Ser Cys Gly Gln Asn Thr Asp Gln
435 440 445
Val Leu Val His Lys Lys Ile Asp Glu Arg Ala Ser His Ser Leu
450 455 460

(2) INFORMATION FOR SEQ ID NO:1138:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 426 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..426

(D) OTHER INFORMATION: / Ceres Seq. ID 1499730

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1138:

Met Gln Lys Asn Pro Gly Ala Lys Thr Ile Glu Gly Glu Leu Glu Glu
1 5 10 15
Ala Leu Phe His Ala Gly Ala Val Pro Glu Ser Ile Arg Gly Lys Pro
20 25 30
Lys Leu Tyr Asp Phe Ala Arg Ser Ala Arg Thr Asp Lys Gly Val Ser
35 40 45
Ala Val Gly Gln Val Val Ser Gly Arg Phe Ile Val Asp Pro Leu Gly
50 55 60
Phe Val Asn Arg Leu Asn Ser Asn Leu Pro Asn Gln Ile Arg Ile Phe
65 70 75 80
Gly Tyr Lys His Val Thr Pro Ser Phe Ser Ser Lys Lys Phe Cys Asp
85 90 95
Arg Arg Arg Tyr Val Tyr Leu Leu Pro Val Phe Ala Leu Asp Pro Ile
100 105 110
Ser His Arg Asp Arg Glu Thr Val Met Ala Ser Leu Gly Pro Gly Glu
115 120 125
Glu Tyr Val Lys Cys Phe Glu Cys Ser Glu Arg Gly Arg Lys Ile Pro
130 135 140
Pro Gly Leu Val Gly Lys Trp Lys Gly Thr Asn Phe Gly Thr Lys Ser
145 150 155 160
Leu Asp Phe Gln Ser Asp Ile Ser Ser Asn Asn Ser Ser Ala Leu Arg
165 170 175
Ser Asp Ile Lys Ile Glu Ala Leu Ser Ser Asn Leu Ala Gly Leu Cys
180 185 190
Ser Val Asp Val Glu Val Gly Arg Ile Gln Glu Asp Ser Cys Lys Leu
195 200 205
Asn Thr Asn Ser Ser Glu Thr Lys Val Lys Ser Lys Phe Cys Tyr Gly
210 215 220
Glu Lys Glu Lys Glu Arg Phe Ser Arg Ile Leu Ser Cys Tyr Val Gly

225					230					235					240
Ser	Tyr	Asn	Phe	His	Asn	Phe	Thr	Thr	Arg	Thr	Lys	Ala	Asp	Asp	Pro
				245					250					255	
Thr	Ala	Asn	Arg	Gln	Ile	Ile	Ser	Phe	Thr	Ala	Asn	Thr	Val	Ile	Asn
			260					265					270		
Leu	Asp	Gly	Ile	Asp	Phe	Ile	Lys	Cys	Glu	Val	Leu	Gly	Lys	Ser	Phe
		275					280					285			
Met	Leu	His	Gln	Ile	Arg	Lys	Met	Met	Gly	Leu	Ala	Val	Ala	Ile	Met
	290					295					300				
Arg	Asn	Cys	Ala	Ser	Glu	Ser	Leu	Ile	Gln	Ser	Ala	Phe	Ser	Lys	Asp
305					310					315					320
Val	Asn	Ile	Thr	Val	Pro	Met	Ala	Pro	Glu	Val	Gly	Leu	Tyr	Leu	Asp
				325					330					335	
Glu	Cys	Phe	Phe	Thr	Ser	Tyr	Asn	Arg	Asn	Phe	Glu	Asp	Ser	His	Glu
				340				345					350		
Glu	Val	Ser	Met	Glu	Ala	Tyr	Lys	Glu	Glu	Ala	Glu	Ala	Phe	Lys	Leu
		355					360					365			
Lys	His	Ile	Tyr	Ser	His	Ile	Gly	Ala	Thr	Glu	Arg	Lys	Tyr	Gly	Asn
	370					375					380				
Met	Ala	Leu	Trp	Leu	His	Ser	Leu	Asn	Tyr	Arg	Asn	Tyr	Pro	Asp	Leu
385					390					395					400
Asn	Phe	Gly	Ser	Cys	Gly	Gln	Asn	Thr	Asp	Gln	Val	Leu	Val	His	Lys
				405					410					415	
Lys	Ile	Asp	Glu	Arg	Ala	Ser	His	Ser	Leu						
			420					425							

(2) INFORMATION FOR SEQ ID NO:1139:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 306 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..306

(D) OTHER INFORMATION: / Ceres Seq. ID 1499731

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1139:

Met	Ala	Ser	Leu	Gly	Pro	Gly	Glu	Glu	Tyr	Val	Lys	Cys	Phe	Glu	Cys
1			5				10							15	
Ser	Glu	Arg	Gly	Arg	Lys	Ile	Pro	Pro	Gly	Leu	Val	Gly	Lys	Trp	Lys
			20				25						30		
Gly	Thr	Asn	Phe	Gly	Thr	Lys	Ser	Leu	Asp	Phe	Gln	Ser	Asp	Ile	Ser
		35				40					45				
Ser	Asn	Asn	Ser	Ser	Ala	Leu	Arg	Ser	Asp	Ile	Lys	Ile	Glu	Ala	Leu
	50					55				60					
Ser	Ser	Asn	Leu	Ala	Gly	Leu	Cys	Ser	Val	Asp	Val	Glu	Val	Gly	Arg
65				70					75					80	
Ile	Gln	Glu	Asp	Ser	Cys	Lys	Leu	Asn	Thr	Asn	Ser	Ser	Glu	Thr	Lys
			85					90					95		
Val	Lys	Ser	Lys	Phe	Cys	Tyr	Gly	Glu	Lys	Glu	Lys	Glu	Arg	Phe	Ser
		100					105					110			
Arg	Ile	Leu	Ser	Cys	Tyr	Val	Gly	Ser	Tyr	Asn	Phe	His	Asn	Phe	Thr
		115					120					125			
Thr	Arg	Thr	Lys	Ala	Asp	Asp	Pro	Thr	Ala	Asn	Arg	Gln	Ile	Ile	Ser
	130					135					140				
Phe	Thr	Ala	Asn	Thr	Val	Ile	Asn	Leu	Asp	Gly	Ile	Asp	Phe	Ile	Lys
145					150					155				160	
Cys	Glu	Val	Leu	Gly	Lys	Ser	Phe	Met	Leu	His	Gln	Ile	Arg	Lys	Met
			165					170						175	
Met	Gly	Leu	Ala	Val	Ala	Ile	Met	Arg	Asn	Cys	Ala	Ser	Glu	Ser	Leu
			180					185					190		

Ile Gln Ser Ala Phe Ser Lys Asp Val Asn Ile Thr Val Pro Met Ala
195 200 205
Pro Glu Val Gly Leu Tyr Leu Asp Glu Cys Phe Phe Thr Ser Tyr Asn
210 215 220
Arg Asn Phe Glu Asp Ser His Glu Glu Val Ser Met Glu Ala Tyr Lys
225 230 235 240
Glu Glu Ala Glu Ala Phe Lys Leu Lys His Ile Tyr Ser His Ile Gly
245 250 255
Ala Thr Glu Arg Lys Tyr Gly Asn Met Ala Leu Trp Leu His Ser Leu
260 265 270
Asn Tyr Arg Asn Tyr Pro Asp Leu Asn Phe Gly Ser Cys Gly Gln Asn
275 280 285
Thr Asp Gln Val Leu Val His Lys Lys Ile Asp Glu Arg Ala Ser His
290 295 300
Ser Leu
305

(2) INFORMATION FOR SEQ ID NO:1140:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1402 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1402
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499732

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1140:

gggatgtttg	tgaccttttg	tctcttcttc	tctaaaattc	tctttctccc	aaaaactaaa	60
aaaacaaaaa	aaacaaaaaa	tgtacgcaat	gaaagaagaa	gactgtcttc	aaacatttca	120
caacttacaa	gactatcaag	accagtttca	tcttcatcat	catccacaaa	ttctcccctg	180
gtcgtcgaca	tctttacctt	cttttgaccc	actccatttc	ccatctaacc	cgacccggtta	240
ttctgacccg	gttactact	tcaacagaag	agcttcttct	tcctcttctt	cttttgacta	300
taacgacggg	tttgtctctc	ctcctccttc	catggatcat	cctcagaacc	atctaaggat	360
tttatccgaa	gctcttgac	ccatcatgcg	tcgtggctcg	tcctttgggt	tcgatgggtga	420
gatcatggga	aaattgagtg	cacaagaagt	catggatgct	aaggctttag	ctgcttcaaa	480
gagtcatagt	gaagctgaga	gaagaagacg	agagagaatc	aacactcatc	ttgctaagct	540
gcgtagtata	ttaccaaaaca	caaccaaacc	ggacaaagct	tctttgctag	cggaagtgat	600
ccaacacatg	aaggagctaa	aacgacaaac	atcacagatc	accgacacgt	atcaagtccc	660
aacagagtgc	gatgatctga	ccgtagattc	gtcttacaac	gacgaggaag	gaaacttggt	720
gataagagca	tccttttgct	gccaagacag	gactgacctc	atgcatgacg	tcataaatgc	780
cttaaagtct	cttcgtcttc	gaactctcaa	agctgagatc	gcaaccgtag	gtggtagagt	840
caagaacatc	ttgttcttga	gccgagaata	cgatgatgaa	gaagatcatg	attcatatcg	900
tagaaacttc	gatggtgatg	acgtggagga	ttatgatgaa	gagaggatga	tgaataatcg	960
tgtgagttcg	atagaagaag	cgttaaaggc	ggttatagag	aagtgtgttc	ataataatga	1020
tgaaagtaac	gataacaata	acttgagaaa	atcatcttca	gggggtatta	agaggcaaa	1080
gactagtaag	atggtgaatc	gatgttataa	ttagttaatt	aagtcaagtc	tttattaact	1140
agggttagtt	aattagactt	gcaaaatggg	atgtgattat	gggttggtga	tattagtatt	1200
attttcggtg	tttttagtag	ttgggattgg	gtttattctt	ctatgttttt	ttaatctatg	1260
aagaaccctt	tgtttagggg	tttatagtga	tgagtttggt	ttatatatgg	tagttaagac	1320
attttatcgt	cttaattaat	ataggaaatg	tatagagctt	gggtttgtat	taatttatca	1380
agaagttttt	tttatcatat	tc				

(2) INFORMATION FOR SEQ ID NO:1141:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 344 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide

(B) LOCATION: 1..344

(D) OTHER INFORMATION: / Ceres Seq. ID 1499733

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1141:

Met	Tyr	Ala	Met	Lys	Glu	Glu	Asp	Cys	Leu	Gln	Thr	Phe	His	Asn	Leu
1				5					10					15	
Gln	Asp	Tyr	Gln	Asp	Gln	Phe	His	Leu	His	His	His	Pro	Gln	Ile	Leu
			20					25					30		
Pro	Trp	Ser	Ser	Thr	Ser	Leu	Pro	Ser	Phe	Asp	Pro	Leu	His	Phe	Pro
		35					40					45			
Ser	Asn	Pro	Thr	Arg	Tyr	Ser	Asp	Pro	Val	His	Tyr	Phe	Asn	Arg	Arg
	50					55					60				
Ala	Ser	Ser	Ser	Ser	Ser	Ser	Phe	Asp	Tyr	Asn	Asp	Gly	Phe	Val	Ser
65					70					75					80
Pro	Pro	Pro	Ser	Met	Asp	His	Pro	Gln	Asn	His	Leu	Arg	Ile	Leu	Ser
			85					90					95		
Glu	Ala	Leu	Gly	Pro	Ile	Met	Arg	Arg	Gly	Ser	Ser	Phe	Gly	Phe	Asp
			100					105					110		
Gly	Glu	Ile	Met	Gly	Lys	Leu	Ser	Ala	Gln	Glu	Val	Met	Asp	Ala	Lys
		115				120						125			
Ala	Leu	Ala	Ala	Ser	Lys	Ser	His	Ser	Glu	Ala	Glu	Arg	Arg	Arg	Arg
	130					135					140				
Glu	Arg	Ile	Asn	Thr	His	Leu	Ala	Lys	Leu	Arg	Ser	Ile	Leu	Pro	Asn
145					150					155					160
Thr	Thr	Lys	Thr	Asp	Lys	Ala	Ser	Leu	Leu	Ala	Glu	Val	Ile	Gln	His
			165						170					175	
Met	Lys	Glu	Leu	Lys	Arg	Gln	Thr	Ser	Gln	Ile	Thr	Asp	Thr	Tyr	Gln
		180					185					190			
Val	Pro	Thr	Glu	Cys	Asp	Asp	Leu	Thr	Val	Asp	Ser	Ser	Tyr	Asn	Asp
		195					200					205			
Glu	Glu	Gly	Asn	Leu	Val	Ile	Arg	Ala	Ser	Phe	Cys	Cys	Gln	Asp	Arg
	210					215					220				
Thr	Asp	Leu	Met	His	Asp	Val	Ile	Asn	Ala	Leu	Lys	Ser	Leu	Arg	Leu
225					230					235					240
Arg	Thr	Leu	Lys	Ala	Glu	Ile	Ala	Thr	Val	Gly	Gly	Arg	Val	Lys	Asn
			245						250					255	
Ile	Leu	Phe	Leu	Ser	Arg	Glu	Tyr	Asp	Asp	Glu	Glu	Asp	His	Asp	Ser
		260						265					270		
Tyr	Arg	Arg	Asn	Phe	Asp	Gly	Asp	Asp	Val	Glu	Asp	Tyr	Asp	Glu	Glu
		275					280					285			
Arg	Met	Met	Asn	Asn	Arg	Val	Ser	Ser	Ile	Glu	Glu	Ala	Leu	Lys	Ala
	290					295					300				
Val	Ile	Glu	Lys	Cys	Val	His	Asn	Asn	Asp	Glu	Ser	Asn	Asp	Asn	Asn
305					310					315					320
Asn	Leu	Glu	Lys	Ser	Ser	Ser	Gly	Gly	Ile	Lys	Arg	Gln	Arg	Thr	Ser
			325						330					335	
Lys	Met	Val	Asn	Arg	Cys	Tyr	Asn								
			340												

(2) INFORMATION FOR SEQ ID NO:1142:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 341 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..341

(D) OTHER INFORMATION: / Ceres Seq. ID 1499734

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1142:

Met	Lys	Glu	Glu	Asp	Cys	Leu	Gln	Thr	Phe	His	Asn	Leu	Gln	Asp	Tyr
1					5				10					15	

Gln Asp Gln Phe His Leu His His His Pro Gln Ile Leu Pro Trp Ser
20 25 30
Ser Thr Ser Leu Pro Ser Phe Asp Pro Leu His Phe Pro Ser Asn Pro
35 40 45
Thr Arg Tyr Ser Asp Pro Val His Tyr Phe Asn Arg Arg Ala Ser Ser
50 55 60
Ser Ser Ser Ser Phe Asp Tyr Asn Asp Gly Phe Val Ser Pro Pro Pro
65 70 75 80
Ser Met Asp His Pro Gln Asn His Leu Arg Ile Leu Ser Glu Ala Leu
85 90 95
Gly Pro Ile Met Arg Arg Gly Ser Ser Phe Gly Phe Asp Gly Glu Ile
100 105 110
Met Gly Lys Leu Ser Ala Gln Glu Val Met Asp Ala Lys Ala Leu Ala
115 120 125
Ala Ser Lys Ser His Ser Glu Ala Glu Arg Arg Arg Glu Arg Ile
130 135 140
Asn Thr His Leu Ala Lys Leu Arg Ser Ile Leu Pro Asn Thr Thr Lys
145 150 155 160
Thr Asp Lys Ala Ser Leu Leu Ala Glu Val Ile Gln His Met Lys Glu
165 170 175
Leu Lys Arg Gln Thr Ser Gln Ile Thr Asp Thr Tyr Gln Val Pro Thr
180 185 190
Glu Cys Asp Asp Leu Thr Val Asp Ser Ser Tyr Asn Asp Glu Glu Gly
195 200 205
Asn Leu Val Ile Arg Ala Ser Phe Cys Cys Gln Asp Arg Thr Asp Leu
210 215 220
Met His Asp Val Ile Asn Ala Leu Lys Ser Leu Arg Leu Arg Thr Leu
225 230 235 240
Lys Ala Glu Ile Ala Thr Val Gly Gly Arg Val Lys Asn Ile Leu Phe
245 250 255
Leu Ser Arg Glu Tyr Asp Asp Glu Glu Asp His Asp Ser Tyr Arg Arg
260 265 270
Asn Phe Asp Gly Asp Asp Val Glu Asp Tyr Asp Glu Glu Arg Met Met
275 280 285
Asn Asn Arg Val Ser Ser Ile Glu Glu Ala Leu Lys Ala Val Ile Glu
290 295 300
Lys Cys Val His Asn Asn Asp Glu Ser Asn Asp Asn Asn Leu Glu
305 310 315 320
Lys Ser Ser Ser Gly Gly Ile Lys Arg Gln Arg Thr Ser Lys Met Val
325 330 335
Asn Arg Cys Tyr Asn
340

(2) INFORMATION FOR SEQ ID NO:1143:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 260 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..260
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499735

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1143:

Met Asp His Pro Gln Asn His Leu Arg Ile Leu Ser Glu Ala Leu Gly
1 5 10 15
Pro Ile Met Arg Arg Gly Ser Ser Phe Gly Phe Asp Gly Glu Ile Met
20 25 30
Gly Lys Leu Ser Ala Gln Glu Val Met Asp Ala Lys Ala Leu Ala Ala
35 40 45
Ser Lys Ser His Ser Glu Ala Glu Arg Arg Arg Arg Glu Arg Ile Asn

50	55	60
Thr His Leu Ala Lys	Leu Arg Ser Ile Leu	Pro Asn Thr Thr Lys Thr
65	70	75
Asp Lys Ala Ser Leu	Leu Ala Glu Val Ile	Gln His Met Lys Glu Leu
85	90	95
Lys Arg Gln Thr Ser	Gln Ile Thr Asp Thr	Tyr Gln Val Pro Thr Glu
100	105	110
Cys Asp Asp Leu Thr	Val Asp Ser Tyr Asn	Asp Glu Glu Gly Asn
115	120	125
Leu Val Ile Arg Ala	Ser Phe Cys Cys Gln	Asp Arg Thr Asp Leu Met
130	135	140
His Asp Val Ile Asn	Ala Leu Lys Ser Leu	Arg Leu Arg Thr Leu Lys
145	150	155
Ala Glu Ile Ala Thr	Val Gly Gly Arg Val	Lys Asn Ile Leu Phe Leu
165	170	175
Ser Arg Glu Tyr Asp	Asp Glu Glu Asp His	Asp Ser Tyr Arg Arg Asn
180	185	190
Phe Asp Gly Asp Asp	Val Glu Asp Tyr Asp	Glu Glu Arg Met Met Asn
195	200	205
Asn Arg Val Ser Ser	Ile Glu Glu Ala Leu	Lys Ala Val Ile Glu Lys
210	215	220
Cys Val His Asn Asn	Asp Glu Ser Asn Asp	Asn Asn Leu Glu Lys
225	230	235
Ser Ser Ser Gly Gly	Ile Lys Arg Gln Arg	Thr Ser Lys Met Val Asn
245	250	255
Arg Cys Tyr Asn		
260		

(2) INFORMATION FOR SEQ ID NO:1144:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1379 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1379
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499740

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1144:

aaattccag	acgtggtgga	gtgaacaacc	aaaaaaacaa	catgattgat	tgattctgaa	60
attcacttta	attttcaaga	gagagtttct	gaggatcttg	atatcagaat	ctgtcatgag	120
agaagcagga	gaagagaaag	tggcgtggaa	gtactttacc	agagatgttg	tgccgtttgc	180
tgcgatgttt	gcggtggagt	gtgccactgt	tgggtcaaac	acgctgttta	aggctgctac	240
tttaagagga	ttgagcttct	atgtctttgt	cttctactct	tatatgtttt	caacacttct	300
ccttcttcca	ctttctgtaa	tctttggaag	gtcaagaaga	ttaccagcag	ctaagtctcc	360
tcttttcttc	aagattttct	tacttgggct	tggtggattg	ctggttgtaa	aggtattgca	420
tacagttccc	caactcttgc	atctgctatc	agcaatctca	caccggcttt	cacattcaca	480
ctcgtctgta	tcttcaggat	ggagcaagta	agggttaagga	gctctgcgac	ycaggctaaa	540
atcattggtg	caatactatc	tatatctggt	gctctggtag	ttgtgctgta	taaaggccca	600
caagttctcg	cctctgcatc	ttttacaact	gtattaccta	ccgttacact	tcaccagcat	660
ttgacctcaa	tagagtcaag	ctggataatc	ggagggtctc	tgcttgcttc	acagtatttt	720
cttatatccg	tctgactcgt	gtcatggagg	tttaccctga	agagataacc	gtagtcttct	780
tctacaattt	atttgcaaca	ctaattctcag	taccagtatg	tctttttgcg	gagagcaact	840
tgacttcttg	ggtgcttaaa	ccagacattt	ccctcgctgc	aatcatatac	tcgggagctc	900
tcgtttcatt	attcagcgcg	cttaccacca	catggggctc	gcactctgaag	ggtccgggat	960
acatatcctt	gttcaggcca	ttgtctattg	cgattgcagt	cgccatgggt	gctatatattc	1020
tcggcgatgc	acttcacctt	gggagtgta	ttggatcaay	gatattgtgc	mttgattctc	1080
acactgtgat	ttggggcaaa	gcaagagagg	atacaatcaa	aactgtagct	ggttctgagc	1140
agtcaccttt	gctgcttaca	catatcatag	aagatggagc	ctttccatta	agctaggatt	1200
gatgcaagtg	aaatccttat	actattttat	aataaatatg	gatccctaaa	agaggtgtac	1260
catatatgtt	tatatatgtc	tatagttaca	tataagatat	ctgttctttt	tttcttgttt	1320

tattttgatg ttacatatga atgagaatta tgaatctata agaaatattt ggctcctttt

(2) INFORMATION FOR SEQ ID NO:1145:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 131 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..131
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499741

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1145:

Met	Arg	Glu	Ala	Gly	Glu	Glu	Lys	Val	Ala	Trp	Lys	Tyr	Phe	Thr	Arg
1				5					10					15	
Asp	Val	Val	Pro	Phe	Ala	Ala	Met	Phe	Ala	Val	Glu	Cys	Ala	Thr	Val
			20					25					30		
Gly	Ser	Asn	Thr	Leu	Phe	Lys	Ala	Ala	Thr	Leu	Arg	Gly	Leu	Ser	Phe
		35				40						45			
Tyr	Val	Phe	Val	Phe	Tyr	Ser	Tyr	Ile	Val	Ser	Thr	Leu	Leu	Leu	Leu
	50					55					60				
Pro	Leu	Ser	Val	Ile	Phe	Gly	Arg	Ser	Arg	Arg	Leu	Pro	Ala	Ala	Lys
65				70					75					80	
Ser	Pro	Leu	Phe	Phe	Lys	Ile	Phe	Leu	Leu	Gly	Leu	Val	Gly	Leu	Leu
			85					90						95	
Val	Val	Lys	Val	Leu	His	Thr	Val	Pro	Gln	Leu	Leu	His	Leu	Leu	Ser
		100					105					110			
Ala	Ile	Ser	His	Arg	Leu	Ser	His	Ser	His	Ser	Leu	Leu	Ser	Ser	Gly
	115					120						125			
Trp	Ser	Lys													
	130														

(2) INFORMATION FOR SEQ ID NO:1146:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 108 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..108
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499742

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1146:

Met	Phe	Ala	Val	Glu	Cys	Ala	Thr	Val	Gly	Ser	Asn	Thr	Leu	Phe	Lys
1				5					10					15	
Ala	Ala	Thr	Leu	Arg	Gly	Leu	Ser	Phe	Tyr	Val	Phe	Val	Phe	Tyr	Ser
		20						25					30		
Tyr	Ile	Val	Ser	Thr	Leu	Leu	Leu	Leu	Pro	Leu	Ser	Val	Ile	Phe	Gly
	35					40						45			
Arg	Ser	Arg	Arg	Leu	Pro	Ala	Ala	Lys	Ser	Pro	Leu	Phe	Phe	Lys	Ile
	50					55					60				
Phe	Leu	Leu	Gly	Leu	Val	Gly	Leu	Leu	Val	Val	Lys	Val	Leu	His	Thr
65				70					75					80	
Val	Pro	Gln	Leu	Leu	His	Leu	Leu	Ser	Ala	Ile	Ser	His	Arg	Leu	Ser
		85						90						95	
His	Ser	His	Ser	Leu	Leu	Ser	Ser	Gly	Trp	Ser	Lys				
	100					105									

(2) INFORMATION FOR SEQ ID NO:1147:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 150 amino acids
- (B) TYPE: amino acid

- (C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..150
(D) OTHER INFORMATION: / Ceres Seq. ID 1499743
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1147:

Met	Glu	Val	Tyr	Pro	Glu	Glu	Ile	Thr	Val	Val	Phe	Phe	Tyr	Asn	Leu
1				5					10					15	
Phe	Ala	Thr	Leu	Ile	Ser	Val	Pro	Val	Cys	Leu	Phe	Ala	Glu	Ser	Asn
			20					25					30		
Leu	Thr	Ser	Trp	Val	Leu	Lys	Pro	Asp	Ile	Ser	Leu	Ala	Ala	Ile	Ile
			35				40					45			
Tyr	Ser	Gly	Val	Phe	Val	Ser	Leu	Phe	Ser	Ala	Leu	Thr	His	Thr	Trp
			50			55					60				
Gly	Leu	His	Leu	Lys	Gly	Pro	Val	Tyr	Ile	Ser	Leu	Phe	Arg	Pro	Leu
65				70					75					80	
Ser	Ile	Ala	Ile	Ala	Val	Ala	Met	Gly	Ala	Ile	Phe	Leu	Gly	Asp	Ala
			85					90						95	
Leu	His	Leu	Gly	Ser	Val	Ile	Gly	Ser	Xaa	Ile	Leu	Cys	Xaa	Gly	Phe
			100					105					110		
Tyr	Thr	Val	Ile	Trp	Gly	Lys	Ala	Arg	Glu	Asp	Thr	Ile	Lys	Thr	Val
			115				120					125			
Ala	Gly	Ser	Glu	Gln	Ser	Pro	Leu	Leu	Leu	Thr	His	Ile	Ile	Glu	Asp
			130				135					140			
Gly	Ala	Phe	Pro	Leu	Ser										
145				150											

- (2) INFORMATION FOR SEQ ID NO:1148:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 685 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
(A) NAME/KEY: -
(B) LOCATION: 1..685
(D) OTHER INFORMATION: / Ceres Seq. ID 1499748
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1148:

attcaatctc	acaacaacca	atctacacac	aaaacaataa	caacaacaac	aacaacaaca	60
acaacaaca	acaacaaca	acaacaaaat	gtttacaaaa	tcaatccttt	taccttttct	120
tctggtaatc	atcttcgtct	cagcatctca	agctagtcgt	caactctggg	atagtggaat	180
cagcgagatg	tttggttcca	aatccgggtt	tcatcatgga	ttttccgggt	tttcgggggtc	240
ctctggaggt	gctggaggtg	ctggaggatc	attcggagat	atgatgaatg	ctggagggtgc	300
acatacatgc	tcggcgcaag	gagcttgtag	cggtaagaag	ctgacatgtc	ccgaggagtg	360
ctacaaatca	accaacgtta	acaaggatgg	ttataaaaagc	accagccgca	gtggaggatg	420
ttcatttgac	tgtacgacca	agtgtgccgc	gacttgttca	aattaacatg	ttaatttgca	480
catatatatt	atatgttcgt	atagtatgtt	gttatgttat	gttatagcat	tatatagtct	540
atatatatgt	caatataata	aaaccggcaa	ggtatatggg	aggtttgtgt	ctccctttgt	600
aattttgtat	ggatcttgat	tagaagcttt	ctatgaatct	atgtacataa	tatgattttg	660
aataaaaagaa	aatttagtgt	ttctc				

- (2) INFORMATION FOR SEQ ID NO:1149:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 125 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide

(B) LOCATION: 1..125

(D) OTHER INFORMATION: / Ceres Seq. ID 1499749

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1149:

Met	Phe	Thr	Lys	Ser	Ile	Leu	Leu	Pro	Phe	Leu	Leu	Val	Ile	Ile	Phe
1				5					10					15	
Val	Ser	Ala	Ser	Gln	Ala	Ser	Arg	Gln	Leu	Trp	Asp	Ser	Gly	Ile	Ser
			20					25					30		
Glu	Met	Phe	Gly	Ser	Lys	Ser	Gly	Phe	His	His	Gly	Phe	Ser	Gly	Phe
		35					40					45			
Ser	Gly	Ser	Ser	Gly	Gly	Ala	Gly	Gly	Ala	Gly	Gly	Ser	Phe	Gly	Asp
	50					55					60				
Met	Met	Asn	Ala	Gly	Gly	Ala	His	Thr	Cys	Ser	Ala	Gln	Gly	Ala	Cys
65					70					75					80
Ser	Gly	Lys	Lys	Leu	Thr	Cys	Pro	Glu	Glu	Cys	Tyr	Lys	Ser	Thr	Asn
			85						90					95	
Val	Asn	Lys	Asp	Gly	Tyr	Lys	Ser	Thr	Ser	Arg	Ser	Gly	Gly	Cys	Ser
			100					105					110		
Phe	Asp	Cys	Thr	Thr	Lys	Cys	Ala	Ala	Thr	Cys	Ser	Asn			
			115					120				125			

(2) INFORMATION FOR SEQ ID NO:1150:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 92 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..92

(D) OTHER INFORMATION: / Ceres Seq. ID 1499750

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1150:

Met	Phe	Gly	Ser	Lys	Ser	Gly	Phe	His	His	Gly	Phe	Ser	Gly	Phe	Ser
1				5					10					15	
Gly	Ser	Ser	Gly	Gly	Ala	Gly	Gly	Ala	Gly	Gly	Ser	Phe	Gly	Asp	Met
			20					25					30		
Met	Asn	Ala	Gly	Gly	Ala	His	Thr	Cys	Ser	Ala	Gln	Gly	Ala	Cys	Ser
		35				40						45			
Gly	Lys	Lys	Leu	Thr	Cys	Pro	Glu	Glu	Cys	Tyr	Lys	Ser	Thr	Asn	Val
	50					55					60				
Asn	Lys	Asp	Gly	Tyr	Lys	Ser	Thr	Ser	Arg	Ser	Gly	Gly	Cys	Ser	Phe
65					70					75					80
Asp	Cys	Thr	Thr	Lys	Cys	Ala	Ala	Thr	Cys	Ser	Asn				
			85						90						

(2) INFORMATION FOR SEQ ID NO:1151:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 741 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..741

(D) OTHER INFORMATION: / Ceres Seq. ID 1499751

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1151:

actttctctt	gatactcac	tgcataca	atggccagag	agaagattgt	ggtggctggt	60
ggtaccacaa	agagctggaa	actactcttg	gggctgagaa	tatttgcatt	catggctact	120
ttagctgcag	ccattgtaat	gtcactaaac	aaagagacaa	agaccttggt	tgtggccacc	180
attggtactg	ttcctattaa	agccacttta	accgctaagt	ttcagcacac	accggctttt	240
gtgttctttg	ttatagctaa	tgtaatgggtg	agcttccaca	atttgttgat	gattgctctt	300
cagattttca	gcccgaaact	ggagtacaaa	ggtctccgtc	tcctctctat	cgctattctc	360

```
gacatgctaa acgcaacact agtatctgcg gctgcaaacg cggcgggtgtt cgtggcagag      420
ctaggaaga acggaacaa gcacgccaag tggaacaaag tctgcgacag gtttgccact      480
tactgtgatc acggcgcagg agcaatcatc gcagcattcg scggagtcac tctaagtctc      540
ctggtgtccg ccgtctccat ttcccgctc ttaatcaatt ctaaaaactt ctccaccacc      600
gccaccacaa cctccgtcgt ctaaaacatc gtggccaaaa attcagcaac atgtgtgtga      660
ccattttata gatgttgtgg cttactttgt gtgtttgtct ctcaagtcac tagcaaattg      720
tgtaatgcac tcctttgttc t
```

(2) INFORMATION FOR SEQ ID NO:1152:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 197 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..197

(D) OTHER INFORMATION: / Ceres Seq. ID 1499752

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1152:

```
Met Ala Arg Glu Lys Ile Val Val Ala Gly Gly Thr Thr Lys Ser Trp
1          5          10          15
Lys Leu Leu Leu Gly Leu Arg Ile Phe Ala Phe Met Ala Thr Leu Ala
20          25          30
Ala Ala Ile Val Met Ser Leu Asn Lys Glu Thr Lys Thr Leu Val Val
35          40          45
Ala Thr Ile Gly Thr Val Pro Ile Lys Ala Thr Leu Thr Ala Lys Phe
50          55          60
Gln His Thr Pro Ala Phe Val Phe Phe Val Ile Ala Asn Val Met Val
65          70          75          80
Ser Phe His Asn Leu Leu Met Ile Ala Leu Gln Ile Phe Ser Pro Lys
85          90          95
Leu Glu Tyr Lys Gly Leu Arg Leu Leu Ser Ile Ala Ile Leu Asp Met
100          105          110
Leu Asn Ala Thr Leu Val Ser Ala Ala Asn Ala Ala Val Phe Val
115          120          125
Ala Glu Leu Gly Lys Asn Gly Asn Lys His Ala Lys Trp Asn Lys Val
130          135          140
Cys Asp Arg Phe Ala Thr Tyr Cys Asp His Gly Ala Gly Ala Ile Ile
145          150          155          160
Ala Ala Phe Xaa Gly Val Ile Leu Met Leu Leu Val Ser Ala Val Ser
165          170          175
Ile Ser Arg Leu Leu Ile Asn Ser Lys Asn Phe Ser Thr Thr Ala Thr
180          185          190
Thr Thr Ser Val Val
195
```

(2) INFORMATION FOR SEQ ID NO:1153:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 170 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..170

(D) OTHER INFORMATION: / Ceres Seq. ID 1499753

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1153:

```
Met Ala Thr Leu Ala Ala Ala Ile Val Met Ser Leu Asn Lys Glu Thr
1          5          10          15
Lys Thr Leu Val Val Ala Thr Ile Gly Thr Val Pro Ile Lys Ala Thr
20          25          30
```

Leu Thr Ala Lys Phe Gln His Thr Pro Ala Phe Val Phe Phe Val Ile
35 40 45
Ala Asn Val Met Val Ser Phe His Asn Leu Leu Met Ile Ala Leu Gln
50 55 60
Ile Phe Ser Pro Lys Leu Glu Tyr Lys Gly Leu Arg Leu Leu Ser Ile
65 70 75 80
Ala Ile Leu Asp Met Leu Asn Ala Thr Leu Val Ser Ala Ala Ala Asn
85 90 95
Ala Ala Val Phe Val Ala Glu Leu Gly Lys Asn Gly Asn Lys His Ala
100 105 110
Lys Trp Asn Lys Val Cys Asp Arg Phe Ala Thr Tyr Cys Asp His Gly
115 120 125
Ala Gly Ala Ile Ile Ala Ala Phe Xaa Gly Val Ile Leu Met Leu Leu
130 135 140
Val Ser Ala Val Ser Ile Ser Arg Leu Leu Ile Asn Ser Lys Asn Phe
145 150 155 160
Ser Thr Thr Ala Thr Thr Thr Ser Val Val
165 170

(2) INFORMATION FOR SEQ ID NO:1154:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 161 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..161

(D) OTHER INFORMATION: / Ceres Seq. ID 1499754

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1154:

Met Ser Leu Asn Lys Glu Thr Lys Thr Leu Val Val Ala Thr Ile Gly
1 5 10 15
Thr Val Pro Ile Lys Ala Thr Leu Thr Ala Lys Phe Gln His Thr Pro
20 25 30
Ala Phe Val Phe Phe Val Ile Ala Asn Val Met Val Ser Phe His Asn
35 40 45
Leu Leu Met Ile Ala Leu Gln Ile Phe Ser Pro Lys Leu Glu Tyr Lys
50 55 60
Gly Leu Arg Leu Leu Ser Ile Ala Ile Leu Asp Met Leu Asn Ala Thr
65 70 75 80
Leu Val Ser Ala Ala Asn Ala Ala Val Phe Val Ala Glu Leu Gly
85 90 95
Lys Asn Gly Asn Lys His Ala Lys Trp Asn Lys Val Cys Asp Arg Phe
100 105 110
Ala Thr Tyr Cys Asp His Gly Ala Gly Ala Ile Ile Ala Ala Phe Xaa
115 120 125
Gly Val Ile Leu Met Leu Leu Val Ser Ala Val Ser Ile Ser Arg Leu
130 135 140
Leu Ile Asn Ser Lys Asn Phe Ser Thr Thr Ala Thr Thr Thr Ser Val
145 150 155 160
Val

(2) INFORMATION FOR SEQ ID NO:1155:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 667 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..667

(D) OTHER INFORMATION: / Ceres Seq. ID 1499755

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1155:

acaacttccc	catttttctgc	ttctttttgt	tcaactccaa	tcacacaatt	cacaacccat	60
tgagaaacca	ataaaataac	ctcaatcaaa	aaaaaaaaaa	aaaaaagatg	aaaatctcaa	120
tttagtaaag	gagaaaaaag	ccatttcgaa	taacttgaaa	aggttttggt	tttgcagaag	180
aaaatgaagg	agaaggcgga	gagtgggtgga	ggagtaggat	acgtgagagc	agatcagata	240
gatttaaaga	gtctggacga	gcaattgcag	agacacttaa	gtaaagcatg	gacgatggag	300
aagaggaaga	gtttgagtga	tgggtgaagat	aacgtcaata	acacccgaca	taaccagaac	360
aacttcggac	atcgacagct	tgtgtttcag	aggccgcttc	cttggtggtg	gatatagcaa	420
caacaacaac	agcagcaaga	acgacataat	taggtcgacc	gaggttgaga	agtcgaggag	480
agagtgggag	attgatcctt	ctaagcttat	aatcaaaaagt	gtgattgcta	gaggctacttt	540
tggtacgggt	caccgtggaa	tctacgatgg	tcaagatgtc	gccgtaaaac	tactagactg	600
gggagaagag	gggcacaggt	cagacgcaga	gatagcttcg	cttagagctg	ctttcactca	660
agaagtt						

(2) INFORMATION FOR SEQ ID NO:1156:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 77 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..77

(D) OTHER INFORMATION: / Ceres Seq. ID 1499756

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1156:

Met	Lys	Glu	Lys	Ala	Glu	Ser	Gly	Gly	Val	Gly	Tyr	Val	Arg	Ala
1			5					10					15	
Asp	Gln	Ile	Asp	Leu	Lys	Ser	Leu	Asp	Glu	Gln	Leu	Gln	Arg	His
			20					25					30	Leu
Ser	Lys	Ala	Trp	Thr	Met	Glu	Lys	Arg	Lys	Ser	Leu	Ser	Asp	Gly
		35					40					45		Glu
Asp	Asn	Val	Asn	Asn	Thr	Arg	His	Asn	Gln	Asn	Asn	Phe	Gly	His
	50					55						60		Arg
Gln	Leu	Val	Phe	Gln	Arg	Pro	Leu	Pro	Trp	Trp	Trp	Ile		
65				70						75				

(2) INFORMATION FOR SEQ ID NO:1157:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 116 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..116

(D) OTHER INFORMATION: / Ceres Seq. ID 1499757

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1157:

Met	Val	Lys	Ile	Thr	Ser	Ile	Thr	Pro	Asp	Ile	Thr	Arg	Thr	Thr	Ser
1			5					10						15	
Asp	Ile	Asp	Ser	Leu	Cys	Phe	Arg	Gly	Arg	Phe	Leu	Gly	Gly	Gly	Tyr
			20					25					30		
Ser	Asn	Asn	Asn	Asn	Ser	Ser	Lys	Asn	Asp	Ile	Ile	Arg	Ser	Thr	Glu
		35					40					45			
Val	Glu	Lys	Ser	Arg	Arg	Glu	Trp	Glu	Ile	Asp	Pro	Ser	Lys	Leu	Ile
	50					55					60				
Ile	Lys	Ser	Val	Ile	Ala	Arg	Gly	Thr	Phe	Gly	Thr	Val	His	Arg	Gly
65				70				75					80		
Ile	Tyr	Asp	Gly	Gln	Asp	Val	Ala	Val	Lys	Leu	Leu	Asp	Trp	Gly	Glu
				85				90						95	

Glu Gly His Arg Ser Asp Ala Glu Ile Ala Ser Leu Arg Ala Ala Phe
100 105 110
Thr Gln Glu Val
115

(2) INFORMATION FOR SEQ ID NO:1158:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 224 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..224
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499758

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1158:

tttttttcgt cgagcagccg cgcttttttg cgcaggaagg ataaagagag acgccatggg	60
aagaagacct gcgaggtggt accgtcagat caagggttaag ccatacccaa agtctcgcta	120
ctgtcgtggt gtgccagatc caaaaatcag gatctacgat gttggtatga agaggaaggg	180
tggtgatgag tttccatggc gtctctcttt atccttcctc ggcc	

(2) INFORMATION FOR SEQ ID NO:1159:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 74 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..74
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499759

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1159:

Phe Phe Arg Arg Ala Ala Ala Leu Phe Gly Arg Gly Arg Ile Lys Arg	
1 5 10 15	
Asp Ala Met Gly Arg Arg Pro Ala Arg Cys Tyr Arg Gln Ile Lys Gly	
20 25 30	
Lys Pro Tyr Pro Lys Ser Arg Tyr Cys Arg Gly Val Pro Asp Pro Lys	
35 40 45	
Ile Arg Ile Tyr Asp Val Gly Met Lys Arg Lys Gly Val Asp Glu Phe	
50 55 60	
Pro Trp Arg Leu Ser Leu Ser Phe Leu Gly	
65 70	

(2) INFORMATION FOR SEQ ID NO:1160:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 56 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..56
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499760

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1160:

Met Gly Arg Arg Pro Ala Arg Cys Tyr Arg Gln Ile Lys Gly Lys Pro	
1 5 10 15	
Tyr Pro Lys Ser Arg Tyr Cys Arg Gly Val Pro Asp Pro Lys Ile Arg	
20 25 30	
Ile Tyr Asp Val Gly Met Lys Arg Lys Gly Val Asp Glu Phe Pro Trp	
35 40 45	
Arg Leu Ser Leu Ser Phe Leu Gly	

50

55

(2) INFORMATION FOR SEQ ID NO:1161:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1331 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1331
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499765

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1161:

```
attttcttct tcttcttcat ttttctattc acattctctg aaactcatat catattttca 60
aagctcttaa cccaaaaaac ctaagtcttt tttttcttca aattattggt tatattaatg 120
ttttaagcta tgatggatat gactcctaca ataacaacaa caacaacacc aactcctaaa 180
tcaccggaac ccgaatccga aactccgacc cggatccaac cggcgaaacc catttccttt 240
agcaacggca tcatcaaaag ccaccaccac caccaccatc ctctcctctt tacttaaaaa 300
gaatgtctca aaaaccacgc ggcggcttta ggtggtcacg ctctcgacgg ttgcggcgaa 360
ttcatgccgt ctccgtcgtc aatctcctcc gatccaactt ctctcaaagt tgctgccttg 420
tggtgccac cgtaatttcc accgccgtga tccagataac aacaacgact cttcccaaat 480
ccctcctcct ccttccactg bcgtagagaa tcaacctcac caccgtcatc atccaccacc 540
accaccacct cctccaccac cagctagtcc taactcagct tctcctccac caatctcttc 600
ctcttacatg ctcttatctc tctccggtag taataacaac aacaacaact tagcttcttt 660
ctccgatctt aacttctcgc ccggaacaaa ccaccaccac caccaccaac atactcttca 720
cggatctcgt aaaagattcc gaacaaaatt cagccagttt cagaaagaga agatgcatga 780
attcgccgaa cgtgttggtt ggaagatgca aaaacgtgac saagacgatg ttcgtgatgt 840
ttgccggcag atcggagttg ataaaagtgt tctcaaagtt tggatgcata acaacaaaaa 900
cacctttaac cgccgtgata tcgccggaac cgagatccgg caaatcgata acggcggagg 960
aaaccacact ccgattctcg ccggcgagat taataaccat aacaatggac accacgggtg 1020
cggaggagga ggagagcttc accagagtgt tagtagcggc ggtggtggcg gaggatttga 1080
tagtgatagc ggaggagcta acggtggtta cggttaacgga tcatcgctcg cgtgaagtta 1140
aagatgagag tgtcaggtta ataagaagct tagagtaagc ttattcgtat tatcatcggt 1200
aataactttc tattaatat taattaagat ctttagcttt gtttgttttt gcattattat 1260
tagttttgat ttaatgttct ttaccacgtc ggtgtctcgc tcgatgagga ataataccat 1320
aacaatgttc g
```

(2) INFORMATION FOR SEQ ID NO:1162:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 175 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..175
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499766

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1162:

```
Met Leu Leu Ser Leu Ser Gly Thr Asn Asn Asn Asn Asn Asn Ala
1      5      10      15
Ser Phe Ser Asp Leu Asn Phe Ser Ala Gly Asn Asn His His His
20     25     30
His Gln His Thr Leu His Gly Ser Arg Lys Arg Phe Arg Thr Lys Phe
35     40     45
Ser Gln Phe Gln Lys Glu Lys Met His Glu Phe Ala Glu Arg Val Gly
50     55     60
Trp Lys Met Gln Lys Arg Asp Xaa Asp Asp Val Arg Asp Phe Cys Arg
65     70     75     80
Gln Ile Gly Val Asp Lys Ser Val Leu Lys Val Trp Met His Asn Asn
85     90     95
Lys Asn Thr Phe Asn Arg Arg Asp Ile Ala Gly Asn Glu Ile Arg Gln
```

	100		105		110										
Ile	Asp	Asn	Gly	Gly	Gly	Asn	His	Thr	Pro	Ile	Leu	Ala	Gly	Glu	Ile
	115						120						125		
Asn	Asn	His	Asn	Asn	Gly	His	His	Gly	Val	Gly	Gly	Gly	Gly	Glu	Leu
	130					135						140			
His	Gln	Ser	Val	Ser	Ser	Gly	Gly	Gly	Gly	Gly	Gly	Phe	Asp	Ser	Asp
145					150					155					160
Ser	Gly	Gly	Ala	Asn	Gly	Gly	Asn	Val	Asn	Gly	Ser	Ser	Ser	Ser	
			165					170							175

(2) INFORMATION FOR SEQ ID NO:1163:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 120 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..120

(D) OTHER INFORMATION: / Ceres Seq. ID 1499767

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1163:

Met	His	Glu	Phe	Ala	Glu	Arg	Val	Gly	Trp	Lys	Met	Gln	Lys	Arg	Asp
1			5					10						15	
Xaa	Asp	Asp	Val	Arg	Asp	Phe	Cys	Arg	Gln	Ile	Gly	Val	Asp	Lys	Ser
			20					25					30		
Val	Leu	Lys	Val	Trp	Met	His	Asn	Asn	Lys	Asn	Thr	Phe	Asn	Arg	Arg
		35				40						45			
Asp	Ile	Ala	Gly	Asn	Glu	Ile	Arg	Gln	Ile	Asp	Asn	Gly	Gly	Gly	Asn
	50					55					60				
His	Thr	Pro	Ile	Leu	Ala	Gly	Glu	Ile	Asn	Asn	His	Asn	Asn	Gly	His
				70					75					80	
His	Gly	Val	Gly	Gly	Gly	Gly	Glu	Leu	His	Gln	Ser	Val	Ser	Ser	Gly
				85				90						95	
Gly	Gly	Gly	Gly	Gly	Phe	Asp	Ser	Asp	Ser	Gly	Gly	Ala	Asn	Gly	Gly
			100					105					110		
Asn	Val	Asn	Gly	Ser	Ser	Ser	Ser								
		115				120									

(2) INFORMATION FOR SEQ ID NO:1164:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 133 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..133

(D) OTHER INFORMATION: / Ceres Seq. ID 1499768

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1164:

Met	Asn	Ser	Pro	Asn	Val	Leu	Val	Gly	Arg	Cys	Lys	Asn	Val	Xaa	Lys
1				5				10						15	
Thr	Met	Phe	Val	Ile	Phe	Ala	Gly	Arg	Ser	Glu	Leu	Ile	Lys	Val	Phe
			20					25					30		
Ser	Lys	Phe	Gly	Cys	Ile	Thr	Thr	Lys	Thr	Pro	Leu	Thr	Ala	Val	Ile
		35				40						45			
Ser	Pro	Glu	Thr	Arg	Ser	Gly	Lys	Ser	Ile	Thr	Ala	Glu	Glu	Thr	Thr
	50					55					60				
Leu	Arg	Phe	Ser	Pro	Ala	Arg	Leu	Ile	Thr	Ile	Thr	Met	Asp	Thr	Thr
				70				75						80	
Val	Ser	Glu	Glu	Glu	Glu	Ser	Phe	Thr	Arg	Val	Leu	Val	Ala	Ala	Val
				85				90						95	

Val Ala Glu Asp Leu Ile Val Ile Ala Ala Glu Leu Thr Val Val Thr
100 105 110
Leu Thr Asp His Arg Arg Arg Glu Val Lys Asp Glu Ser Val Arg Leu
115 120 125
Ile Arg Ser Leu Glu
130

(2) INFORMATION FOR SEQ ID NO:1165:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 491 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..491
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499769

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1165:

aatttgctaa ggaaaaaaa aacgaaaacg tgtgtctgtc tcttctcgta gcgctctctca	60
agctcagatg aattttgggt tgccaagtat atcttggttt ggtagcatca gcacaaagaa	120
agatgtagct atgattgatt ccgtagacacc aacaacaact tctctatttg aacagccaga	180
gcaagagaaa gcaacaacct ttcttctcaa acagccagag aaagagaaa gcttatttga	240
tataaagata tggacttggc cctccttcag ttcagttctt ccttggtctg caaatgcctc	300
tgatggtaag cagaaaccca ctactatcaa cagagggtta aaaaggcatg ctctttctcg	360
gaggtcatca aggatcaaat ggtgtgaata ctgtttatcg gtttagacct tatgggtgtct	420
aaggttccgt ggcatacagg gacgarggcg tttckgtcac agcttttccc gagatatgga	480
catttattgt g	

(2) INFORMATION FOR SEQ ID NO:1166:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 112 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..112
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499770

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1166:

Met Asn Phe Gly Leu Pro Ser Ile Ser Trp Phe Gly Ser Ile Ser Thr	
1 5 10 15	
Lys Lys Asp Val Ala Met Ile Asp Ser Val Thr Pro Thr Thr Ser	
20 25 30	
Leu Leu Glu Gln Pro Glu Gln Glu Lys Ala Thr Thr Phe Leu Leu Lys	
35 40 45	
Gln Pro Glu Lys Glu Lys Gly Leu Phe Asp Ile Lys Ile Trp Thr Trp	
50 55 60	
Ser Ser Phe Ser Ser Val Leu Pro Trp Ser Ala Asn Ala Ser Asp Gly	
65 70 75 80	
Lys Gln Lys Pro Thr Thr Ile Asn Arg Gly Leu Lys Arg His Ala Leu	
85 90 95	
Ser Arg Arg Ser Ser Arg Ile Lys Trp Cys Glu Tyr Cys Leu Ser Val	
100 105 110	

(2) INFORMATION FOR SEQ ID NO:1167:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 91 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..91

(D) OTHER INFORMATION: / Ceres Seq. ID 1499771

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1167:

Met	Ile	Asp	Ser	Val	Thr	Pro	Thr	Thr	Thr	Ser	Leu	Leu	Glu	Gln	Pro
1				5					10					15	
Glu	Gln	Glu	Lys	Ala	Thr	Thr	Phe	Leu	Leu	Lys	Gln	Pro	Glu	Lys	Glu
			20					25					30		
Lys	Gly	Leu	Phe	Asp	Ile	Lys	Ile	Trp	Thr	Trp	Ser	Ser	Phe	Ser	Ser
			35				40					45			
Val	Leu	Pro	Trp	Ser	Ala	Asn	Ala	Ser	Asp	Gly	Lys	Gln	Lys	Pro	Thr
			50			55					60				
Thr	Ile	Asn	Arg	Gly	Leu	Lys	Arg	His	Ala	Leu	Ser	Arg	Arg	Ser	Ser
65					70					75					80
Arg	Ile	Lys	Trp	Cys	Glu	Tyr	Cys	Leu	Ser	Val					
				85						90					

(2) INFORMATION FOR SEQ ID NO:1168:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1277 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1277

(D) OTHER INFORMATION: / Ceres Seq. ID 1499772

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1168:

atttcttctt	caccgttaga	tttttcctcg	cttaatttct	caataacgct	ctcagagaga	60
ccatttgatg	aagcttctcg	cttctggaat	ttgaaaagga	tttgataaga	cgagttcata	120
gaagattacc	gcaagttcat	caactttttg	aacttggtat	ggagataatc	tcactgaacg	180
ttgtgcccc	gtgctctgtg	gttacttgga	gtagtaaatt	agcaacgata	agattgggtc	240
caaatcggtc	aagtttggtt	ttctcagggg	tcaaaaaatc	cagacttggtg	attcgaagtg	300
gaaattccga	tggttatggt	gttggtgaga	atgatgactt	gggtcgtata	gccagaagag	360
gagaatcaac	gtcaaagggt	ttgattcctg	gtttgcctga	tgaatcaaat	ggtgaaattg	420
ctgctcgaat	cagtcattct	cactgcgagt	ggaagcccaa	gcttagagta	cattatgaga	480
aagccggttg	tgacaatctc	gatgctcctg	cggtgtgtgt	tcttcctggc	tttggcggtg	540
gttcatttca	ctatgagaag	cagcttaccg	atttggaag	ggattatcga	gtatgggcta	600
ttgattttct	tggacagggt	ttatctctcc	ctactgaaga	tcctactacc	atgactgaag	660
aaaccagttc	ctcgaagat	aaggaaccat	tttggggatt	tggtgacaaa	actgaaccgt	720
gggctgatca	acttgatttc	tctctggatc	tctggaggga	tcaagttcag	tattttgtag	780
aagaggttat	cggtagacct	gtgtacattg	ctgggaactc	acttgagggg	tatgtagctc	840
tctactttgc	agcaacccat	cctcacctgg	ttaagggtgt	taccttgctt	aatgcaacac	900
ctttctgggg	tttcttccct	aatccagtaa	gatcccaaaa	gctagcacgt	ctctttccat	960
ggcccggagc	attccctctg	cgggaaagag	tgaaaaaaaa	tcacagaatt	gggtgtggcaa	1020
aagataagtg	atcctgaaaag	catagctgag	atacttaaac	aggtctacac	agaccattct	1080
accaatgttg	ataaagtatt	ctcacgtatt	gtggaggcca	cacagcatcc	ggctgctgca	1140
gcatcgtttg	cttcaattat	gcttgctcct	ggtagagagc	tatctttctc	cgaagcttta	1200
tctaggtgta	aggaaaacaa	tgttcagata	tgtctcatgt	atggaagaga	agatccatgg	1260
gtgagaccgt	tatggggg					

(2) INFORMATION FOR SEQ ID NO:1169:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 290 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..290

(D) OTHER INFORMATION: / Ceres Seq. ID 1499773

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1169:

Met Glu Ile Ile Ser Leu Asn Val Val Pro Gln Cys Ser Val Val Thr
1 5 10 15
Trp Ser Ser Lys Leu Ala Thr Ile Arg Leu Val Pro Asn Arg Ser Ser
20 25 30
Leu Leu Phe Ser Gly Val Lys Lys Ser Arg Leu Val Ile Arg Ser Gly
35 40 45
Asn Ser Asp Gly Tyr Val Val Gly Glu Asn Asp Asp Leu Gly Arg Ile
50 55 60
Ala Arg Arg Gly Glu Ser Thr Ser Lys Val Leu Ile Pro Gly Leu Pro
65 70 75 80
Asp Glu Ser Asn Gly Glu Ile Ala Ala Arg Ile Ser His Ser His Cys
85 90 95
Glu Trp Lys Pro Lys Leu Arg Val His Tyr Glu Lys Ala Gly Cys Asp
100 105 110
Asn Leu Asp Ala Pro Ala Val Leu Phe Leu Pro Gly Phe Gly Val Gly
115 120 125
Ser Phe His Tyr Glu Lys Gln Leu Thr Asp Leu Gly Arg Asp Tyr Arg
130 135 140
Val Trp Ala Ile Asp Phe Leu Gly Gln Gly Leu Ser Leu Pro Thr Glu
145 150 155 160
Asp Pro Thr Thr Met Thr Glu Glu Thr Ser Ser Ser Glu Asp Lys Glu
165 170 175
Pro Phe Trp Gly Phe Gly Asp Lys Thr Glu Pro Trp Ala Asp Gln Leu
180 185 190
Val Phe Ser Leu Asp Leu Trp Arg Asp Gln Val Gln Tyr Phe Val Glu
195 200 205
Glu Val Ile Gly Glu Pro Val Tyr Ile Ala Gly Asn Ser Leu Gly Gly
210 215 220
Tyr Val Ala Leu Tyr Phe Ala Ala Thr His Pro His Leu Val Lys Gly
225 230 235 240
Val Thr Leu Leu Asn Ala Thr Pro Phe Trp Gly Phe Phe Pro Asn Pro
245 250 255
Val Arg Ser Pro Lys Leu Ala Arg Leu Phe Pro Trp Pro Gly Ala Phe
260 265 270
Pro Leu Pro Glu Arg Val Lys Lys Asn His Arg Ile Gly Val Ala Lys
275 280 285
Asp Lys
290

(2) INFORMATION FOR SEQ ID NO:1170:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1843 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1843

(D) OTHER INFORMATION: / Ceres Seq. ID 1499777

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1170:

acacaaccaa agcgtttaga aaaaaaacag cgataaaacc gaaacatcaa gcaaacaaaa	60
aaaaagagga gaattttttt tttttgtttt cgttttcaaa aacaaaatct ttgaatttta	120
tggaaccccg tcttctccga acaaaacttta tccggcgatc ttaccgttta cccgctttta	180
gcccgggtggg tcctcccacc gtgactgctt ccaccgccgt cgtcccggag attctctcct	240
ttggacaaca agcaccggaa ccacctcttc accacccaaa acccactgag caatctcacg	300
atggtctcga tctctccgat caagcccgtc ttttctcctc tatcccaacc tctgatctcc	360
tccgttccac cgccgtgttg catgcggcgg cgataggtcc tatggtcgac ctaggacgt	420
gggtcatgag ctctaaactt atggacgctt ccgtgacgcy tggcatggtt ttagggcttg	480

tgaaaagtac gttttatgac catttttgcg ccggtgaaga tgccgacgca gccgctgagc 540
gcgtgagaag cgtttatgaa gctaccggtc ttaaagggat gcttgtctat ggcgtcgaac 600
acgccgatga cgctgtatct tgtgatgata acatgcaaca attcattcga accattgaag 660
ctgccaaatc tttaccaaca tctcacttta gctcagtggt tgtgaagata actgccattt 720
gtccaattag tcttctgaaa cgagtgaagc atctgcttcg gtgggaatac aaaagtccaa 780
acttcaaaact ctcatggaag ctcaaactcg ttccggtttt ctccgattcg agtcctctct 840
accacacaaa ctcagaaccg gaaccgttaa ccgcggaaga agaacgggag ctccaagcag 900
ctcatggaag gattcaagaa atctgttaga aatgccaaag agtccaatgt accattgttg 960
attgatgcgg aagacacaat cctccaaccc gcgatcgatt acatggctta ttcacggcg 1020
atcatgttca atgctgacaa agaccgacca atcgtttaca acacgattca ggcgtacttg 1080
agagacgccg gtgagagact gcatttggca gtacaaaatg ctgagaaaga gaatgttcct 1140
atgggggttca agttggtgag aggggcttac atgtctagcg aagctagctt ggcggattcc 1200
ctgggttgca agtcgccagt ccacgacaca attcaggata ctactcttg ttacaatgat 1260
tgtatgacat tcctgatgga gaaagcatca aacggttctg gtttcggtgt cgttctcgca 1320
acacataacg ctgattcggg gagacttgcg tcgaggaaag cgagtgdhct cgggattgat 1380
aaacagaacg ggaagataga gtttgcacag ctatatggtat tgcggatgc attgtcttcg 1440
gtttaaagag agccgggttc aatgttagca agtacatgcc gtttggaccc gtcgcaaccg 1500
ctataccgta tcttctccga cgcgcttatg agaaccgggg aatgatggcc accggagctc 1560
atgaccgtca actcatgagg atggaactta agaggagatt aatcgccggg attgcgtaaa 1620
gagagagtat ggagccatta aatgaaattg ggaaatgtag atgaataaat ttcttctatg 1680
tagtttaaga aattgaaaac aaaaaattat aatataagaa atggagtagg taagaacatt 1740
tcctgtggct aaatatcttt catgagggac tatgttttta ctatcaatat atcattcaca 1800
aatgtatatt caccttatca ataaaaatgt tttttacttt ttt

(2) INFORMATION FOR SEQ ID NO:1171:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 320 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..320

(D) OTHER INFORMATION: / Ceres Seq. ID 1499778

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1171:

Thr Thr Lys Ala Phe Arg Lys Lys Thr Ala Ile Lys Pro Lys His Gln
1 5 10 15
Ala Asn Lys Lys Lys Glu Glu Asn Phe Phe Phe Leu Phe Ser Phe Ser
20 25 30
Lys Thr Lys Ser Leu Asn Phe Met Ala Thr Arg Leu Leu Arg Thr Asn
35 40 45
Phe Ile Arg Arg Ser Tyr Arg Leu Pro Ala Phe Ser Pro Val Gly Pro
50 55 60
Pro Thr Val Thr Ala Ser Thr Ala Val Val Pro Glu Ile Leu Ser Phe
65 70 75 80
Gly Gln Gln Ala Pro Glu Pro Pro Leu His His Pro Lys Pro Thr Glu
85 90 95
Gln Ser His Asp Gly Leu Asp Leu Ser Asp Gln Ala Arg Leu Phe Ser
100 105 110
Ser Ile Pro Thr Ser Asp Leu Leu Arg Ser Thr Ala Val Leu His Ala
115 120 125
Ala Ala Ile Gly Pro Met Val Asp Leu Gly Thr Trp Val Met Ser Ser
130 135 140
Lys Leu Met Asp Ala Ser Val Thr Arg Gly Met Val Leu Gly Leu Val
145 150 155 160
Lys Ser Thr Phe Tyr Asp His Phe Cys Ala Gly Glu Asp Ala Asp Ala
165 170 175
Ala Ala Glu Arg Val Arg Ser Val Tyr Glu Ala Thr Gly Leu Lys Gly
180 185 190
Met Leu Val Tyr Gly Val Glu His Ala Asp Asp Ala Val Ser Cys Asp
195 200 205

Asp	Asn	Met	Gln	Gln	Phe	Ile	Arg	Thr	Ile	Glu	Ala	Ala	Lys	Ser	Leu
210						215					220				
Pro	Thr	Ser	His	Phe	Ser	Ser	Val	Val	Val	Lys	Ile	Thr	Ala	Ile	Cys
225					230					235					240
Pro	Ile	Ser	Leu	Leu	Lys	Arg	Val	Ser	Asp	Leu	Leu	Arg	Trp	Glu	Tyr
				245					250					255	
Lys	Ser	Pro	Asn	Phe	Lys	Leu	Ser	Trp	Lys	Leu	Lys	Ser	Phe	Pro	Val
			260					265					270		
Phe	Ser	Asp	Ser	Ser	Pro	Leu	Tyr	His	Thr	Asn	Ser	Glu	Pro	Glu	Pro
		275					280					285			
Leu	Thr	Ala	Glu	Glu	Glu	Arg	Glu	Leu	Glu	Ala	Ala	His	Gly	Arg	Ile
290						295					300				
Gln	Glu	Ile	Cys	Arg	Lys	Cys	Gln	Arg	Val	Gln	Cys	Thr	Ile	Val	Asp
305					310					315					320

(2) INFORMATION FOR SEQ ID NO:1172:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 281 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..281

(D) OTHER INFORMATION: / Ceres Seq. ID 1499779

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1172:

Met	Ala	Thr	Arg	Leu	Leu	Arg	Thr	Asn	Phe	Ile	Arg	Arg	Ser	Tyr	Arg
1				5				10					15		
Leu	Pro	Ala	Phe	Ser	Pro	Val	Gly	Pro	Pro	Thr	Val	Thr	Ala	Ser	Thr
		20					25					30			
Ala	Val	Val	Pro	Glu	Ile	Leu	Ser	Phe	Gly	Gln	Gln	Ala	Pro	Glu	Pro
		35				40					45				
Pro	Leu	His	His	Pro	Lys	Pro	Thr	Glu	Gln	Ser	His	Asp	Gly	Leu	Asp
50					55					60					
Leu	Ser	Asp	Gln	Ala	Arg	Leu	Phe	Ser	Ser	Ile	Pro	Thr	Ser	Asp	Leu
65				70						75				80	
Leu	Arg	Ser	Thr	Ala	Val	Leu	His	Ala	Ala	Ala	Ile	Gly	Pro	Met	Val
			85					90					95		
Asp	Leu	Gly	Thr	Trp	Val	Met	Ser	Ser	Lys	Leu	Met	Asp	Ala	Ser	Val
		100					105					110			
Thr	Arg	Gly	Met	Val	Leu	Gly	Leu	Val	Lys	Ser	Thr	Phe	Tyr	Asp	His
		115				120						125			
Phe	Cys	Ala	Gly	Glu	Asp	Ala	Asp	Ala	Ala	Ala	Glu	Arg	Val	Arg	Ser
		130				135					140				
Val	Tyr	Glu	Ala	Thr	Gly	Leu	Lys	Gly	Met	Leu	Val	Tyr	Gly	Val	Glu
145				150						155				160	
His	Ala	Asp	Asp	Ala	Val	Ser	Cys	Asp	Asp	Asn	Met	Gln	Gln	Phe	Ile
			165					170						175	
Arg	Thr	Ile	Glu	Ala	Ala	Lys	Ser	Leu	Pro	Thr	Ser	His	Phe	Ser	Ser
		180						185					190		
Val	Val	Val	Lys	Ile	Thr	Ala	Ile	Cys	Pro	Ile	Ser	Leu	Leu	Lys	Arg
		195					200					205			
Val	Ser	Asp	Leu	Leu	Arg	Trp	Glu	Tyr	Lys	Ser	Pro	Asn	Phe	Lys	Leu
		210				215					220				
Ser	Trp	Lys	Leu	Lys	Ser	Phe	Pro	Val	Phe	Ser	Asp	Ser	Ser	Pro	Leu
225				230						235				240	
Tyr	His	Thr	Asn	Ser	Glu	Pro	Glu	Pro	Leu	Thr	Ala	Glu	Glu	Glu	Arg
			245						250					255	
Glu	Leu	Glu	Ala	Ala	His	Gly	Arg	Ile	Gln	Glu	Ile	Cys	Arg	Lys	Cys

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260 265 270
Gln Arg Val Gln Cys Thr Ile Val Asp
275 280
(2) INFORMATION FOR SEQ ID NO:1173:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 187 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..187
(D) OTHER INFORMATION: / Ceres Seq. ID 1499780
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1173:
Met Val Asp Leu Gly Thr Trp Val Met Ser Ser Lys Leu Met Asp Ala
1 5 10 15
Ser Val Thr Arg Gly Met Val Leu Gly Leu Val Lys Ser Thr Phe Tyr
20 25 30
Asp His Phe Cys Ala Gly Glu Asp Ala Ala Ala Glu Arg Val
35 40 45
Arg Ser Val Tyr Glu Ala Thr Gly Leu Lys Gly Met Leu Val Tyr Gly
50 55 60
Val Glu His Ala Asp Asp Ala Val Ser Cys Asp Asp Asn Met Gln Gln
65 70 75 80
Phe Ile Arg Thr Ile Glu Ala Ala Lys Ser Leu Pro Thr Ser His Phe
85 90 95
Ser Ser Val Val Val Lys Ile Thr Ala Ile Cys Pro Ile Ser Leu Leu
100 105 110
Lys Arg Val Ser Asp Leu Leu Arg Trp Glu Tyr Lys Ser Pro Asn Phe
115 120 125
Lys Leu Ser Trp Lys Leu Lys Ser Phe Pro Val Phe Ser Asp Ser Ser
130 135 140
Pro Leu Tyr His Thr Asn Ser Glu Pro Glu Pro Leu Thr Ala Glu Glu
145 150 155 160
Glu Arg Glu Leu Glu Ala Ala His Gly Arg Ile Gln Glu Ile Cys Arg
165 170 175
Lys Cys Gln Arg Val Gln Cys Thr Ile Val Asp
180 185

(2) INFORMATION FOR SEQ ID NO:1174:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 553 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
(A) NAME/KEY: -
(B) LOCATION: 1..553
(D) OTHER INFORMATION: / Ceres Seq. ID 1499785
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1174:
gacgttggttt cttatatcgt tgccagagag agtttgacgg cggagagata tggcggcggtt 60
gatggagtgca gtcgtcggcc gagctctaaa attctcatcg acggcgaatt tcagggtcaat 120
ccgacgcggc gaaacaccaa cactctgtat caaatcattc tccaccatta tgtcaccacc 180
gtcaaaagcc atcgtctacg aagaacacgg ctctcccgat tccgtcacca gattggtgaa 240
tctcccgccg gtggaagtga aagaaaacga cgtttgtgtt aaaatgatcg ccgctccgat 300
caaccctcc gatatacaatc gaattgaagg tgtgtatccg gtgaggccac cggtaggcagc 360
ggttggtggt tatgaaggtg ttggtgaagt ttatgcagtt ggctccaatg ttaatggttt 420
ttctcctggt gattgggtca ttccatctcc accttcttca gggacttggc agacttatgt 480
tgtgaaggaa gagagtggtg ggcacaaaat cgataaagag tgtccaatgg agtatgcagc 540
gacgattact gtt

(2) INFORMATION FOR SEQ ID NO:1175:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 168 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..168
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499786

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1175:

Met	Ala	Ala	Leu	Met	Glu	Ser	Val	Val	Gly	Arg	Ala	Leu	Lys	Phe	Ser
1				5					10					15	
Ser	Thr	Ala	Asn	Phe	Arg	Ser	Ile	Arg	Arg	Gly	Glu	Thr	Pro	Thr	Leu
			20					25					30		
Cys	Ile	Lys	Ser	Phe	Ser	Thr	Ile	Met	Ser	Pro	Pro	Ser	Lys	Ala	Ile
		35					40					45			
Val	Tyr	Glu	Glu	His	Gly	Ser	Pro	Asp	Ser	Val	Thr	Arg	Leu	Val	Asn
	50					55					60				
Leu	Pro	Pro	Val	Glu	Val	Lys	Glu	Asn	Asp	Val	Cys	Val	Lys	Met	Ile
65					70					75					80
Ala	Ala	Pro	Ile	Asn	Pro	Ser	Asp	Ile	Asn	Arg	Ile	Glu	Gly	Val	Tyr
				85					90					95	
Pro	Val	Arg	Pro	Pro	Val	Pro	Ala	Val	Gly	Gly	Tyr	Glu	Gly	Val	Gly
			100					105						110	
Glu	Val	Tyr	Ala	Val	Gly	Ser	Asn	Val	Asn	Gly	Phe	Ser	Pro	Gly	Asp
		115					120					125			
Trp	Val	Ile	Pro	Ser	Pro	Pro	Ser	Ser	Gly	Thr	Trp	Gln	Thr	Tyr	Val
	130					135					140				
Val	Lys	Glu	Glu	Ser	Val	Trp	His	Lys	Ile	Asp	Lys	Glu	Cys	Pro	Met
145					150					155					160
Glu	Tyr	Ala	Ala	Thr	Ile	Thr	Val								
															165

(2) INFORMATION FOR SEQ ID NO:1176:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 164 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..164
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499787

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1176:

Met	Glu	Ser	Val	Val	Gly	Arg	Ala	Leu	Lys	Phe	Ser	Ser	Thr	Ala	Asn
1				5					10					15	
Phe	Arg	Ser	Ile	Arg	Arg	Gly	Glu	Thr	Pro	Thr	Leu	Cys	Ile	Lys	Ser
			20					25					30		
Phe	Ser	Thr	Ile	Met	Ser	Pro	Pro	Ser	Lys	Ala	Ile	Val	Tyr	Glu	Glu
		35					40					45			
His	Gly	Ser	Pro	Asp	Ser	Val	Thr	Arg	Leu	Val	Asn	Leu	Pro	Pro	Val
	50					55					60				
Glu	Val	Lys	Glu	Asn	Asp	Val	Cys	Val	Lys	Met	Ile	Ala	Ala	Pro	Ile
65				70					75						80
Asn	Pro	Ser	Asp	Ile	Asn	Arg	Ile	Glu	Gly	Val	Tyr	Pro	Val	Arg	Pro
				85					90					95	
Pro	Val	Pro	Ala	Val	Gly	Gly	Tyr	Glu	Gly	Val	Gly	Glu	Val	Tyr	Ala
			100					105					110		
Val	Gly	Ser	Asn	Val	Asn	Gly	Phe	Ser	Pro	Gly	Asp	Trp	Val	Ile	Pro

	115					120						125					
Ser	Pro	Pro	Ser	Ser	Gly	Thr	Trp	Gln	Thr	Tyr	Val	Val	Lys	Glu	Glu		
	130					135					140						
Ser	Val	Trp	His	Lys	Ile	Asp	Lys	Glu	Cys	Pro	Met	Glu	Tyr	Ala	Ala		
145					150					155					160		
Thr	Ile	Thr	Val														

(2) INFORMATION FOR SEQ ID NO:1177:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 128 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..128

(D) OTHER INFORMATION: / Ceres Seq. ID 1499788

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1177:

Met	Ser	Pro	Pro	Ser	Lys	Ala	Ile	Val	Tyr	Glu	Glu	His	Gly	Ser	Pro
1				5					10					15	
Asp	Ser	Val	Thr	Arg	Leu	Val	Asn	Leu	Pro	Pro	Val	Glu	Val	Lys	Glu
			20				25					30			
Asn	Asp	Val	Cys	Val	Lys	Met	Ile	Ala	Ala	Pro	Ile	Asn	Pro	Ser	Asp
		35				40					45				
Ile	Asn	Arg	Ile	Glu	Gly	Val	Tyr	Pro	Val	Arg	Pro	Pro	Val	Pro	Ala
	50				55					60					
Val	Gly	Gly	Tyr	Glu	Gly	Val	Gly	Glu	Val	Tyr	Ala	Val	Gly	Ser	Asn
65				70				75						80	
Val	Asn	Gly	Phe	Ser	Pro	Gly	Asp	Trp	Val	Ile	Pro	Ser	Pro	Pro	Ser
			85				90						95		
Ser	Gly	Thr	Trp	Gln	Thr	Tyr	Val	Val	Lys	Glu	Glu	Ser	Val	Trp	His
		100					105						110		
Lys	Ile	Asp	Lys	Glu	Cys	Pro	Met	Glu	Tyr	Ala	Ala	Thr	Ile	Thr	Val
	115						120						125		

(2) INFORMATION FOR SEQ ID NO:1178:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1910 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1910

(D) OTHER INFORMATION: / Ceres Seq. ID 1499789

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1178:

atttataaaaaa	gaaaaaagaa	gaaaagagag	agagagactc	acaaatcata	atatctcctt	60
cattaactca	taatcacttt	aaagaacatt	ggaatcagat	tcattacata	gggattgata	120
tggaaaagtc	aaaccaacca	gttcatgtaa	ccttggtccga	attgaaggac	ggagataaag	180
aaatcggtga	tgctgaattt	ttgggtgatc	ttcttgagag	ctatagattt	ggtaaagata	240
atgttccccgc	ccgagaattt	cgatccaagg	cggcagcgac	ggctccggcg	ccgggtcaaca	300
ccaccgagat	agagttggaa	gaggataatg	atggatctca	agctcaaggt	aacaattctg	360
ttagtgaaaag	tacatcatcg	ctattttccg	attcagatcc	aatagtactt	gagagtactg	420
tgagcgaaaac	cggttcaaac	gaagaatctg	aaaccggttc	aaacgaagaa	aatggtaata	480
attgggttaga	gtcgagctcc	acaaacttgc	caaagttaga	gaacaaaagg	caacgggaatg	540
gagaagattg	tgagatagaa	gaggaagaag	aaaataacga	gagatcatta	tcggatttcag	600
aagagaagtc	aaacctagag	aagttgcttg	ggacacaaga	aaactatgag	cttggaaatg	660
aggatgaaga	aaagaacgag	agatcatcgt	cagattcaga	agagaagtca	aacctagaga	720

attttcttgc	gacacaagaa	aactacgagc	tttactgtcc	tagctgtagc	acatgtatca	780
ccagaaatgt	ggttctcaag	aaaagaaaac	gaggggaagca	cgtaattca	tctctggatc	840
tgaaccgga	tataccggtt	gttgaaccgg	acgaaccaag	cgacattgag	gagatggaat	900
caccagttaa	ggtttatgtc	cctgagactc	ggattgagga	tgatcaagaa	gataaagagg	960
gaactatctt	tacttgcttg	gtttgtgatc	taaagtactt	catccgggta	ggaacaaagt	1020
tcttacaact	tgattatata	aggggaaaac	cggttgagaa	atcagttgaa	gaatatatag	1080
atgtgaggaa	gagtataaac	accacacaat	caccaccaca	aattcaaccg	gacggagaaa	1140
gattcgccat	tgagttgtta	aagagcaccg	tctacggcgg	tctcactgag	accatcacca	1200
gcctcggcgt	tgtatcatct	gcttctgcct	ctggttcctc	caccatgaat	atattgsctc	1260
ttgctgtcgc	aaatttggcc	gggtgggtca	tcgtcctcgc	tcaaaacttt	caagatctaa	1320
gaaacagttc	agatcaagag	aaagataggt	acgaggaatt	gttagggaga	cgtactaaat	1380
cccggataca	tatcttagta	gcggtcatgt	cttacatttt	cttcggccta	attcctccgt	1440
tagtttacgc	attttccttc	tacgaaaccg	gaatcaagaa	ctacaagctc	atctcggttt	1500
tcttggttgc	tctggtttgc	gtaattttgc	tcggttcgat	caaggtctat	gtccgaaaac	1560
caaccaattc	atgtggatcg	actaaagctt	atctcaaata	tgcggttat	tatacgtcta	1620
ttgttgttgc	ttcttgcgga	atctcatatc	ttgtcggaga	tattatggga	gagtatatcg	1680
agaagctcag	tttggttggg	ttagaccaga	tcagtataac	ttcaccatgt	tatggaatta	1740
aacccgagga	gtgccggttt	acttcctttt	aatatacagt	gggactaaga	accgggtctga	1800
ccaacgttgt	ataatttctg	ttctaattac	ttactaaatc	tctgtatctt	ttctagtaaa	1860
aatcaaaaac	taatgctttc	atagaataaa	tgtgttttga	ggtttttctc		

(2) INFORMATION FOR SEQ ID NO:1179:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 589 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..589
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499790

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1179:

Leu	Lys	Lys	Lys	Lys	Glu	Glu	Lys	Arg	Glu	Arg	Asp	Ser	Gln	Ile	Ile
1				5					10					15	
Ile	Ser	Pro	Ser	Leu	Thr	His	Asn	His	Phe	Lys	Glu	His	Trp	Asn	Gln
				20				25					30		
Ile	His	Tyr	Ile	Gly	Ile	Asp	Met	Glu	Lys	Ser	Asn	Gln	Pro	Val	His
		35					40					45			
Val	Thr	Leu	Ser	Glu	Leu	Lys	Asp	Gly	Asp	Lys	Glu	Ile	Val	Asp	Ala
		50				55					60				
Glu	Phe	Leu	Val	Asp	Leu	Glu	Ser	Tyr	Arg	Phe	Gly	Lys	Asp	Asn	
65					70				75					80	
Val	Pro	Ala	Arg	Glu	Phe	Arg	Ser	Lys	Ala	Ala	Ala	Thr	Ala	Pro	Ala
				85					90					95	
Pro	Val	Asn	Thr	Thr	Glu	Ile	Glu	Leu	Glu	Glu	Asp	Asn	Asp	Gly	Ser
				100				105					110		
Gln	Ala	Gln	Gly	Asn	Asn	Ser	Val	Ser	Glu	Ser	Thr	Ser	Ser	Leu	Phe
		115					120					125			
Ser	Asp	Ser	Asp	Pro	Ile	Val	Leu	Glu	Ser	Thr	Val	Ser	Glu	Thr	Gly
		130				135					140				
Ser	Asn	Glu	Glu	Ser	Glu	Thr	Gly	Ser	Asn	Glu	Glu	Asn	Gly	Asn	Asn
145					150					155				160	
Trp	Leu	Glu	Ser	Ser	Ser	Thr	Asn	Leu	Pro	Asn	Val	Glu	Asn	Lys	Arg
				165					170					175	
Gln	Arg	Asn	Gly	Glu	Asp	Cys	Glu	Ile	Glu	Glu	Glu	Glu	Glu	Asn	Asn
			180				185					190			
Glu	Arg	Ser	Leu	Ser	Asp	Ser	Glu	Glu	Lys	Ser	Asn	Leu	Glu	Lys	Leu
		195					200					205			
Leu	Gly	Thr	Gln	Glu	Asn	Tyr	Glu	Leu	Gly	Asn	Glu	Asp	Glu	Glu	Lys
		210				215					220				
Asn	Glu	Arg	Ser	Ser	Ser	Asp	Ser	Glu	Glu	Lys	Ser	Asn	Leu	Glu	Asn

225		230		235		240									
Phe	Leu	Ala	Thr	Gln	Glu	Asn	Tyr	Glu	Leu	Tyr	Cys	Pro	Ser	Cys	Ser
				245				250						255	
Thr	Cys	Ile	Thr	Arg	Asn	Val	Val	Leu	Lys	Lys	Arg	Lys	Arg	Gly	Lys
			260					265						270	
His	Val	Asn	Ser	Ser	Leu	Asp	Leu	Lys	Pro	Asp	Ile	Pro	Val	Val	Glu
		275						280					285		
Pro	Asp	Glu	Pro	Ser	Asp	Ile	Glu	Glu	Met	Glu	Ser	Pro	Val	Lys	Val
	290					295					300				
Tyr	Val	Pro	Glu	Thr	Arg	Ile	Glu	Asp	Asp	Gln	Glu	Asp	Lys	Glu	Gly
305					310					315					320
Thr	Ile	Phe	Thr	Cys	Leu	Val	Cys	Asp	Leu	Lys	Tyr	Phe	Ile	Arg	Leu
				325						330					335
Gly	Thr	Lys	Phe	Leu	Gln	Leu	Asp	Tyr	Ile	Arg	Gly	Lys	Pro	Val	Glu
			340					345					350		
Lys	Ser	Val	Glu	Glu	Tyr	Ile	Asp	Val	Arg	Lys	Ser	Ile	Asn	Thr	Thr
		355					360					365			
Gln	Ser	Pro	Pro	Gln	Ile	Gln	Pro	Asp	Gly	Glu	Arg	Phe	Ala	Ile	Glu
	370					375					380				
Leu	Leu	Lys	Ser	Thr	Val	Tyr	Gly	Gly	Leu	Thr	Glu	Thr	Ile	Thr	Ser
385					390					395					400
Leu	Gly	Val	Val	Ser	Ser	Ala	Ser	Ala	Ser	Gly	Ser	Ser	Thr	Met	Asn
			405							410				415	
Ile	Leu	Xaa	Leu	Ala	Val	Ala	Asn	Leu	Ala	Gly	Gly	Leu	Ile	Val	Leu
			420						425					430	
Ala	Gln	Asn	Phe	Gln	Asp	Leu	Arg	Asn	Ser	Ser	Asp	Gln	Glu	Lys	Asp
		435					440					445			
Arg	Tyr	Glu	Glu	Leu	Leu	Gly	Arg	Arg	Thr	Lys	Ser	Arg	Ile	His	Ile
	450					455					460				
Leu	Val	Ala	Val	Met	Ser	Tyr	Ile	Phe	Phe	Gly	Leu	Ile	Pro	Pro	Leu
465					470					475					480
Val	Tyr	Ala	Phe	Ser	Phe	Tyr	Glu	Thr	Gly	Ile	Lys	Asn	Tyr	Lys	Leu
			485						490					495	
Ile	Ser	Val	Phe	Leu	Gly	Ser	Leu	Val	Cys	Val	Ile	Leu	Leu	Gly	Ser
		500						505					510		
Ile	Lys	Val	Tyr	Val	Arg	Lys	Pro	Thr	Asn	Ser	Cys	Gly	Ser	Thr	Lys
		515					520					525			
Ala	Tyr	Leu	Lys	Ser	Ala	Ala	Tyr	Tyr	Thr	Ser	Ile	Val	Val	Ala	Ser
	530					535					540				
Cys	Gly	Ile	Ser	Tyr	Val	Val	Gly	Asp	Ile	Met	Gly	Glu	Tyr	Ile	Glu
545					550					555					560
Lys	Leu	Ser	Leu	Val	Gly	Leu	Asp	Gln	Ile	Ser	Ile	Thr	Ser	Pro	Cys
			565						570					575	
Tyr	Gly	Ile	Lys	Pro	Glu	Glu	Cys	Arg	Phe	Thr	Ser	Phe			
		580						585							

(2) INFORMATION FOR SEQ ID NO:1180:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 550 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..550
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499791

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1180:

Met	Glu	Lys	Ser	Asn	Gln	Pro	Val	His	Val	Thr	Leu	Ser	Glu	Leu	Lys
1				5				10					15		
Asp	Gly	Asp	Lys	Glu	Ile	Val	Asp	Ala	Glu	Phe	Leu	Val	Asp	Leu	Leu
			20					25					30		

Glu	Ser	Tyr	Arg	Phe	Gly	Lys	Asp	Asn	Val	Pro	Ala	Arg	Glu	Phe	Arg
		35					40					45			
Ser	Lys	Ala	Ala	Ala	Thr	Ala	Pro	Ala	Pro	Val	Asn	Thr	Thr	Glu	Ile
	50					55					60				
Glu	Leu	Glu	Glu	Asp	Asn	Asp	Gly	Ser	Gln	Ala	Gln	Gly	Asn	Asn	Ser
65					70				75					80	
Val	Ser	Glu	Ser	Thr	Ser	Ser	Leu	Phe	Ser	Asp	Ser	Asp	Pro	Ile	Val
				85					90					95	
Leu	Glu	Ser	Thr	Val	Ser	Glu	Thr	Gly	Ser	Asn	Glu	Glu	Ser	Glu	Thr
			100					105					110		
Gly	Ser	Asn	Glu	Glu	Asn	Gly	Asn	Asn	Trp	Leu	Glu	Ser	Ser	Ser	Thr
		115					120					125			
Asn	Leu	Pro	Asn	Val	Glu	Asn	Lys	Arg	Gln	Arg	Asn	Gly	Glu	Asp	Cys
	130					135					140				
Glu	Ile	Glu	Glu	Glu	Glu	Glu	Asn	Asn	Glu	Arg	Ser	Leu	Ser	Asp	Ser
145					150				155					160	
Glu	Glu	Lys	Ser	Asn	Leu	Glu	Lys	Leu	Leu	Gly	Thr	Gln	Glu	Asn	Tyr
				165				170						175	
Glu	Leu	Gly	Asn	Glu	Asp	Glu	Glu	Lys	Asn	Glu	Arg	Ser	Ser	Ser	Asp
			180					185					190		
Ser	Glu	Glu	Lys	Ser	Asn	Leu	Glu	Asn	Phe	Leu	Ala	Thr	Gln	Glu	Asn
		195					200					205			
Tyr	Glu	Leu	Tyr	Cys	Pro	Ser	Cys	Ser	Thr	Cys	Ile	Thr	Arg	Asn	Val
	210					215					220				
Val	Leu	Lys	Lys	Arg	Lys	Arg	Gly	Lys	His	Val	Asn	Ser	Ser	Leu	Asp
225					230					235				240	
Leu	Lys	Pro	Asp	Ile	Pro	Val	Val	Glu	Pro	Asp	Glu	Pro	Ser	Asp	Ile
				245				250						255	
Glu	Glu	Met	Glu	Ser	Pro	Val	Lys	Val	Tyr	Val	Pro	Glu	Thr	Arg	Ile
			260					265					270		
Glu	Asp	Asp	Gln	Glu	Asp	Lys	Glu	Gly	Thr	Ile	Phe	Thr	Cys	Leu	Val
			275				280					285			
Cys	Asp	Leu	Lys	Tyr	Phe	Ile	Arg	Leu	Gly	Thr	Lys	Phe	Leu	Gln	Leu
	290					295					300				
Asp	Tyr	Ile	Arg	Gly	Lys	Pro	Val	Glu	Lys	Ser	Val	Glu	Glu	Tyr	Ile
305					310					315				320	
Asp	Val	Arg	Lys	Ser	Ile	Asn	Thr	Thr	Gln	Ser	Pro	Pro	Gln	Ile	Gln
				325					330					335	
Pro	Asp	Gly	Glu	Arg	Phe	Ala	Ile	Glu	Leu	Leu	Lys	Ser	Thr	Val	Tyr
			340					345					350		
Gly	Gly	Leu	Thr	Glu	Thr	Ile	Thr	Ser	Leu	Gly	Val	Val	Ser	Ser	Ala
		355					360					365			
Ser	Ala	Ser	Gly	Ser	Ser	Thr	Met	Asn	Ile	Leu	Xaa	Leu	Ala	Val	Ala
	370					375					380				
Asn	Leu	Ala	Gly	Gly	Leu	Ile	Val	Leu	Ala	Gln	Asn	Phe	Gln	Asp	Leu
385					390					395				400	
Arg	Asn	Ser	Ser	Asp	Gln	Glu	Lys	Asp	Arg	Tyr	Glu	Glu	Leu	Leu	Gly
				405				410						415	
Arg	Arg	Thr	Lys	Ser	Arg	Ile	His	Ile	Leu	Val	Ala	Val	Met	Ser	Tyr
			420					425					430		
Ile	Phe	Phe	Gly	Leu	Ile	Pro	Pro	Leu	Val	Tyr	Ala	Phe	Ser	Phe	Tyr
		435					440					445			
Glu	Thr	Gly	Ile	Lys	Asn	Tyr	Lys	Leu	Ile	Ser	Val	Phe	Leu	Gly	Ser
	450					455					460				
Leu	Val	Cys	Val	Ile	Leu	Leu	Gly	Ser	Ile	Lys	Val	Tyr	Val	Arg	Lys
465					470					475				480	
Pro	Thr	Asn	Ser	Cys	Gly	Ser	Thr	Lys	Ala	Tyr	Leu	Lys	Ser	Ala	Ala
				485					490					495	
Tyr	Tyr	Thr	Ser	Ile	Val	Val	Ala	Ser	Cys	Gly	Ile	Ser	Tyr	Val	Val
			500					505					510		
Gly	Asp	Ile	Met	Gly	Glu	Tyr	Ile	Glu	Lys	Leu	Ser	Leu	Val	Gly	Leu

515 520 525
Asp Gln Ile Ser Ile Thr Ser Pro Cys Tyr Gly Ile Lys Pro Glu Glu
530 535 540
Cys Arg Phe Thr Ser Phe
545 550

(2) INFORMATION FOR SEQ ID NO:1181:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1500 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1500
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499792

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1181:

atctcttggt	ctctccgccc	atctctgctc	tcttttattt	tcccagaaag	tttttttttt	60
tttcccgaat	tccgttaatc	tcaattgggt	ttccattgat	agcaatggcg	acggctttcg	120
ctcccactaa	gctcactgcc	acggttcctc	tgcatggatc	ccatgagaat	cgtctcttgc	180
tcccgatccg	attggtcctt	ccttcttctt	tcctcggatc	cacccgttcc	ctctcccttc	240
gcagactcaa	tcactccaac	gccaccgctc	gatctcccgt	cgtctctgtc	caggaagtgt	300
gtcaaggaga	agcaatccac	caataatacc	agcctgttga	taaccaaaaga	ggaaggattg	360
gagttgtatg	aagatatgat	actaggtaga	tctttcgaag	acatgtgtgc	tcaaagtgtat	420
taccgaggca	agatgttttg	ttttgttcac	ttgtacaatg	gccaagaggc	tgtttctact	480
ggctttatca	agctccttac	caagtctgac	tctgtcggtt	gtacctaccg	tgacctgtc	540
catgccctca	gcaaagggtg	ctctgctcgt	gctgttatga	gcgagctctt	cggcaagggt	600
actggatgct	gcagaggcca	aggtggatcc	atgcacatgt	tctccaaaga	acacaacatg	660
cttggtggct	ttgcttttat	tggtgaaggc	attcctgtcg	ccactgggtg	tgcccttagc	720
tccaagtaca	ggaggggaag	cttgaaacag	gattgtgatg	atgtcactgt	cgcctttttc	780
ggagatggaa	cttgtaacaa	cggacagttc	ttcgagtgtc	tcaacatggc	tgctctctat	840
aaactgccta	ttatctttgt	tgctcgagaat	aacttgtggg	ccattgggat	gtctcacttg	900
agagccactt	ctgaccccca	gatttgggaag	aaaggtcctg	catttgggat	gcctgggtgt	960
catgttgacg	gtvtggatgt	cttgaaggtc	agggaaagtcg	ctaaagaggc	gtgcactaga	1020
gctagaagag	gagaagggtc	aaccttggtt	gaatgtgaga	cttatagatt	tagaggacac	1080
tccttggtcg	atcccgatga	gctccgtgat	gctgctgaga	aagccaaata	cgcggctaga	1140
gacccaatcg	cagcattgaa	gaagtatttg	atagagaaca	agcttgcaaa	ggaagcagag	1200
ctaaagtcaa	tagagaaaaa	gatagacgag	ttggtggagg	aagcggttga	gtttgcagac	1260
gctagtccac	agcccggctc	cagtcagttg	ctagagaatg	tgtttgctga	tccaaaagga	1320
tttggaaattg	gacctgatgg	acggtacaga	tgtgaggacc	ccaagtttac	cgaaggcaca	1380
gctcaagtct	gagaagacaa	gtttaaccat	aagctgtcta	ctgtctcttc	gatgtttcta	1440
tatatcttat	taagttaaat	gctacagaga	atcagtttga	atcatttgca	ctttttgctg	1500

(2) INFORMATION FOR SEQ ID NO:1182:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 412 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..412
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499793

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1182:

Met Asp Pro Met Arg Ile Val Ser Cys Ser Arg Ser Asp Trp Leu Leu	
1 5 10 15	
Leu Leu Leu Ser Ser Asp Pro Pro Val Pro Ser Pro Phe Ala Asp Ser	
20 25 30	
Ile Thr Pro Thr Pro Pro Val Asp Leu Pro Ser Ser Leu Ser Arg Lys	
35 40 45	

Leu	Val	Lys	Glu	Lys	Gln	Ser	Thr	Asn	Asn	Thr	Ser	Leu	Leu	Ile	Thr
50						55					60				
Lys	Glu	Glu	Gly	Leu	Glu	Leu	Tyr	Glu	Asp	Met	Ile	Leu	Gly	Arg	Ser
65					70					75					80
Phe	Glu	Asp	Met	Cys	Ala	Gln	Met	Tyr	Tyr	Arg	Gly	Lys	Met	Phe	Gly
				85					90					95	
Phe	Val	His	Leu	Tyr	Asn	Gly	Gln	Glu	Ala	Val	Ser	Thr	Gly	Phe	Ile
			100					105					110		
Lys	Leu	Leu	Thr	Lys	Ser	Asp	Ser	Val	Val	Ser	Thr	Tyr	Arg	Asp	His
			115				120					125			
Val	His	Ala	Leu	Ser	Lys	Gly	Val	Ser	Ala	Arg	Ala	Val	Met	Ser	Glu
			130			135					140				
Leu	Phe	Gly	Lys	Val	Thr	Gly	Cys	Cys	Arg	Gly	Gln	Gly	Gly	Ser	Met
145					150					155					160
His	Met	Phe	Ser	Lys	Glu	His	Asn	Met	Leu	Gly	Gly	Phe	Ala	Phe	Ile
				165					170					175	
Gly	Glu	Gly	Ile	Pro	Val	Ala	Thr	Gly	Ala	Ala	Phe	Ser	Ser	Lys	Tyr
			180					185					190		
Arg	Arg	Glu	Val	Leu	Lys	Gln	Asp	Cys	Asp	Asp	Val	Thr	Val	Ala	Phe
		195					200					205			
Phe	Gly	Asp	Gly	Thr	Cys	Asn	Asn	Gly	Gln	Phe	Phe	Glu	Cys	Leu	Asn
		210				215					220				
Met	Ala	Ala	Leu	Tyr	Lys	Leu	Pro	Ile	Ile	Phe	Val	Val	Glu	Asn	Asn
225					230					235					240
Leu	Trp	Ala	Ile	Gly	Met	Ser	His	Leu	Arg	Ala	Thr	Ser	Asp	Pro	Glu
				245					250					255	
Ile	Trp	Lys	Lys	Gly	Pro	Ala	Phe	Gly	Met	Pro	Gly	Val	His	Val	Asp
			260					265					270		
Gly	Xaa	Asp	Val	Leu	Lys	Val	Arg	Glu	Val	Ala	Lys	Glu	Ala	Val	Thr
		275					280					285			
Arg	Ala	Arg	Arg	Gly	Glu	Gly	Pro	Thr	Leu	Val	Glu	Cys	Glu	Thr	Tyr
		290				295					300				
Arg	Phe	Arg	Gly	His	Ser	Leu	Ala	Asp	Pro	Asp	Glu	Leu	Arg	Asp	Ala
305					310					315					320
Ala	Glu	Lys	Ala	Lys	Tyr	Ala	Ala	Arg	Asp	Pro	Ile	Ala	Ala	Leu	Lys
				325					330					335	
Lys	Tyr	Leu	Ile	Glu	Asn	Lys	Leu	Ala	Lys	Glu	Ala	Glu	Leu	Lys	Ser
			340					345				350			
Ile	Glu	Lys	Lys	Ile	Asp	Glu	Leu	Val	Glu	Glu	Ala	Val	Glu	Phe	Ala
		355				360						365			
Asp	Ala	Ser	Pro	Gln	Pro	Gly	Arg	Ser	Gln	Leu	Leu	Glu	Asn	Val	Phe
		370				375					380				
Ala	Asp	Pro	Lys	Gly	Phe	Gly	Ile	Gly	Pro	Asp	Gly	Arg	Tyr	Arg	Cys
385					390					395					400
Glu	Asp	Pro	Lys	Phe	Thr	Glu	Gly	Thr	Ala	Gln	Val				
				405					410						

(2) INFORMATION FOR SEQ ID NO:1183:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 409 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..409

(D) OTHER INFORMATION: / Ceres Seq. ID 1499794

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1183:

Met	Arg	Ile	Val	Ser	Cys	Ser	Arg	Ser	Asp	Trp	Leu	Leu	Leu	Leu	Leu
1			5						10					15	
Ser	Ser	Asp	Pro	Pro	Val	Pro	Ser	Pro	Phe	Ala	Asp	Ser	Ile	Thr	Pro

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1184:

Met Ile Leu Gly Arg Ser Phe Glu Asp Met Cys Ala Gln Met Tyr Tyr
1 5 10 15
Arg Gly Lys Met Phe Gly Phe Val His Leu Tyr Asn Gly Gln Glu Ala
20 25 30
Val Ser Thr Gly Phe Ile Lys Leu Thr Lys Ser Asp Ser Val Val
35 40 45
Ser Thr Tyr Arg Asp His Val His Ala Leu Ser Lys Gly Val Ser Ala
50 55 60
Arg Ala Val Met Ser Glu Leu Phe Gly Lys Val Thr Gly Cys Cys Arg
65 70 75 80
Gly Gln Gly Gly Ser Met His Met Phe Ser Lys Glu His Asn Met Leu
85 90 95
Gly Gly Phe Ala Phe Ile Gly Glu Gly Ile Pro Val Ala Thr Gly Ala
100 105 110
Ala Phe Ser Ser Lys Tyr Arg Arg Glu Val Leu Lys Gln Asp Cys Asp
115 120 125
Asp Val Thr Val Ala Phe Phe Gly Asp Gly Thr Cys Asn Asn Gly Gln
130 135 140
Phe Phe Glu Cys Leu Asn Met Ala Ala Leu Tyr Lys Leu Pro Ile Ile
145 150 155 160
Phe Val Val Glu Asn Asn Leu Trp Ala Ile Gly Met Ser His Leu Arg
165 170 175
Ala Thr Ser Asp Pro Glu Ile Trp Lys Lys Gly Pro Ala Phe Gly Met
180 185 190
Pro Gly Val His Val Asp Gly Xaa Asp Val Leu Lys Val Arg Glu Val
195 200 205
Ala Lys Glu Ala Val Thr Arg Ala Arg Arg Gly Glu Gly Pro Thr Leu
210 215 220
Val Glu Cys Glu Thr Tyr Arg Phe Arg Gly His Ser Leu Ala Asp Pro
225 230 235 240
Asp Glu Leu Arg Asp Ala Ala Glu Lys Ala Lys Tyr Ala Ala Arg Asp
245 250 255
Pro Ile Ala Ala Leu Lys Lys Tyr Leu Ile Glu Asn Lys Leu Ala Lys
260 265 270
Glu Ala Glu Leu Lys Ser Ile Glu Lys Lys Ile Asp Glu Leu Val Glu
275 280 285
Glu Ala Val Glu Phe Ala Asp Ala Ser Pro Gln Pro Gly Arg Ser Gln
290 295 300
Leu Leu Glu Asn Val Phe Ala Asp Pro Lys Gly Phe Gly Ile Gly Pro
305 310 315 320
Asp Gly Arg Tyr Arg Cys Glu Asp Pro Lys Phe Thr Glu Gly Thr Ala
325 330 335
Gln Val

(2) INFORMATION FOR SEQ ID NO:1185:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1319 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1319
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499800

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1185:

gggtttgaga gttatcgttt cgaagcttga tcctaattatt caacaatgac gataatgtca	60
gatctttccac gggatttggt agcggagatt ctccagtaggg ttccggttgac atctctaaga	120
gcagtgcgat tgacttgcaa aaagtggaac gatttatcca aagatcggag ctttctcaag	180
aagcaaatacg tcgaaacaaa gaagaagcaa ttggaatcga aggagattga ggtgatcatg	240
atgaggaatt ttaggggttta tctaacaagc atcgatatcc acaacaatgt tgatctatca	300

(2) INFORMATION FOR SEQ ID NO:1186:

(A) LENGTH: 292 amino acids

(C) STRANDEDNESS:

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..292

(D) OTHER INFORMATION: / Ceres Seq. ID 1499801

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1186:

Met	Met	Gln	Thr	Ile	Lys	Ser	Ile	Met	Tyr	Leu	Glu	Ser	Phe	Thr	
1				5				10					15		
Ala	Met	Val	Tyr	Tyr	Tyr	Ala	Ser	Pro	Lys	Thr	Ser	Thr	Ile	Gly	Leu
			20					25					30		
Xaa	Val	Trp	Asn	Pro	Tyr	Phe	Gly	Gln	Thr	Arg	Trp	Ile	Gln	Pro	Arg
			35				40					45			
Asn	Ser	Tyr	His	Arg	Lys	Asp	Asn	Tyr	Ala	Leu	Gly	Tyr	Asp	Glu	Lys
						55					60				
Lys	Asn	His	Lys	Ile	Leu	Arg	Leu	Lys	Asp	Asp	Tyr	Tyr	Ala	Pro	Arg
65					70					75				80	
Glu	Arg	Ile	Cys	Glu	Phe	Glu	Leu	Tyr	Ser	Phe	Glu	Ser	Asn	Ser	Trp
				85					90					95	
Lys	Val	Val	Leu	Asp	Val	Ser	Pro	Asp	Trp	Tyr	Ile	Pro	Ser	Tyr	Asn
			100					105					110		
Arg	Gly	Leu	Ser	Leu	Lys	Gly	Asn	Thr	Tyr	Trp	Tyr	Ala	Thr	Glu	Lys
			115				120					125			
His	Val	Asn	Val	Asp	Phe	Leu	Ile	Cys	Phe	Asp	Phe	Thr	Thr	Glu	Lys
					135						140				
Phe	Gly	Pro	Arg	Leu	Pro	Leu	Pro	Phe	Asn	Ala	Thr	Glu	Ser	Pro	Thr
145					150					155					160
Tyr	Glu	Asp	Val	Val	Thr	Leu	Ser	Ser	Val	Gly	Glu	Glu	Gln	Leu	Ala
				165					170					175	
Val	Leu	Phe	Gln	Ser	Glu	Tyr	Thr	Leu	Met	Met	Glu	Ile	Trp	Val	Thr
			180					185					190		
Ser	Lys	Val	Glu	Ser	Thr	Glu	Val	Leu	Trp	Asn	Lys	Leu	Phe	Leu	Glu
			195				200					205			
Val	Asp	Leu	Ile	Ala	Ile	Ser	Ser	His	Phe	Gln	Phe	Leu	Ala	Glu	Ala
					215						220				
Gly	Ser	Phe	Phe	Ile	Asp	Gln	Lys	Lys	Asn	Val	Val	Val	Val	Phe	Asp
225					230					235				240	
Lys	Asp	Met	Asp	Glu	Ala	Thr	Asp	Arg	Asp	Met	Ala	Tyr	Val	Val	Gly
				245					250					255	

Lys Asn Gly Tyr Phe Lys Lys Val Asp Ile Gly Glu Glu Ala Tyr Thr
260 265 270
Ser Cys Phe Pro Leu Val Cys Ser Tyr Val Pro Ser Ser Glu Gln Ile
275 280 285
Arg Gln Leu Thr
290

(2) INFORMATION FOR SEQ ID NO:1187:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 291 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..291
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499802

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1187:

Met Gln Thr Ile Ile Lys Ser Ile Met Tyr Leu Glu Ser Phe Thr Ala
1 5 10 15
Met Val Tyr Tyr Tyr Ala Ser Pro Lys Thr Ser Thr Ile Gly Leu Xaa
20 25 30
Val Trp Asn Pro Tyr Phe Gly Gln Thr Arg Trp Ile Gln Pro Arg Asn
35 40 45
Ser Tyr His Arg Lys Asp Asn Tyr Ala Leu Gly Tyr Asp Glu Lys Lys
50 55 60
Asn His Lys Ile Leu Arg Leu Lys Asp Asp Tyr Tyr Ala Pro Arg Glu
65 70 75 80
Arg Ile Cys Glu Phe Glu Leu Tyr Ser Phe Glu Ser Asn Ser Trp Lys
85 90 95
Val Val Leu Asp Val Ser Pro Asp Trp Tyr Ile Pro Ser Tyr Asn Arg
100 105 110
Gly Leu Ser Leu Lys Gly Asn Thr Tyr Trp Tyr Ala Thr Glu Lys His
115 120 125
Val Asn Val Asp Phe Leu Ile Cys Phe Asp Phe Thr Thr Glu Lys Phe
130 135 140
Gly Pro Arg Leu Pro Leu Pro Phe Asn Ala Thr Glu Ser Pro Thr Tyr
145 150 155 160
Glu Asp Val Val Thr Leu Ser Ser Val Gly Glu Glu Gln Leu Ala Val
165 170 175
Leu Phe Gln Ser Glu Tyr Thr Leu Met Met Glu Ile Trp Val Thr Ser
180 185 190
Lys Val Glu Ser Thr Glu Val Leu Trp Asn Lys Leu Phe Leu Glu Val
195 200 205
Asp Leu Ile Ala Ile Ser Ser His Phe Gln Phe Leu Ala Glu Ala Gly
210 215 220
Ser Phe Phe Ile Asp Gln Lys Lys Asn Val Val Val Val Phe Asp Lys
225 230 235 240
Asp Met Asp Glu Ala Thr Asp Arg Asp Met Ala Tyr Val Val Gly Lys
245 250 255
Asn Gly Tyr Phe Lys Lys Val Asp Ile Gly Glu Glu Ala Tyr Thr Ser
260 265 270
Cys Phe Pro Leu Val Cys Ser Tyr Val Pro Ser Ser Glu Gln Ile Arg
275 280 285
Gln Leu Thr
290

(2) INFORMATION FOR SEQ ID NO:1188:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 283 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:

- (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..283
(D) OTHER INFORMATION: / Ceres Seq. ID 1499803
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1188:

Met	Tyr	Leu	Glu	Ser	Phe	Thr	Ala	Met	Val	Tyr	Tyr	Tyr	Ala	Ser	Pro
1				5				10					15		
Lys	Thr	Ser	Thr	Ile	Gly	Leu	Xaa	Val	Trp	Asn	Pro	Tyr	Phe	Gly	Gln
		20				25						30			
Thr	Arg	Trp	Ile	Gln	Pro	Arg	Asn	Ser	Tyr	His	Arg	Lys	Asp	Asn	Tyr
	35					40					45				
Ala	Leu	Gly	Tyr	Asp	Glu	Lys	Lys	Asn	His	Lys	Ile	Leu	Arg	Leu	Lys
	50					55					60				
Asp	Asp	Tyr	Tyr	Ala	Pro	Arg	Glu	Arg	Ile	Cys	Glu	Phe	Glu	Leu	Tyr
65				70					75					80	
Ser	Phe	Glu	Ser	Asn	Ser	Trp	Lys	Val	Val	Leu	Asp	Val	Ser	Pro	Asp
			85					90						95	
Trp	Tyr	Ile	Pro	Ser	Tyr	Asn	Arg	Gly	Leu	Ser	Leu	Lys	Gly	Asn	Thr
		100						105					110		
Tyr	Trp	Tyr	Ala	Thr	Glu	Lys	His	Val	Asn	Val	Asp	Phe	Leu	Ile	Cys
	115						120					125			
Phe	Asp	Phe	Thr	Thr	Glu	Lys	Phe	Gly	Pro	Arg	Leu	Pro	Leu	Pro	Phe
	130					135					140				
Asn	Ala	Thr	Glu	Ser	Pro	Thr	Tyr	Glu	Asp	Val	Val	Thr	Leu	Ser	Ser
145				150					155					160	
Val	Gly	Glu	Glu	Gln	Leu	Ala	Val	Leu	Phe	Gln	Ser	Glu	Tyr	Thr	Leu
			165					170						175	
Met	Met	Glu	Ile	Trp	Val	Thr	Ser	Lys	Val	Glu	Ser	Thr	Glu	Val	Leu
		180						185					190		
Trp	Asn	Lys	Leu	Phe	Leu	Glu	Val	Asp	Leu	Ile	Ala	Ile	Ser	Ser	His
	195					200						205			
Phe	Gln	Phe	Leu	Ala	Glu	Ala	Gly	Ser	Phe	Phe	Ile	Asp	Gln	Lys	Lys
	210					215					220				
Asn	Val	Val	Val	Val	Phe	Asp	Lys	Asp	Met	Asp	Glu	Ala	Thr	Asp	Arg
225					230					235				240	
Asp	Met	Ala	Tyr	Val	Val	Gly	Lys	Asn	Gly	Tyr	Phe	Lys	Lys	Val	Asp
			245						250					255	
Ile	Gly	Glu	Glu	Ala	Tyr	Thr	Ser	Cys	Phe	Pro	Leu	Val	Cys	Ser	Tyr
		260					265						270		
Val	Pro	Ser	Ser	Glu	Gln	Ile	Arg	Gln	Leu	Thr					
		275					280								

(2) INFORMATION FOR SEQ ID NO:1189:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 957 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
 (A) NAME/KEY: -
 (B) LOCATION: 1..957
(D) OTHER INFORMATION: / Ceres Seq. ID 1499811

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1189:

aaatgaaatg	tatagagagg	taaagtggga	atatttgacat	tggtgggttt	agggaaaaaa	60
cagagagaaa	gagatggatt	cgtcgtcagt	agggaacacc	aacaggtact	gggtcctccg	120
ccacggcaag	agcattccca	acgagagagg	cctcgtcgtc	tcttccatgg	aaaatgggtg	180
cctccccgag	taccagttag	cccctgatgg	tgctcgctcag	gctcgtctcg	ccggcgaaatc	240
gttcctccag	caacttaagg	aaagtaacat	agaactggac	aaggttcggc	atttgctact	300
cccccttctc	cagaaccact	cacaccgcta	gggttggtgc	tgaggtcctc	aatctccctc	360

```
ttgatgctcc tcaatgcaag atgatggaag atctgcgca acgctatattt ggacctacat 420
ttgaactcaa gtcccatgac aagtaccag agatatgggc tcttgatgaa aaagatcctt 480
ttatgggacc agaaggaggt gaaagtgtgt atgatgttgt tccccgactt gccactgcca 540
tgaaatccat ggaagctgaa tatcaaaggt gtgcaattct ggtggtgagt catggagatc 600
ctctgcagat gttgcagaac gttttccatt cagcaaagca acaggaagga gatgggttgg 660
cagagaagtt tcagttgagc agagttgctt ctgtcttgtc acagcaccgc aagtttgctt 720
tgctcactgg ggaactccga cccctcatct gattggcaat caatgtattc agcttttgga 780
atgtctttcc ttgaactctt ttgttatcaa ttcctatttc tctcccattg gcattcttgc 840
aattgccaaa cttggattag cctgtttatt atcacctctg tttgttagag aaaacatgaa 900
gatttactcc tgtaataaga aatcatgctc atttatgtta tatgtatctt caaatct
```

(2) INFORMATION FOR SEQ ID NO:1190:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 123 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..123

(D) OTHER INFORMATION: / Ceres Seq. ID 1499812

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1190:

```
Met Met Glu Asp Leu Arg Glu Arg Tyr Phe Gly Pro Thr Phe Glu Leu
1      5      10      15
Lys Ser His Asp Lys Tyr Pro Glu Ile Trp Ala Leu Asp Glu Lys Asp
20     25     30
Pro Phe Met Gly Pro Glu Gly Gly Glu Ser Ala Asp Asp Val Val Ser
35     40     45
Arg Leu Ala Thr Ala Met Lys Ser Met Glu Ala Glu Tyr Gln Arg Cys
50     55     60
Ala Ile Leu Val Val Ser His Gly Asp Pro Leu Gln Met Leu Gln Asn
65     70     75     80
Val Phe His Ser Ala Lys Gln Gln Glu Gly Asp Gly Leu Ala Glu Lys
85     90     95
Phe Gln Leu Ser Arg Val Ala Ser Val Leu Ser Gln His Arg Lys Phe
100    105    110
Ala Leu Leu Thr Gly Glu Leu Arg Pro Leu Ile
115    120
```

(2) INFORMATION FOR SEQ ID NO:1191:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 122 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..122

(D) OTHER INFORMATION: / Ceres Seq. ID 1499813

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1191:

```
Met Glu Asp Leu Arg Glu Arg Tyr Phe Gly Pro Thr Phe Glu Leu Lys
1      5      10      15
Ser His Asp Lys Tyr Pro Glu Ile Trp Ala Leu Asp Glu Lys Asp Pro
20     25     30
Phe Met Gly Pro Glu Gly Gly Glu Ser Ala Asp Asp Val Val Ser Arg
35     40     45
Leu Ala Thr Ala Met Lys Ser Met Glu Ala Glu Tyr Gln Arg Cys Ala
50     55     60
Ile Leu Val Val Ser His Gly Asp Pro Leu Gln Met Leu Gln Asn Val
65     70     75     80
Phe His Ser Ala Lys Gln Gln Glu Gly Asp Gly Leu Ala Glu Lys Phe
```

85 90 95
Gln Leu Ser Arg Val Ala Ser Val Leu Ser Gln His Arg Lys Phe Ala
100 105 110
Leu Leu Thr Gly Glu Leu Arg Pro Leu Ile
115 120

(2) INFORMATION FOR SEQ ID NO:1192:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 89 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..89
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499814

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1192:

Met Gly Pro Glu Gly Gly Glu Ser Ala Asp Asp Val Val Ser Arg Leu
1 5 10 15
Ala Thr Ala Met Lys Ser Met Glu Ala Glu Tyr Gln Arg Cys Ala Ile
20 25 30
Leu Val Val Ser His Gly Asp Pro Leu Gln Met Leu Gln Asn Val Phe
35 40 45
His Ser Ala Lys Gln Gln Glu Gly Asp Gly Leu Ala Glu Lys Phe Gln
50 55 60
Leu Ser Arg Val Ala Ser Val Leu Ser Gln His Arg Lys Phe Ala Leu
65 70 75 80
Leu Thr Gly Glu Leu Arg Pro Leu Ile
85

(2) INFORMATION FOR SEQ ID NO:1193:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1112 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1112
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499823

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1193:

gagttcttcc ttcggtggaa agagcaaatt ttacttttaa gaaatttgaa aacaaagttt 60
cattaaacag attggtggga ttttaaattt gaattttgat cagtgaatca acgataaacg 120
attcgtcgtt atggaaggag ttggtgcacg gttaggtagg tcctcgacac ggtacggacc 180
ggcaacgggt ttcaccggac cgggtgaggaa gtggaagaag aagtgggtac acgtctctcc 240
ttcctctaag aaagacaata ataatagctc ctccggttcc gccgctgctc ccgccgctgc 300
tgcagcttcc gtcgttaacg gtggttcgaa ttctgacggt agtaatggat cgcatttggt 360
gctgtataag tgggcaccat tgtctcagaa tggtaacggc aatgaagatg gtaaaagtga 420
gagtaattct ccgagcggag atacgggtggc aacgggtggca gaagatcctc cacggcggag 480
attcaaatag gttccgatag cagtacttga ggaacagaag aaggaaatta cagaaattga 540
ggaagatgat aagattgagc aggatgacaa gattgatgag gataataagg ttgagcagga 600
agacaagggt gatgaggaca aaactgtaga ggagtcgagc gagaagaaat cggaagtgga 660
agtggaggaa aagcctgaca tcaatgatgt tccgatggaa gatattcagc aggttgaaga 720
aaaaatagta caggatgatg aagaaaaagt agtgcgacaa gatttgaacg aaagcactgt 780
ggatttagga ctgaacttaa atgcaaacga tgctgatgct gatgcagaaa acgacccgaa 840
agaggacaag ccattagaag aatgataaac tgggtgcatt gttttggttc ctcaccctca 900
actctcaata tgaattagga agaaagacat tacagaaaga acaaagcagt cattagatat 960
ggacgcagat ccttgatttg gtctgtaacc ccatggctta ttccttttga tgttaattga 1020
aatgactcat tgattcagac tgatcattca attcatagga gattcttgtc tttttgtctg 1080
aattttatth tgattcaaca ttcagaacat tt

(2) INFORMATION FOR SEQ ID NO:1194:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 244 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..244
 (D) OTHER INFORMATION: / Ceres Seq. ID 1499824
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1194:

Met	Glu	Gly	Val	Gly	Ala	Arg	Leu	Gly	Arg	Ser	Ser	Thr	Arg	Tyr	Gly
1				5				10						15	
Pro	Ala	Thr	Val	Phe	Thr	Gly	Pro	Val	Arg	Lys	Trp	Lys	Lys	Lys	Trp
			20				25						30		
Val	His	Val	Ser	Pro	Ser	Ser	Lys	Asp	Asn	Asn	Asn	Ser	Ser	Ser	
		35					40				45				
Gly	Ser	Ala	Ala	Ala	Pro	Ala	Ala	Ala	Ala	Ser	Val	Val	Asn	Gly	
	50				55					60					
Gly	Ser	Asn	Ser	Asp	Gly	Ser	Asn	Gly	Ser	His	Leu	Leu	Leu	Tyr	Lys
65					70				75					80	
Trp	Ala	Pro	Leu	Ser	Gln	Asn	Gly	Asn	Gly	Asn	Glu	Asp	Gly	Lys	Ser
			85					90						95	
Glu	Ser	Asn	Ser	Pro	Ser	Glu	Asp	Thr	Val	Ala	Thr	Val	Ala	Glu	Asp
			100					105					110		
Pro	Pro	Arg	Arg	Arg	Phe	Lys	Tyr	Val	Pro	Ile	Ala	Val	Leu	Glu	Glu
			115				120					125			
Gln	Lys	Lys	Glu	Ile	Thr	Glu	Ile	Glu	Glu	Asp	Asp	Lys	Ile	Glu	Gln
	130				135						140				
Asp	Asp	Lys	Ile	Asp	Glu	Asp	Asn	Lys	Val	Glu	Gln	Glu	Asp	Lys	Val
145					150					155					160
Asp	Glu	Asp	Lys	Thr	Val	Glu	Glu	Ser	Ser	Glu	Lys	Lys	Ser	Glu	Val
			165					170						175	
Glu	Val	Glu	Glu	Lys	Pro	Asp	Ile	Asn	Asp	Val	Pro	Met	Glu	Asp	Ile
			180					185					190		
Gln	Gln	Val	Glu	Glu	Lys	Ile	Val	Gln	Asp	Asp	Glu	Glu	Lys	Val	Val
		195					200					205			
Arg	Gln	Asp	Leu	Asn	Glu	Ser	Thr	Val	Asp	Leu	Gly	Leu	Asn	Leu	Asn
	210				215						220				
Ala	Asn	Asp	Ala	Asp	Ala	Asp	Ala	Glu	Asn	Asp	Pro	Lys	Glu	Asp	Lys
225					230					235					240
Pro	Leu	Glu	Glu												

(2) INFORMATION FOR SEQ ID NO:1195:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1851 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
 (A) NAME/KEY: -
 (B) LOCATION: 1..1851
 (D) OTHER INFORMATION: / Ceres Seq. ID 1499825
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1195:

aaaaaaacat	tcaactcgta	actcttctcc	tccatccaat	ttcactttct	ctcactcatt	60
tttattcgtc	gtcgtcgtct	cctctgattt	gttctttttt	ctctaaattc	gcttcgcttc	120
ttctcagttc	tacgaatctt	cgattctctt	tggtttttct	catccccgta	tacgtttaag	180
aacattgcaa	gaaagtgaag	aaaaaaaatg	caggaaggga	ctgatccgta	tggtgagatt	240
gagataagtt	ttggttatca	atgcaataat	aagaagatag	gaatccctga	agataaaatt	300
gctgatggtc	gtgaggttct	tggtgggttt	aggctacaaa	agactagcag	tttctcttgt	360

ttatcaggag	ctgctttaag	tggaaacccc	acttttagcca	atactaatat	ctgcaatgga	420
gtcattggtt	ctgagatatt	gccgtctctg	gatttctccga	aatcttttcag	gaaagttccg	480
tcttcgcctg	cgctttcgaa	gcttgatata	ctctctcctt	ctctccatgg	aagtatggtg	540
agtctaagct	gcagctcgtc	tactagtccg	agtcctcctg	agcctgaatc	ttgttacttg	600
acgtcaatga	gttctccttc	ttctgttaat	gaagggtttc	ttctctctgc	tatggaagtt	660
caagttgcgg	gtggtgctgc	aggggaagat	agagttcaag	ctgtttgctc	tgaggagaat	720
ggttggttgt	tttgcgctat	ctatgatgga	ttcaacggaa	gagatgctgc	tgatttcttg	780
gcatgtactt	ttatgatgct	cattgtgttt	catcttcagt	tgcttgatcg	tcaaataag	840
caaacaaagt	ccgatgatga	tggcgaaaag	ttggaattgt	tatcaaatat	aagtaatgta	900
gattactctt	ccactgattt	gttcaggcaa	ggagtactag	attgcttgaa	ccgtgcgctt	960
tttcaggcgg	aaaccgattt	cctaaggatg	gttgagcaag	aaatggaaga	aagaccggat	1020
ttagtatccg	ttggatcttg	tgttttggtc	actctcctgg	ttgggaagga	tctatacgtc	1080
cttaatcttg	gtgatagcag	agctgttcta	gcgacctaca	atggtaataa	gaagctgcaa	1140
gctgttcagc	tcacagagga	tcatacagtt	gataacgaag	tcgaagaagc	tagactctta	1200
agtgagcadc	ttgatgatcc	taagatcggt	attggtggga	aaatcaaagg	aaagcttaaa	1260
gttactcgtg	ctctcggagt	tggttacttg	aagaaggaga	aactaaatga	tgactcatg	1320
gagatcctcc	gcgttcgtaa	ccttttgagc	ccgccttatg	tttcagtgga	accatcgatg	1380
agagttcaca	agataacgga	atcagatcac	tttgttatag	ttgcaagcga	tggtttgttt	1440
gatttcttca	gcaacgagga	agcgattggg	ctcgtccatt	ccttcgtttc	tagtaatcct	1500
tctggtgatc	cagcaaagtt	tctgcttgaa	cgctctgtag	ctaaagctgc	tgctcgtgct	1560
ggctttacct	tggaagaatt	gacgaatggt	ccggctggta	ggagaaggag	atatcatgac	1620
gatgtgacta	taatggtaat	cactctaggt	accgatcaac	gtacctcaaa	agcttctacg	1680
ttcgtgtgat	tttgatgatg	atggcgacaa	atgttggtt	ggtaaaattg	taattagtct	1740
cactgatctt	cttttagact	ttggaactga	tcatcagttt	ttcaattctt	tgggaactggt	1800
ataatattat	ttcatgtata	gtccgtatat	atatatcatt	gtagtagtct	t	

(2) INFORMATION FOR SEQ ID NO:1196:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 493 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..493

(D) OTHER INFORMATION: / Ceres Seq. ID 1499826

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1196:

Met	Gln	Glu	Gly	Thr	Asp	Pro	Tyr	Gly	Glu	Ile	Glu	Ile	Ser	Phe	Gly
1				5				10						15	
Tyr	Gln	Cys	Asn	Asn	Lys	Lys	Ile	Gly	Ile	Pro	Glu	Asp	Lys	Ile	Ala
			20					25					30		
Asp	Gly	Arg	Glu	Val	Leu	Gly	Gly	Phe	Arg	Leu	Gln	Lys	Thr	Ser	Ser
		35				40					45				
Phe	Ser	Cys	Leu	Ser	Gly	Ala	Ala	Leu	Ser	Gly	Asn	Pro	Thr	Leu	Ala
	50					55					60				
Asn	Thr	Asn	Ile	Cys	Asn	Gly	Val	Ile	Gly	Ser	Glu	Ile	Leu	Pro	Ser
65					70					75				80	
Leu	Asp	Ser	Pro	Lys	Ser	Phe	Arg	Lys	Val	Pro	Ser	Ser	Pro	Ala	Leu
			85						90					95	
Ser	Lys	Leu	Asp	Ile	Leu	Ser	Pro	Ser	Leu	His	Gly	Ser	Met	Val	Ser
		100						105					110		
Leu	Ser	Cys	Ser	Ser	Ser	Thr	Ser	Pro	Ser	Pro	Pro	Glu	Pro	Glu	Ser
		115						120				125			
Cys	Tyr	Leu	Thr	Ser	Met	Ser	Ser	Pro	Ser	Ser	Val	Asn	Glu	Gly	Phe
	130					135					140				
Leu	Leu	Ser	Ala	Met	Glu	Val	Gln	Val	Ala	Gly	Gly	Ala	Ala	Gly	Glu
145					150					155					160
Asp	Arg	Val	Gln	Ala	Val	Cys	Ser	Glu	Glu	Asn	Gly	Trp	Leu	Phe	Cys
			165						170					175	
Ala	Ile	Tyr	Asp	Gly	Phe	Asn	Gly	Arg	Asp	Ala	Ala	Asp	Phe	Leu	Ala
		180						185						190	

Cys Thr Leu Tyr Glu Ser Ile Val Phe His Leu Gln Leu Leu Asp Arg
195 200 205
Gln Met Lys Gln Thr Lys Ser Asp Asp Asp Gly Glu Lys Leu Glu Leu
210 215 220
Leu Ser Asn Ile Ser Asn Val Asp Tyr Ser Ser Thr Asp Leu Phe Arg
225 230 235 240
Gln Gly Val Leu Asp Cys Leu Asn Arg Ala Leu Phe Gln Ala Glu Thr
245 250 255
Asp Phe Leu Arg Met Val Glu Gln Glu Met Glu Glu Arg Pro Asp Leu
260 265 270
Val Ser Val Gly Ser Cys Val Leu Val Thr Leu Leu Val Gly Lys Asp
275 280 285
Leu Tyr Val Leu Asn Leu Gly Asp Ser Arg Ala Val Leu Ala Thr Tyr
290 295 300
Asn Gly Asn Lys Lys Leu Gln Ala Val Gln Leu Thr Glu Asp His Thr
305 310 315 320
Val Asp Asn Glu Val Glu Glu Ala Arg Leu Leu Ser Glu His Leu Asp
325 330 335
Asp Pro Lys Ile Val Ile Gly Gly Lys Ile Lys Gly Lys Leu Lys Val
340 345 350
Thr Arg Ala Leu Gly Val Gly Tyr Leu Lys Lys Glu Lys Leu Asn Asp
355 360 365
Ala Leu Met Glu Ile Leu Arg Val Arg Asn Leu Leu Ser Pro Pro Tyr
370 375 380
Val Ser Val Glu Pro Ser Met Arg Val His Lys Ile Thr Glu Ser Asp
385 390 395 400
His Phe Val Ile Val Ala Ser Asp Gly Leu Phe Asp Phe Phe Ser Asn
405 410 415
Glu Glu Ala Ile Gly Leu Val His Ser Phe Val Ser Ser Asn Pro Ser
420 425 430
Gly Asp Pro Ala Lys Phe Leu Leu Glu Arg Leu Val Ala Lys Ala Ala
435 440 445
Ala Arg Ala Gly Phe Thr Leu Glu Glu Leu Thr Asn Val Pro Ala Gly
450 455 460
Arg Arg Arg Arg Tyr His Asp Asp Val Thr Ile Met Val Ile Thr Leu
465 470 475 480
Gly Thr Asp Gln Arg Thr Ser Lys Ala Ser Thr Phe Val
485 490

(2) INFORMATION FOR SEQ ID NO:1197:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 384 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..384

(D) OTHER INFORMATION: / Ceres Seq. ID 1499827

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1197:

Met Val Ser Leu Ser Cys Ser Ser Ser Thr Ser Pro Ser Pro Pro Glu
1 5 10 15
Pro Glu Ser Cys Tyr Leu Thr Ser Met Ser Ser Pro Ser Ser Val Asn
20 25 30
Glu Gly Phe Leu Leu Ser Ala Met Glu Val Gln Val Ala Gly Gly Ala
35 40 45
Ala Gly Glu Asp Arg Val Gln Ala Val Cys Ser Glu Glu Asn Gly Trp
50 55 60
Leu Phe Cys Ala Ile Tyr Asp Gly Phe Asn Gly Arg Asp Ala Ala Asp
65 70 75 80
Phe Leu Ala Cys Thr Leu Tyr Glu Ser Ile Val Phe His Leu Gln Leu

			85					90					95		
Leu	Asp	Arg	Gln	Met	Lys	Gln	Thr	Lys	Ser	Asp	Asp	Asp	Gly	Glu	Lys
			100					105					110		
Leu	Glu	Leu	Leu	Ser	Asn	Ile	Ser	Asn	Val	Asp	Tyr	Ser	Ser	Thr	Asp
			115				120					125			
Leu	Phe	Arg	Gln	Gly	Val	Leu	Asp	Cys	Leu	Asn	Arg	Ala	Leu	Phe	Gln
			130				135				140				
Ala	Glu	Thr	Asp	Phe	Leu	Arg	Met	Val	Glu	Gln	Glu	Met	Glu	Glu	Arg
			145			150				155					160
Pro	Asp	Leu	Val	Ser	Val	Gly	Ser	Cys	Val	Leu	Val	Thr	Leu	Leu	Val
			165					170					175		
Gly	Lys	Asp	Leu	Tyr	Val	Leu	Asn	Leu	Gly	Asp	Ser	Arg	Ala	Val	Leu
			180					185					190		
Ala	Thr	Tyr	Asn	Gly	Asn	Lys	Lys	Leu	Gln	Ala	Val	Gln	Leu	Thr	Glu
			195				200					205			
Asp	His	Thr	Val	Asp	Asn	Glu	Val	Glu	Glu	Ala	Arg	Leu	Leu	Ser	Glu
			210				215				220				
His	Leu	Asp	Asp	Pro	Lys	Ile	Val	Ile	Gly	Gly	Lys	Ile	Lys	Gly	Lys
			225			230				235					240
Leu	Lys	Val	Thr	Arg	Ala	Leu	Gly	Val	Gly	Tyr	Leu	Lys	Lys	Glu	Lys
			245					250						255	
Leu	Asn	Asp	Ala	Leu	Met	Glu	Ile	Leu	Arg	Val	Arg	Asn	Leu	Leu	Ser
			260					265					270		
Pro	Pro	Tyr	Val	Ser	Val	Glu	Pro	Ser	Met	Arg	Val	His	Lys	Ile	Thr
			275				280					285			
Glu	Ser	Asp	His	Phe	Val	Ile	Val	Ala	Ser	Asp	Gly	Leu	Phe	Asp	Phe
			290				295				300				
Phe	Ser	Asn	Glu	Glu	Ala	Ile	Gly	Leu	Val	His	Ser	Phe	Val	Ser	Ser
			305			310				315					320
Asn	Pro	Ser	Gly	Asp	Pro	Ala	Lys	Phe	Leu	Glu	Arg	Leu	Val	Ala	
			325					330					335		
Lys	Ala	Ala	Ala	Arg	Ala	Gly	Phe	Thr	Leu	Glu	Glu	Leu	Thr	Asn	Val
			340					345					350		
Pro	Ala	Gly	Arg	Arg	Arg	Arg	Tyr	His	Asp	Asp	Val	Thr	Ile	Met	Val
			355				360					365			
Ile	Thr	Leu	Gly	Thr	Asp	Gln	Arg	Thr	Ser	Lys	Ala	Ser	Thr	Phe	Val
			370			375					380				

(2) INFORMATION FOR SEQ ID NO:1198:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 360 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..360

(D) OTHER INFORMATION: / Ceres Seq. ID 1499828

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1198:

Met	Ser	Ser	Pro	Ser	Ser	Val	Asn	Glu	Gly	Phe	Leu	Leu	Ser	Ala	Met
1			5						10					15	
Glu	Val	Gln	Val	Ala	Gly	Gly	Ala	Ala	Gly	Glu	Asp	Arg	Val	Gln	Ala
			20					25					30		
Val	Cys	Ser	Glu	Glu	Asn	Gly	Trp	Leu	Phe	Cys	Ala	Ile	Tyr	Asp	Gly
			35				40					45			
Phe	Asn	Gly	Arg	Asp	Ala	Ala	Asp	Phe	Leu	Ala	Cys	Thr	Leu	Tyr	Glu
			50			55				60					
Ser	Ile	Val	Phe	His	Leu	Gln	Leu	Leu	Asp	Arg	Gln	Met	Lys	Gln	Thr
			65			70				75				80	

Lys Ser Asp Asp Asp Gly Glu Lys Leu Glu Leu Leu Ser Asn Ile Ser
85 90 95
Asn Val Asp Tyr Ser Ser Thr Asp Leu Phe Arg Gln Gly Val Leu Asp
100 105 110
Cys Leu Asn Arg Ala Leu Phe Gln Ala Glu Thr Asp Phe Leu Arg Met
115 120 125
Val Glu Gln Glu Met Glu Glu Arg Pro Asp Leu Val Ser Val Gly Ser
130 135 140
Cys Val Leu Val Thr Leu Leu Val Gly Lys Asp Leu Tyr Val Leu Asn
145 150 155 160
Leu Gly Asp Ser Arg Ala Val Leu Ala Thr Tyr Asn Gly Asn Lys Lys
165 170 175
Leu Gln Ala Val Gln Leu Thr Glu Asp His Thr Val Asp Asn Glu Val
180 185 190
Glu Glu Ala Arg Leu Leu Ser Glu His Leu Asp Asp Pro Lys Ile Val
195 200 205
Ile Gly Gly Lys Ile Lys Gly Lys Leu Lys Val Thr Arg Ala Leu Gly
210 215 220
Val Gly Tyr Leu Lys Lys Glu Lys Leu Asn Asp Ala Leu Met Glu Ile
225 230 235 240
Leu Arg Val Arg Asn Leu Leu Ser Pro Pro Tyr Val Ser Val Glu Pro
245 250 255
Ser Met Arg Val His Lys Ile Thr Glu Ser Asp His Phe Val Ile Val
260 265 270
Ala Ser Asp Gly Leu Phe Asp Phe Phe Ser Asn Glu Glu Ala Ile Gly
275 280 285
Leu Val His Ser Phe Val Ser Ser Asn Pro Ser Gly Asp Pro Ala Lys
290 295 300
Phe Leu Leu Glu Arg Leu Val Ala Lys Ala Ala Arg Ala Gly Phe
305 310 315 320
Thr Leu Glu Glu Leu Thr Asn Val Pro Ala Gly Arg Arg Arg Arg Tyr
325 330 335
His Asp Asp Val Thr Ile Met Val Ile Thr Leu Gly Thr Asp Gln Arg
340 345 350
Thr Ser Lys Ala Ser Thr Phe Val
355 360

(2) INFORMATION FOR SEQ ID NO:1199:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1810 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1810
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499829

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1199:

atacctacaa	gacgacgagt	gttcccattt	ccttggtcta	tttcaagaca	tggactcttc	60
tccttctgct	ttcggattag	aagggtttta	tagcaacgac	aataatacta	atcaaaagaa	120
acgccaaga	aaagacgacg	aaggcggttg	tggtggcggc	ggaggaacag	aagttctagg	180
agctgttaat	ggtaataata	aggctgcttt	tggagatata	ctcgcgacgc	ttttgttggt	240
agacgaggaa	gctaaacagc	aacaagaaca	gtgggatttt	gaatctatta	aagagaagtc	300
tttacttgaa	gctaatacata	agaagaaagt	gaaaacaatg	gatgggttatt	acaatcaaatt	360
gcaagatcat	tactctgcag	ctggtgaaac	cgatgggttcg	cgttcaaaac	gcgcacggaa	420
aaccgcggtt	gcggctgtgg	tttccgcggt	agcttccggg	gcggacacaa	ccggttttagc	480
tgctccgggt	ccgaccgcgg	atatoctag	cggttccggg	tcaggaccga	gtcataggag	540
gttatgggtt	aaagaacgaa	ccacggactg	gtgggacaga	gtaagccggc	ctgattttcc	600
agaagacgag	tttcggcgag	agttccgtat	gagcaaatcg	acgtttaacc	taatatgcga	660
ggagctagat	acgacggtga	cgaagaaaaa	cacgatgtta	agagacgcga	ttccagctcc	720
aaaacgcgta	ggcgtttgcg	tttggcgttt	ggcgacagga	gctccgcttc	gccacgtgtc	780

ggagcgtttc	ggtctgggaa	tctcaacttg	ccacaaacta	gtcatcgaag	tctgccgcgc	840
gatctacgac	gttctcatgc	ccaagtatct	cctctggccg	tcggattcag	agataaactc	900
aacgaaagcc	aaattcgaat	cgggtccaca	aataccaaac	gtcgtcggat	caatctacac	960
cacacatatt	ccgatcatcg	ctccgaaagt	ccacgtggcg	gcgtatttta	acaagagaca	1020
cacggagagg	aatcagaaga	cgctgtactc	gataacagta	caaggagtgg	tcaacgccga	1080
cgggatcttc	accgacgttt	gtatcggaaa	cccaggatct	ctcaccgacg	atcagatcct	1140
ggagaaatct	tcgctttcac	ggcaaagagc	ggcgcgtggg	atgttacgtg	acagctggat	1200
agttggaac	tctgggtttc	cgttgactga	ttatcttctt	gtaccgtaca	cgagacagaa	1260
tctgacgtgg	agcagcacg	cgtttaacga	gagtatcgga	gagattcagg	ggattgcgac	1320
ggctgcgttt	gagaggctca	aaggacggtg	ggcttggttg	cagaaacgga	cggaggtgaa	1380
gcttcaggat	ctgccgtacg	tgcttgagac	ttgttggttg	ttgcataaca	tttgtgagat	1440
gaggaaggag	gagatgttgc	cggagttgaa	gtttgaggtt	tttgatgatg	tggcggtgcc	1500
ggagaataat	atccgatctg	ctagtgcggt	taatacgagg	gatcatatct	ctcacaatct	1560
cttgcacgtg	ggacttgccg	ggacaagaac	tctataggct	ctgtttttca	cctttttctta	1620
ttttgaaact	gattttttat	tgcaaattct	ttttccaaat	taggaataaa	aacatttttag	1680
ggattgggtg	gatacagaaa	gaatagttga	attgagagta	gaagtggctg	atgatattgt	1740
ttgtgttact	tattagcatt	gtgtaatctt	tagttcatgt	attttctata	caaattgaat	1800
ctgaaacctt						

(2) INFORMATION FOR SEQ ID NO:1200:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 531 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..531

(D) OTHER INFORMATION: / Ceres Seq. ID 1499830

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1200:

Tyr	Leu	Gln	Asp	Asp	Glu	Cys	Ser	His	Phe	Leu	Gly	Leu	Phe	Gln	Asp
1				5					10					15	
Met	Asp	Ser	Ser	Pro	Ser	Ala	Phe	Gly	Leu	Glu	Gly	Phe	Asn	Ser	Asn
			20					25					30		
Asp	Asn	Asn	Thr	Asn	Gln	Lys	Lys	Arg	Pro	Arg	Lys	Asp	Asp	Glu	Gly
		35					40					45			
Gly	Gly	Gly	Gly	Gly	Gly	Gly	Thr	Glu	Val	Leu	Gly	Ala	Val	Asn	Gly
	50					55					60				
Asn	Asn	Lys	Ala	Ala	Phe	Gly	Asp	Ile	Leu	Ala	Thr	Leu	Leu	Leu	Leu
65					70				75					80	
Asp	Glu	Glu	Ala	Lys	Gln	Gln	Gln	Glu	Gln	Trp	Asp	Phe	Glu	Ser	Ile
			85					90					95		
Lys	Glu	Lys	Ser	Leu	Leu	Glu	Ala	Asn	His	Lys	Lys	Lys	Val	Lys	Thr
		100						105					110		
Met	Asp	Gly	Tyr	Tyr	Asn	Gln	Met	Gln	Asp	His	Tyr	Ser	Ala	Ala	Gly
		115				120						125			
Glu	Thr	Asp	Gly	Ser	Arg	Ser	Lys	Arg	Ala	Arg	Lys	Thr	Ala	Val	Ala
	130					135					140				
Ala	Val	Val	Ser	Ala	Val	Ala	Ser	Gly	Ala	Asp	Thr	Thr	Gly	Leu	Ala
145					150					155				160	
Ala	Pro	Val	Pro	Thr	Ala	Asp	Ile	Ala	Ser	Gly	Ser	Gly	Ser	Gly	Pro
			165					170					175		
Ser	His	Arg	Arg	Leu	Trp	Val	Lys	Glu	Arg	Thr	Thr	Asp	Trp	Trp	Asp
		180						185				190			
Arg	Val	Ser	Arg	Pro	Asp	Phe	Pro	Glu	Asp	Glu	Phe	Arg	Arg	Glu	Phe
	195					200					205				
Arg	Met	Ser	Lys	Ser	Thr	Phe	Asn	Leu	Ile	Cys	Glu	Glu	Leu	Asp	Thr
	210					215					220				
Thr	Val	Thr	Lys	Lys	Asn	Thr	Met	Leu	Arg	Asp	Ala	Ile	Pro	Ala	Pro
225					230					235				240	
Lys	Arg	Val	Gly	Val	Cys	Val	Trp	Arg	Leu	Ala	Thr	Gly	Ala	Pro	Leu

				245				250					255		
Arg	His	Val	Ser	Glu	Arg	Phe	Gly	Leu	Gly	Ile	Ser	Thr	Cys	His	Lys
			260					265					270		
Leu	Val	Ile	Glu	Val	Cys	Arg	Ala	Ile	Tyr	Asp	Val	Leu	Met	Pro	Lys
		275					280					285			
Tyr	Leu	Leu	Trp	Pro	Ser	Asp	Ser	Glu	Ile	Asn	Ser	Thr	Lys	Ala	Lys
	290					295					300				
Phe	Glu	Ser	Val	His	Lys	Ile	Pro	Asn	Val	Val	Gly	Ser	Ile	Tyr	Thr
305					310					315					320
Thr	His	Ile	Pro	Ile	Ile	Ala	Pro	Lys	Val	His	Val	Ala	Ala	Tyr	Phe
				325					330					335	
Asn	Lys	Arg	His	Thr	Glu	Arg	Asn	Gln	Lys	Thr	Ser	Tyr	Ser	Ile	Thr
			340				345					350			
Val	Gln	Gly	Val	Val	Asn	Ala	Asp	Gly	Ile	Phe	Thr	Asp	Val	Cys	Ile
		355				360					365				
Gly	Asn	Pro	Gly	Ser	Leu	Thr	Asp	Asp	Gln	Ile	Leu	Glu	Lys	Ser	Ser
	370					375					380				
Leu	Ser	Arg	Gln	Arg	Ala	Ala	Arg	Gly	Met	Leu	Arg	Asp	Ser	Trp	Ile
385					390					395					400
Val	Gly	Asn	Ser	Gly	Phe	Pro	Leu	Thr	Asp	Tyr	Leu	Leu	Val	Pro	Tyr
				405					410					415	
Thr	Arg	Gln	Asn	Leu	Thr	Trp	Thr	Gln	His	Ala	Phe	Asn	Glu	Ser	Ile
			420					425					430		
Gly	Glu	Ile	Gln	Gly	Ile	Ala	Thr	Ala	Ala	Phe	Glu	Arg	Leu	Lys	Gly
		435				440					445				
Arg	Trp	Ala	Cys	Leu	Gln	Lys	Arg	Thr	Glu	Val	Lys	Leu	Gln	Asp	Leu
	450					455					460				
Pro	Tyr	Val	Leu	Gly	Ala	Cys	Cys	Val	Leu	His	Asn	Ile	Cys	Glu	Met
465					470					475					480
Arg	Lys	Glu	Glu	Met	Leu	Pro	Glu	Leu	Lys	Phe	Glu	Val	Phe	Asp	Asp
				485					490					495	
Val	Ala	Val	Pro	Glu	Asn	Asn	Ile	Arg	Ser	Ala	Ser	Ala	Val	Asn	Thr
			500					505					510		
Arg	Asp	His	Ile	Ser	His	Asn	Leu	Leu	His	Arg	Gly	Leu	Ala	Gly	Thr
		515					520					525			
Arg	Thr	Leu													
		530													

(2) INFORMATION FOR SEQ ID NO:1201:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 515 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..515
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499831

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1201:

Met	Asp	Ser	Ser	Pro	Ser	Ala	Phe	Gly	Leu	Glu	Gly	Phe	Asn	Ser	Asn
1				5				10					15		
Asp	Asn	Asn	Thr	Asn	Gln	Lys	Lys	Arg	Pro	Arg	Lys	Asp	Asp	Glu	Gly
			20					25				30			
Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Thr	Glu	Val	Leu	Gly	Ala	Val	Asn
			35				40					45			
Asn	Asn	Lys	Ala	Ala	Phe	Gly	Asp	Ile	Leu	Ala	Thr	Leu	Leu	Leu	Leu
			50			55					60				
Asp	Glu	Glu	Ala	Lys	Gln	Gln	Gln	Glu	Gln	Trp	Asp	Phe	Glu	Ser	Ile
65				70				75						80	
Lys	Glu	Lys	Ser	Leu	Leu	Glu	Ala	Asn	His	Lys	Lys	Lys	Val	Lys	Thr
				85				90						95	

Met	Asp	Gly	Tyr	Tyr	Asn	Gln	Met	Gln	Asp	His	Tyr	Ser	Ala	Ala	Gly			
			100					105					110					
Glu	Thr	Asp	Gly	Ser	Arg	Ser	Lys	Arg	Ala	Arg	Lys	Thr	Ala	Val	Ala			
		115					120					125						
Ala	Val	Val	Ser	Ala	Val	Ala	Ser	Gly	Ala	Asp	Thr	Thr	Gly	Leu	Ala			
		130				135					140							
Ala	Pro	Val	Pro	Thr	Ala	Asp	Ile	Ala	Ser	Gly	Ser	Gly	Ser	Gly	Pro			
145					150					155					160			
Ser	His	Arg	Arg	Leu	Trp	Val	Lys	Glu	Arg	Thr	Thr	Asp	Trp	Trp	Asp			
			165					170					175					
Arg	Val	Ser	Arg	Pro	Asp	Phe	Pro	Glu	Asp	Glu	Phe	Arg	Arg	Glu	Phe			
			180					185				190						
Arg	Met	Ser	Lys	Ser	Thr	Phe	Asn	Leu	Ile	Cys	Glu	Glu	Leu	Asp	Thr			
		195					200					205						
Thr	Val	Thr	Lys	Lys	Asn	Thr	Met	Leu	Arg	Asp	Ala	Ile	Pro	Ala	Pro			
		210				215					220							
Lys	Arg	Val	Gly	Val	Cys	Val	Trp	Arg	Leu	Ala	Thr	Gly	Ala	Pro	Leu			
225					230					235					240			
Arg	His	Val	Ser	Glu	Arg	Phe	Gly	Leu	Gly	Ile	Ser	Thr	Cys	His	Lys			
			245					250						255				
Leu	Val	Ile	Glu	Val	Cys	Arg	Ala	Ile	Tyr	Asp	Val	Leu	Met	Pro	Lys			
		260						265					270					
Tyr	Leu	Leu	Trp	Pro	Ser	Asp	Ser	Glu	Ile	Asn	Ser	Thr	Lys	Ala	Lys			
		275				280						285						
Phe	Glu	Ser	Val	His	Lys	Ile	Pro	Asn	Val	Val	Gly	Ser	Ile	Tyr	Thr			
		290				295					300							
Thr	His	Ile	Pro	Ile	Ile	Ala	Pro	Lys	Val	His	Val	Ala	Ala	Tyr	Phe			
305					310					315					320			
Asn	Lys	Arg	His	Thr	Glu	Arg	Asn	Gln	Lys	Thr	Ser	Tyr	Ser	Ile	Thr			
			325					330						335				
Val	Gln	Gly	Val	Val	Asn	Ala	Asp	Gly	Ile	Phe	Thr	Asp	Val	Cys	Ile			
		340						345					350					
Gly	Asn	Pro	Gly	Ser	Leu	Thr	Asp	Asp	Gln	Ile	Leu	Glu	Lys	Ser	Ser			
		355					360					365						
Leu	Ser	Arg	Gln	Arg	Ala	Ala	Arg	Gly	Met	Leu	Arg	Asp	Ser	Trp	Ile			
		370				375					380							
Val	Gly	Asn	Ser	Gly	Phe	Pro	Leu	Thr	Asp	Tyr	Leu	Leu	Val	Pro	Tyr			
385					390					395					400			
Thr	Arg	Gln	Asn	Leu	Thr	Trp	Thr	Gln	His	Ala	Phe	Asn	Glu	Ser	Ile			
			405					410					415					
Gly	Glu	Ile	Gln	Gly	Ile	Ala	Thr	Ala	Ala	Phe	Glu	Arg	Leu	Lys	Gly			
		420				425							430					
Arg	Trp	Ala	Cys	Leu	Gln	Lys	Arg	Thr	Glu	Val	Lys	Leu	Gln	Asp	Leu			
		435				440						445						
Pro	Tyr	Val	Leu	Gly	Ala	Cys	Cys	Val	Leu	His	Asn	Ile	Cys	Glu	Met			
		450				455					460							
Arg	Lys	Glu	Glu	Met	Leu	Pro	Glu	Leu	Lys	Phe	Glu	Val	Phe	Asp	Asp			
465					470					475					480			
Val	Ala	Val	Pro	Glu	Asn	Asn	Ile	Arg	Ser	Ala	Ser	Ala	Val	Asn	Thr			
			485					490						495				
Arg	Asp	His	Ile	Ser	His	Asn	Leu	Leu	His	Arg	Gly	Leu	Ala	Gly	Thr			
		500					505						510					
Arg	Thr	Leu																
		515																

(2) INFORMATION FOR SEQ ID NO:1202:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 419 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..419

(D) OTHER INFORMATION: / Ceres Seq. ID 1499832

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1202:

Met	Asp	Gly	Tyr	Tyr	Asn	Gln	Met	Gln	Asp	His	Tyr	Ser	Ala	Ala	Gly	
1				5				10						15		
Glu	Thr	Asp	Gly	Ser	Arg	Ser	Lys	Arg	Ala	Arg	Lys	Thr	Ala	Val	Ala	
		20						25					30			
Ala	Val	Val	Ser	Ala	Val	Ala	Ser	Gly	Ala	Asp	Thr	Thr	Gly	Leu	Ala	
		35					40					45				
Ala	Pro	Val	Pro	Thr	Ala	Asp	Ile	Ala	Ser	Gly	Ser	Gly	Ser	Gly	Pro	
	50					55					60					
Ser	His	Arg	Arg	Leu	Trp	Val	Lys	Glu	Arg	Thr	Thr	Asp	Trp	Trp	Asp	
65					70					75					80	
Arg	Val	Ser	Arg	Pro	Asp	Phe	Pro	Glu	Asp	Glu	Phe	Arg	Arg	Glu	Phe	
				85					90					95		
Arg	Met	Ser	Lys	Ser	Thr	Phe	Asn	Leu	Ile	Cys	Glu	Glu	Leu	Asp	Thr	
			100					105					110			
Thr	Val	Thr	Lys	Lys	Asn	Thr	Met	Leu	Arg	Asp	Ala	Ile	Pro	Ala	Pro	
		115					120					125				
Lys	Arg	Val	Gly	Val	Cys	Val	Trp	Arg	Leu	Ala	Thr	Gly	Ala	Pro	Leu	
	130					135						140				
Arg	His	Val	Ser	Glu	Arg	Phe	Gly	Leu	Gly	Ile	Ser	Thr	Cys	His	Lys	
145					150					155					160	
Leu	Val	Ile	Glu	Val	Cys	Arg	Ala	Ile	Tyr	Asp	Val	Leu	Met	Pro	Lys	
				165					170					175		
Tyr	Leu	Leu	Trp	Pro	Ser	Asp	Ser	Glu	Ile	Asn	Ser	Thr	Lys	Ala	Lys	
			180					185					190			
Phe	Glu	Ser	Val	His	Lys	Ile	Pro	Asn	Val	Val	Gly	Ser	Ile	Tyr	Thr	
		195					200					205				
Thr	His	Ile	Pro	Ile	Ile	Ala	Pro	Lys	Val	His	Val	Ala	Ala	Tyr	Phe	
	210					215					220					
Asn	Lys	Arg	His	Thr	Glu	Arg	Asn	Gln	Lys	Thr	Ser	Tyr	Ser	Ile	Thr	
225					230					235					240	
Val	Gln	Gly	Val	Val	Asn	Ala	Asp	Gly	Ile	Phe	Thr	Asp	Val	Cys	Ile	
				245					250					255		
Gly	Asn	Pro	Gly	Ser	Leu	Thr	Asp	Asp	Gln	Ile	Leu	Glu	Lys	Ser	Ser	
		260						265					270			
Leu	Ser	Arg	Gln	Arg	Ala	Ala	Arg	Gly	Met	Leu	Arg	Asp	Ser	Trp	Ile	
		275					280					285				
Val	Gly	Asn	Ser	Gly	Phe	Pro	Leu	Thr	Asp	Tyr	Leu	Leu	Val	Pro	Tyr	
	290					295					300					
Thr	Arg	Gln	Asn	Leu	Thr	Trp	Thr	Gln	His	Ala	Phe	Asn	Glu	Ser	Ile	
305				310					315						320	
Gly	Glu	Ile	Gln	Gly	Ile	Ala	Thr	Ala	Ala	Phe	Glu	Arg	Leu	Lys	Gly	
			325					330						335		
Arg	Trp	Ala	Cys	Leu	Gln	Lys	Arg	Thr	Glu	Val	Lys	Leu	Gln	Asp	Leu	
		340						345					350			
Pro	Tyr	Val	Leu	Gly	Ala	Cys	Cys	Val	Leu	His	Asn	Ile	Cys	Glu	Met	
		355					360					365				
Arg	Lys	Glu	Glu	Met	Leu	Pro	Glu	Leu	Lys	Phe	Glu	Val	Phe	Asp	Asp	
	370					375					380					
Val	Ala	Val	Pro	Glu	Asn	Asn	Ile	Arg	Ser	Ala	Ser	Ala	Val	Asn	Thr	
385					390					395					400	
Arg	Asp	His	Ile	Ser	His	Asn	Leu	Leu	His	Arg	Gly	Leu	Ala	Gly	Thr	
				405					410					415		
Arg	Thr	Leu														

(2) INFORMATION FOR SEQ ID NO:1203:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1540 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
(A) NAME/KEY: -
(B) LOCATION: 1..1540
(D) OTHER INFORMATION: / Ceres Seq. ID 1499833
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1203:

```
aaaaaatctg aaattctcag gcgagattcc ggaagcaaaa cattcctaaa tttcgccaag      60
tgatccgcca tgggagaaga gaagtctctg cttcagttcc gtagttttcc ttcactcaag     120
acctctgatt tcgctctcac cgaagaacct tcatggaggc tggagaacaa cgtgtcgtcg     180
aatcgccgga gaggaacaa gagaaagcgt ggcgttttta ccaattttgc gtccctttcc     240
gtagcgatta ggagagatcg gagakaatct acatttaacg gtcgtaatgg cggcgagggc     300
cgagcgttcg cgtcggtttc ggtggtgatt ccgaagggaag aggatgaatt cgcgcctacc     360
tcggcccagc tgttgaaaaa ccccatgtgt ttactgtcga tagtaccgaa agacgccgca     420
ctattcttcg ccggagcgtt cgcgggagcc gccgcaaagt cagtgcggc accgcttgac     480
cgaataaagc tcctaattgca gacacatggt gttcgagctg ggcaacaaag tgctaagaag     540
gctattgggt tcattgaggc cattactctt atcggaaaag aagaaggat taaaggttat     600
tggaaggaa atctacctca ggtgataagg attgtacctt atagcgcagt ccagttgttt     660
gcatatgaaa catacaagaa actcttcagc gggaaagacg gtcaattgtc agtcctcgga     720
aggctcggtg ctggtgcttg tgctggcatg acgtctactc tgattacata ccctttagat     780
gtgctgagat tgaggttagc tgttgaaacca ggttatcgaa ccatgtccca ggttgacctg     840
aacatgctgc gggaggaagg agttgcatca ttctacaacg gtctaggtcc ttcgctttta     900
agtatagctc cttacattgc catcaacttc tgcgtctttg atctggtaaa gaaatctctg     960
ccagagaagt atcaacaaaa gacacaatca tctttgttaa cagcagtagt agctgctgct    1020
attgctaccg gtacttgcta tccattggat accattagaa gacagatgca attgaagggt    1080
actccatata aatcgggtatt agacgctttc tcaggatatca ttgcgcgtga aggagttgtt    1140
ggcttgctacc ttggctttgt ccccaatgca ctcaaaagca tgccaaacag cagtattaag    1200
cttacaacat tcgacatcgt caagaaactc atagcagcga gtgagaagga gatccaaaga    1260
atcgcggatg ataaccgcaa gaaagcaagt cctaacacaa ccgatgaaca aacctgaaga    1320
cgcaattttg gatttccaca aggtcatttt tgcccgttat cttatgacct ttgtttgtgt    1380
gttttgtaat ttggaatgta ataagttgta tgttctcctc ataattcaaa atgtgcttga    1440
attgaatcct gaagccagag agggtaataa atggctgttt gtgttacgtt tggtcgcgct    1500
ggttttgtat aaaccgaatt taaccgggtt gctacactcg
```

(2) INFORMATION FOR SEQ ID NO:1204:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 415 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..415
(D) OTHER INFORMATION: / Ceres Seq. ID 1499834
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1204:

```
Met Gly Glu Glu Lys Ser Leu Leu Gln Phe Arg Ser Phe Pro Ser Leu
1          5          10          15
Lys Thr Ser Asp Phe Ala Leu Thr Glu Glu Pro Ser Trp Arg Leu Glu
20          25          30
Asn Asn Val Ser Ser Asn Arg Arg Arg Gly Asn Lys Arg Ser Gly Gly
35          40          45
Val Phe Thr Asn Phe Ala Ser Leu Ser Val Ala Ile Arg Arg Asp Arg
50          55          60
Arg Xaa Ser Thr Phe Asn Gly Arg Asn Gly Gly Gly Gly Ala Phe
65          70          75          80
Ala Ser Val Ser Val Val Ile Pro Lys Glu Glu Asp Glu Phe Ala Pro
85          90          95
Thr Ser Ala Gln Leu Leu Lys Asn Pro Ile Ala Leu Leu Ser Ile Val
```

100	105	110
Pro Lys Asp Ala Ala Leu Phe Phe Ala Gly Ala Phe Ala Gly Ala Ala		
115	120	125
Ala Lys Ser Val Thr Ala Pro Leu Asp Arg Ile Lys Leu Leu Met Gln		
130	135	140
Thr His Gly Val Arg Ala Gly Gln Gln Ser Ala Lys Lys Ala Ile Gly		
145	150	155
Phe Ile Glu Ala Ile Thr Leu Ile Gly Lys Glu Glu Gly Ile Lys Gly		
165	170	175
Tyr Trp Lys Gly Asn Leu Pro Gln Val Ile Arg Ile Val Pro Tyr Ser		
180	185	190
Ala Val Gln Leu Phe Ala Tyr Glu Thr Tyr Lys Lys Leu Phe Arg Gly		
195	200	205
Lys Asp Gly Gln Leu Ser Val Leu Gly Arg Leu Gly Ala Gly Ala Cys		
210	215	220
Ala Gly Met Thr Ser Thr Leu Ile Thr Tyr Pro Leu Asp Val Leu Arg		
225	230	235
Leu Arg Leu Ala Val Glu Pro Gly Tyr Arg Thr Met Ser Gln Val Ala		
245	250	255
Leu Asn Met Leu Arg Glu Glu Gly Val Ala Ser Phe Tyr Asn Gly Leu		
260	265	270
Gly Pro Ser Leu Leu Ser Ile Ala Pro Tyr Ile Ala Ile Asn Phe Cys		
275	280	285
Val Phe Asp Leu Val Lys Lys Ser Leu Pro Glu Lys Tyr Gln Gln Lys		
290	295	300
Thr Gln Ser Ser Leu Leu Thr Ala Val Val Ala Ala Ala Ile Ala Thr		
305	310	315
Gly Thr Cys Tyr Pro Leu Asp Thr Ile Arg Arg Gln Met Gln Leu Lys		
325	330	335
Gly Thr Pro Tyr Lys Ser Val Leu Asp Ala Phe Ser Gly Ile Ile Ala		
340	345	350
Arg Glu Gly Val Val Gly Leu Tyr Arg Gly Phe Val Pro Asn Ala Leu		
355	360	365
Lys Ser Met Pro Asn Ser Ser Ile Lys Leu Thr Thr Phe Asp Ile Val		
370	375	380
Lys Lys Leu Ile Ala Ala Ser Glu Lys Glu Ile Gln Arg Ile Ala Asp		
385	390	395
Asp Asn Arg Lys Lys Ala Ser Pro Asn Thr Thr Asp Glu Gln Thr		
405	410	415

(2) INFORMATION FOR SEQ ID NO:1205:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 273 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..273

(D) OTHER INFORMATION: / Ceres Seq. ID 1499835

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1205:

Met	Gln	Thr	His	Gly	Val	Arg	Ala	Gly	Gln	Ser	Ala	Lys	Lys	Ala
1				5				10					15	
Ile	Gly	Phe	Ile	Glu	Ala	Ile	Thr	Leu	Ile	Gly	Lys	Glu	Glu	Gly
			20					25					30	
Lys	Gly	Tyr	Trp	Lys	Gly	Asn	Leu	Pro	Gln	Val	Ile	Arg	Ile	Val
			35				40					45		
Tyr	Ser	Ala	Val	Gln	Leu	Phe	Ala	Tyr	Glu	Thr	Tyr	Lys	Lys	Leu
			50				55				60			
Arg	Gly	Lys	Asp	Gly	Gln	Leu	Ser	Val	Leu	Gly	Arg	Leu	Gly	Ala
65					70					75				80

Ala Cys Ala Gly Met Thr Ser Thr Leu Ile Thr Tyr Pro Leu Asp Val
85 90 95
Leu Arg Leu Arg Leu Ala Val Glu Pro Gly Tyr Arg Thr Met Ser Gln
100 105 110
Val Ala Leu Asn Met Leu Arg Glu Glu Gly Val Ala Ser Phe Tyr Asn
115 120 125
Gly Leu Gly Pro Ser Leu Leu Ser Ile Ala Pro Tyr Ile Ala Ile Asn
130 135 140
Phe Cys Val Phe Asp Leu Val Lys Lys Ser Leu Pro Glu Lys Tyr Gln
145 150 155 160
Gln Lys Thr Gln Ser Ser Leu Leu Thr Ala Val Val Ala Ala Ala Ile
165 170 175
Ala Thr Gly Thr Cys Tyr Pro Leu Asp Thr Ile Arg Arg Gln Met Gln
180 185 190
Leu Lys Gly Thr Pro Tyr Lys Ser Val Leu Asp Ala Phe Ser Gly Ile
195 200 205
Ile Ala Arg Glu Gly Val Val Gly Leu Tyr Arg Gly Phe Val Pro Asn
210 215 220
Ala Leu Lys Ser Met Pro Asn Ser Ser Ile Lys Leu Thr Thr Phe Asp
225 230 235 240
Ile Val Lys Lys Leu Ile Ala Ala Ser Glu Lys Glu Ile Gln Arg Ile
245 250 255
Ala Asp Asp Asn Arg Lys Lys Ala Ser Pro Asn Thr Thr Asp Glu Gln
260 265 270
Thr

(2) INFORMATION FOR SEQ ID NO:1206:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1109 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1109
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499844

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1206:

aaaaaaacca ataaaattgg tgcgttcgca aaaactgaga tvtgagttct tccttcgggtg	60
gaaagagcaa attttacttt taagaaattt gaaaacaaag ttctattaaa cagattgggtg	120
ggattttaaa tttgaatttt gatcagtgaa tcaacgataa acgattcgtc gttatggaag	180
gagttgggtgc acggttaggc aggtcctcga cacggtacgg accggcaacg gttttcaccg	240
gtccggtgcg gaagtggaag aagaagtggg tacacgtctc tccatccact aagaaagaca	300
ataataatag ctccctccgtg tccgcccgtg ctgcagcttc cgtcgttaat ggtgggttoga	360
attctgacgg cagtaatgga tcgcatttgt tgctgtataa gtgggcacca ttgtcccaga	420
acggtaacgg gaatgaagat ggtaaaagtg agagtaattc tccgagcgag gacacgggtg	480
cgacggtggc agaagatcct ccgcggcgga gattcaaata cgttccgata gcagtacttg	540
aggaacagaa gaaggaaatt acagaaattg aggacgatga taagattgag gaggatgaca	600
agattgatga ggataataag gtcgagcagg aagacaaggt tgatgaggac aaaactgtag	660
aggagtcgag cgagaagaaa gcggaagtgt aagtggaagt ggaggaaaag cctgatatca	720
atgatgttcc aatggaagat attcagcagg atgaagaaaa aatagtagac gatgatgaag	780
aaaaagtagt gcgacaagat ttgaacgaaa gcaactgtgga tttaggactg aacttaaatg	840
caaacgatgc tgatgctgat gcagaaaacg acccgaaaga ggacaagcca ttagaagaat	900
gataaactgg gtgcattggt ttgggttctc accctcaact ctcaatatca attaggaaga	960
aagacattac agaaagaaca aagcagtcac tagatatgga cgcagatcct tgatttggtc	1020
tgtaacccca tggcttattc cttttgatgt taatggaaat gactcattga ttcagactga	1080
tcattcaatt cataggcaga ttcttggtc	

(2) INFORMATION FOR SEQ ID NO:1207:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 242 amino acids
- (B) TYPE: amino acid

- (C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..242
(D) OTHER INFORMATION: / Ceres Seq. ID 1499845
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1207:

Met Glu Gly Val 5 Ala Arg Leu Gly 10 Arg Ser Ser Thr Arg Tyr Gly
1 5 10 15
Pro Ala Thr Val Phe Thr Gly Pro Val Arg Lys Trp Lys Lys Lys Trp
20 25 30
Val His Val Ser Pro Ser Thr Lys Lys Asp Asn Asn Asn Ser Ser Ser
35 40 45
Gly Ser Ala Ala Ala Ala Ser Val Val Asn Gly Gly Ser Asn Ser
50 55 60
Asp Gly Ser Asn Gly Ser His Leu Leu Leu Tyr Lys Trp Ala Pro Leu
65 70 75 80
Ser Gln Asn Gly Asn Gly Asn Glu Asp Gly Lys Ser Glu Ser Asn Ser
85 90 95
Pro Ser Glu Asp Thr Val Ala Thr Val Ala Glu Asp Pro Pro Arg Arg
100 105 110
Arg Phe Lys Tyr Val Pro Ile Ala Val Leu Glu Glu Gln Lys Lys Glu
115 120 125
Ile Thr Glu Ile Glu Asp Asp Asp Lys Ile Glu Glu Asp Asp Lys Ile
130 135 140
Asp Glu Asp Asn Lys Val Glu Gln Glu Asp Lys Val Asp Glu Asp Lys
145 150 155 160
Thr Val Glu Glu Ser Ser Glu Lys Lys Ala Glu Val Glu Val Glu Val
165 170 175
Glu Glu Lys Pro Asp Ile Asn Asp Val Pro Met Glu Asp Ile Gln Gln
180 185 190
Asp Glu Glu Lys Ile Val Gln Asp Asp Glu Glu Lys Val Val Arg Gln
195 200 205
Asp Leu Asn Glu Ser Thr Val Asp Leu Gly Leu Asn Leu Asn Ala Asn
210 215 220
Asp Ala Asp Ala Asp Ala Glu Asn Asp Pro Lys Glu Asp Lys Pro Leu
225 230 235 240
Glu Glu

(2) INFORMATION FOR SEQ ID NO:1208:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 604 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
(A) NAME/KEY: -
(B) LOCATION: 1..604
(D) OTHER INFORMATION: / Ceres Seq. ID 1499850
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1208:

gcactgcttc attctctata accaagtata agcttgagg gggttatttt tctaaaaggg 60
attgagtttt taagatcatg tctatgacag tggagataag agttccaaac ttggattgtg 120
aaggatgtgc ttctaagctt aggaagactc tactcaagct taaaggagtg gaagaagtgg 180
aaagtagaga tggaaccaca aaaagtgcg gctcgaggat accgggttaga ggaaaagaag 240
gtattgaaag cggtacgacg tgccggtaag cgagctgaac tgtggccata ccggttagg 300
aatagccatt ttgcctcttt ctataaatat ccttcttacg tgaccaacca ctattactct 360
gatgcacacc gtacggatcc caccggtggt gtccacactt tcttccacac tcctgcggtt 420
tactcggttg ctgtggctgg agatgagatc gcggcttcga tgttttagcga tgataatccc 480
catgcttgta ctattatgta gtcttttagt atacaaaaat atgttttcag ttcattctct 540

tcgtccaaat ttgatttgat gtgatttttt ttgtacaact aatgttggaa tgagaaagta 600
aaat

(2) INFORMATION FOR SEQ ID NO:1209:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 63 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..63
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499851

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1209:

Met	Ser	Met	Thr	Val	Glu	Ile	Arg	Val	Pro	Asn	Leu	Asp	Cys	Glu	Gly
1				5					10					15	
Cys	Ala	Ser	Lys	Leu	Arg	Lys	Thr	Leu	Leu	Lys	Leu	Lys	Gly	Val	Glu
			20					25					30		
Glu	Val	Glu	Ser	Arg	Asp	Gly	Asn	Pro	Lys	Ser	Asp	Gly	Ser	Arg	Ile
		35					40					45			
Pro	Val	Arg	Gly	Lys	Glu	Gly	Ile	Glu	Ser	Gly	Thr	Thr	Cys	Arg	
		50				55					60				

(2) INFORMATION FOR SEQ ID NO:1210:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 103 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..103
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499852

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1210:

Met	Glu	Thr	Gln	Lys	Val	Thr	Ala	Arg	Gly	Tyr	Arg	Leu	Glu	Glu	Lys
1				5					10					15	
Lys	Val	Leu	Lys	Ala	Val	Arg	Arg	Ala	Gly	Lys	Ala	Ala	Glu	Leu	Trp
			20					25					30		
Pro	Tyr	Arg	Leu	Gly	Asn	Ser	His	Phe	Ala	Ser	Phe	Tyr	Lys	Tyr	Pro
		35					40					45			
Ser	Tyr	Val	Thr	Asn	His	Tyr	Tyr	Ser	Asp	Ala	His	Arg	Thr	Asp	Pro
		50				55					60				
Thr	Gly	Gly	Val	His	Thr	Phe	Phe	His	Thr	Pro	Ala	Val	Tyr	Ser	Val
65				70						75				80	
Ala	Val	Ala	Gly	Asp	Glu	Ile	Ala	Ala	Ser	Met	Phe	Ser	Asp	Asp	Asn
			85						90					95	
Pro	His	Ala	Cys	Thr	Ile	Met									
			100												

(2) INFORMATION FOR SEQ ID NO:1211:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 65 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..65
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499853

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1211:

Met His Thr Val Arg Ile Pro Pro Val Val Ser Thr Leu Ser Ser Thr

[illegible]

(2) INFORMATION FOR SEQ ID NO:1212:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 835 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
(B) LOCATION: 1..835
(D) OTHER INFORMATION: / Ceres Seq. ID 1499854

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1212:

aacttaattt	atttttaggc	catgggaaga	aaagtcttct	gcgtaataa	tttctagatc	60
tttccacaac	attcatacgc	aactccctta	aatcttgaaa	cgaccaattt	cttcaaaaca	120
atagtttggt	tgcgatggcg	acagaacaag	acgctgaagt	tggaacagag	acaccctctg	180
tttccggaag	gtttttgagg	aacagagatt	tatatctctt	cttgcctttt	ctcttaggct	240
tctctgatca	agaatcatca	aacggagatg	atgatgatgt	tgettcatcg	cgtgagagaa	300
tcattttagt	caaccctttt	acacaaggaa	tgattgtgct	cgaaggctca	tcaggatga	360
atcctctgct	tcgtagctta	ctggagtcac	gtgaggaagg	tcgtctctct	gcgtccaagg	420
cttccatcga	tgcgatgccg	atcgttgaga	ttgatggctg	tgaaggagag	tgtgtgatct	480
gtttggagga	gtggaagtcc	gaggagacgg	tgaaggagat	gccgtgtaag	cataggtttc	540
acggtggatg	tatagagaaa	tggttagggt	ttcatgggtc	gtgtctctgt	tgtaggtacg	600
agatgcctgt	tgatggagat	gagattggga	agaaaagaaa	cgatgggaat	gagatttggg	660
ttaggttcag	tttcaacgat	ggtcggagaa	ttagagattt	ttctgcgcag	gacggtggaa	720
acagttagtg	tgttgagctc	gagaattagg	atttacataa	gaagctttttg	taaaaaaaac	780
tttgtccctt	ttttgttctt	qttctqgqaa	aagqttqatg	aacttttttt	qtctt	

(2) INFORMATION FOR SEQ ID NO:1213:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 204 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..204
(D) OTHER INFORMATION: / Ceres Seq. ID 1499855

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1213:

Met	Ala	Thr	Glu	Gln	Asp	Ala	Glu	Val	Gly	Thr	Glu	Thr	Pro	Ser	Val
1				5					10					15	
Ser	Gly	Arg	Phe	Leu	Arg	Asn	Arg	Asp	Leu	Tyr	Leu	Phe	Leu	Pro	Phe
			20					25					30		
Leu	Leu	Gly	Phe	Ser	Asp	Gln	Glu	Ser	Ser	Asn	Gly	Asp	Asp	Asp	Asp
		35					40					45			
Val	Ala	Ser	Ser	Arg	Glu	Arg	Ile	Ile	Leu	Val	Asn	Pro	Phe	Thr	Gln
	50					55					60				
Gly	Met	Ile	Val	Leu	Glu	Gly	Ser	Ser	Gly	Met	Asn	Pro	Leu	Leu	Arg
65					70					75					80
Ser	Leu	Leu	Glu	Ser	Arg	Glu	Glu	Gly	Arg	Pro	Pro	Ala	Ser	Lys	Ala
				85					90					95	
Ser	Ile	Asp	Ala	Met	Pro	Ile	Val	Glu	Ile	Asp	Gly	Cys	Glu	Gly	Glu
			100					105					110		

Cys Val Ile Cys Leu Glu Glu Trp Lys Ser Glu Glu Thr Val Lys Glu
115 120 125
Met Pro Cys Lys His Arg Phe His Gly Gly Cys Ile Glu Lys Trp Leu
130 135 140
Gly Phe His Gly Ser Cys Pro Val Cys Arg Tyr Glu Met Pro Val Asp
145 150 155 160
Gly Asp Glu Ile Gly Lys Lys Arg Asn Asp Gly Asn Glu Ile Trp Val
165 170 175
Arg Phe Ser Phe Asn Asp Gly Arg Arg Ile Arg Asp Phe Ser Ala Gln
180 185 190
Asp Gly Gly Asn Ser Asp Gly Val Glu Ser Glu Asn
195 200

(2) INFORMATION FOR SEQ ID NO:1214:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 139 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..139
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499856

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1214:

Met Ile Val Leu Glu Gly Ser Ser Gly Met Asn Pro Leu Leu Arg Ser
1 5 10 15
Leu Leu Glu Ser Arg Glu Glu Gly Arg Pro Pro Ala Ser Lys Ala Ser
20 25 30
Ile Asp Ala Met Pro Ile Val Glu Ile Asp Gly Cys Glu Gly Glu Cys
35 40 45
Val Ile Cys Leu Glu Glu Trp Lys Ser Glu Glu Thr Val Lys Glu Met
50 55 60
Pro Cys Lys His Arg Phe His Gly Gly Cys Ile Glu Lys Trp Leu Gly
65 70 75 80
Phe His Gly Ser Cys Pro Val Cys Arg Tyr Glu Met Pro Val Asp Gly
85 90 95
Asp Glu Ile Gly Lys Lys Arg Asn Asp Gly Asn Glu Ile Trp Val Arg
100 105 110
Phe Ser Phe Asn Asp Gly Arg Arg Ile Arg Asp Phe Ser Ala Gln Asp
115 120 125
Gly Gly Asn Ser Asp Gly Val Glu Ser Glu Asn
130 135

(2) INFORMATION FOR SEQ ID NO:1215:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 130 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..130
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499857

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1215:

Met Asn Pro Leu Leu Arg Ser Leu Leu Glu Glu Gly Arg
1 5 10 15
Pro Pro Ala Ser Lys Ala Ser Ile Asp Ala Met Pro Ile Val Glu Ile
20 25 30
Asp Gly Cys Glu Gly Glu Cys Val Ile Cys Leu Glu Glu Trp Lys Ser
35 40 45
Glu Glu Thr Val Lys Glu Met Pro Cys Lys His Arg Phe His Gly Gly

50 55 60
Cys Ile Glu Lys Trp Leu Gly Phe His Gly Ser Cys Pro Val Cys Arg
65 70 75 80
Tyr Glu Met Pro Val Asp Gly Asp Glu Ile Gly Lys Lys Arg Asn Asp
85 90 95
Gly Asn Glu Ile Trp Val Arg Phe Ser Phe Asn Asp Gly Arg Arg Ile
100 105 110
Arg Asp Phe Ser Ala Gln Asp Gly Gly Asn Ser Asp Gly Val Glu Ser
115 120 125
Glu Asn
130

(2) INFORMATION FOR SEQ ID NO:1216:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1745 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1745
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499875

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1216:

aaacaagaaa	gagattagga	agagagagac	ggcgatggcg	gctacaggat	ctggacggtc	60
tcaattcatt	tccagttccg	gcggtaacgc	aagcttctcc	aattctccac	tcacgagaa	120
ctctgattct	aatcagatta	ttgtctctga	gaagaagagc	tggaagaatt	tctttgctta	180
cttaggccct	ggttttcttg	tttcaatcgc	atatattgat	cctggaaaact	ttgagactga	240
tctgcaagct	ggagcacact	acaagtatga	attacttttg	atcatattgg	tggcctcatg	300
tgcggttttg	gtgattcaat	ctctggctgc	taactttggt	gttgtcacag	gaaaacattt	360
ggctgagcaa	tgtagagccg	agtactccaa	agttccaaaac	tttatgttat	gggtcgttgc	420
tgaatttgca	gtagttgctt	gtgacatacc	ggaagttatc	ggaacagctt	ttgctctgaa	480
catgctcttt	agcataccgg	tgtggatcgg	tggtcttctg	acaggcttaa	gtacgctgat	540
tcttctcgca	cttcaaaaat	acggggtgag	aaagctggag	ttcttgatag	cgtttcttgt	600
gttcacaatt	gctatatgct	tctttgttga	gcttcattac	tcaaagccag	acccaggaga	660
agtcctacat	ggctctcttg	ttcctcaact	taaaggaaat	ggtgcaactg	gtctcgcaat	720
ctcttttgct	ggagccatgg	ttatgcccga	taatctcttc	ctccactcgg	ccttggttct	780
ctcgaggaaa	atccctcggt	ccgcttcttg	tatcaaggaa	gcttgacagg	tttacttgat	840
agaaagtgga	ttggctctaa	tgggtggcct	tctcataaac	gtctctgtaa	tatcagtaag	900
cggggctgtt	tgtaatgccc	ccaacttaag	ccctgaagat	cgagctaatt	gtgaggattt	960
ggacttaaac	aaggcttcgt	ttctgctacg	gaacgttggt	ggaaaatgga	gctcaaagct	1020
atttgcaatc	gcgcttcttg	cttctgggtc	gagctcgacg	ataaccggaa	cttatgctgg	1080
acaatatgta	atgcagggct	ttcttgatct	cagactcgag	ccatggctca	gaaacttact	1140
aacaagatgt	ttagctataa	tcccagagtct	aattgttgct	ctcatcggtg	gttcagctgg	1200
agctggaaa	ttaatcatca	ttgcctcgat	gatcttatcc	tttgagctcc	cgtttgctgt	1260
ggttcctctt	ctaaaattca	caagttgcaa	aaccaagatg	ggttcacatg	tcaacccaat	1320
ggcgattaca	gctttgactt	gggtcattgg	tggtttaatc	atgggaataa	acataacta	1380
tctagtaagc	agtttcatca	aactgcttat	ccacagtcac	atgaagctta	tcctcgctgt	1440
cttctgtgga	attcttgggt	tcgcaggcat	tgctctctat	ttagccgcca	tagcttacct	1500
tgtcttccgg	aaaaacagag	tagccacttc	tcttcttatt	tcaagagact	cacaaaatgt	1560
ggagacactt	ccaagacagg	acattgtcaa	catgcagtta	ccatgtagag	tatctacctc	1620
cgatgttggc	tgagtcacat	ttaagcttag	gattccaata	aagttagatc	taaaccaagt	1680
tcataaaaaac	ctttcgatag	tgtactagaa	taaaggttat	atgaatcggt	ttgcgtcttt	1740
tcttt						

(2) INFORMATION FOR SEQ ID NO:1217:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 543 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..543

(D) OTHER INFORMATION: / Ceres Seq. ID 1499876

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1217:

Asn	Lys	Lys	Glu	Ile	Arg	Lys	Arg	Glu	Thr	Ala	Met	Ala	Ala	Thr	Gly
1			5					10						15	
Ser	Gly	Arg	Ser	Gln	Phe	Ile	Ser	Ser	Gly	Gly	Asn	Arg	Ser	Phe	
			20					25				30			
Ser	Asn	Ser	Pro	Leu	Ile	Glu	Asn	Ser	Asp	Ser	Asn	Gln	Ile	Ile	Val
		35					40					45			
Ser	Glu	Lys	Lys	Ser	Trp	Lys	Asn	Phe	Phe	Ala	Tyr	Leu	Gly	Pro	Gly
	50					55					60				
Phe	Leu	Val	Ser	Ile	Ala	Tyr	Ile	Asp	Pro	Gly	Asn	Phe	Glu	Thr	Asp
65					70				75						80
Leu	Gln	Ala	Gly	Ala	His	Tyr	Lys	Tyr	Glu	Leu	Leu	Trp	Ile	Ile	Leu
				85					90					95	
Val	Ala	Ser	Cys	Ala	Ala	Leu	Val	Ile	Gln	Ser	Leu	Ala	Ala	Asn	Leu
			100					105					110		
Gly	Val	Val	Thr	Gly	Lys	His	Leu	Ala	Glu	Gln	Cys	Arg	Ala	Glu	Tyr
		115					120					125			
Ser	Lys	Val	Pro	Asn	Phe	Met	Leu	Trp	Val	Val	Ala	Glu	Ile	Ala	Val
	130					135					140				
Val	Ala	Cys	Asp	Ile	Pro	Glu	Val	Ile	Gly	Thr	Ala	Phe	Ala	Leu	Asn
145					150					155					160
Met	Leu	Phe	Ser	Ile	Pro	Val	Trp	Ile	Gly	Val	Leu	Leu	Thr	Gly	Leu
				165					170					175	
Ser	Thr	Leu	Ile	Leu	Leu	Ala	Leu	Gln	Lys	Tyr	Gly	Val	Arg	Lys	Leu
		180						185					190		
Glu	Phe	Leu	Ile	Ala	Phe	Leu	Val	Phe	Thr	Ile	Ala	Ile	Cys	Phe	Phe
		195					200					205			
Val	Glu	Leu	His	Tyr	Ser	Lys	Pro	Asp	Pro	Gly	Glu	Val	Leu	His	Gly
	210					215					220				
Leu	Phe	Val	Pro	Gln	Leu	Lys	Gly	Asn	Gly	Ala	Thr	Gly	Leu	Ala	Ile
225					230					235					240
Ser	Leu	Leu	Gly	Ala	Met	Val	Met	Pro	His	Asn	Leu	Phe	Leu	His	Ser
				245					250					255	
Ala	Leu	Val	Leu	Ser	Arg	Lys	Ile	Pro	Arg	Ser	Ala	Ser	Gly	Ile	Lys
			260					265					270		
Glu	Ala	Cys	Arg	Phe	Tyr	Leu	Ile	Glu	Ser	Gly	Leu	Ala	Leu	Met	Val
		275					280					285			
Ala	Phe	Leu	Ile	Asn	Val	Ser	Val	Ile	Ser	Val	Ser	Gly	Ala	Val	Cys
	290					295					300				
Asn	Ala	Pro	Asn	Leu	Ser	Pro	Glu	Asp	Arg	Ala	Asn	Cys	Glu	Asp	Leu
305				310						315					320
Asp	Leu	Asn	Lys	Ala	Ser	Phe	Leu	Leu	Arg	Asn	Val	Val	Gly	Lys	Trp
			325						330					335	
Ser	Ser	Lys	Leu	Phe	Ala	Ile	Ala	Leu	Leu	Ala	Ser	Gly	Gln	Ser	Ser
		340						345					350		
Thr	Ile	Thr	Gly	Thr	Tyr	Ala	Gly	Gln	Tyr	Val	Met	Gln	Gly	Phe	Leu
		355					360					365			
Asp	Leu	Arg	Leu	Glu	Pro	Trp	Leu	Arg	Asn	Leu	Leu	Thr	Arg	Cys	Leu
	370					375					380				
Ala	Ile	Ile	Pro	Ser	Leu	Ile	Val	Ala	Leu	Ile	Gly	Gly	Ser	Ala	Gly
385					390					395					400
Ala	Gly	Lys	Leu	Ile	Ile	Ala	Ser	Met	Ile	Leu	Ser	Phe	Glu	Leu	
				405				410					415		
Pro	Phe	Ala	Leu	Val	Pro	Leu	Leu	Lys	Phe	Thr	Ser	Cys	Lys	Thr	Lys
			420					425					430		
Met	Gly	Ser	His	Val	Asn	Pro	Met	Ala	Ile	Thr	Ala	Leu	Thr	Trp	Val
		435					440					445			
Ile	Gly	Gly	Leu	Ile	Met	Gly	Ile	Asn	Ile	Tyr	Tyr	Leu	Val	Ser	Ser

450		455		460										
Phe	Ile	Lys	Leu	Ile	His	Ser	His	Met	Lys	Leu	Ile	Leu	Val	Val
465				470				475					480	
Phe	Cys	Gly	Ile	Leu	Gly	Phe	Ala	Gly	Ile	Ala	Leu	Tyr	Leu	Ala
			485					490					495	
Ile	Ala	Tyr	Leu	Val	Phe	Arg	Lys	Asn	Arg	Val	Ala	Thr	Ser	Leu
			500					505					510	
Ile	Ser	Arg	Asp	Ser	Gln	Asn	Val	Glu	Thr	Leu	Pro	Arg	Gln	Asp
			515					520					525	
Val	Asn	Met	Gln	Leu	Pro	Cys	Arg	Val	Ser	Thr	Ser	Asp	Val	Gly
			530					535					540	

(2) INFORMATION FOR SEQ ID NO:1218:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 532 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..532

(D) OTHER INFORMATION: / Ceres Seq. ID 1499877

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1218:

Met	Ala	Ala	Thr	Gly	Ser	Gly	Arg	Ser	Gln	Phe	Ile	Ser	Ser	Ser	Gly
1				5				10						15	
Gly	Asn	Arg	Ser	Phe	Ser	Asn	Ser	Pro	Leu	Ile	Glu	Asn	Ser	Asp	Ser
			20					25					30		
Asn	Gln	Ile	Ile	Val	Ser	Glu	Lys	Ser	Trp	Lys	Asn	Phe	Phe	Ala	
			35					40				45			
Tyr	Leu	Gly	Pro	Gly	Phe	Leu	Val	Ser	Ile	Ala	Tyr	Ile	Asp	Pro	Gly
			50					55				60			
Asn	Phe	Glu	Thr	Asp	Leu	Gln	Ala	Gly	Ala	His	Tyr	Lys	Tyr	Glu	Leu
65								70				75			80
Leu	Trp	Ile	Ile	Leu	Val	Ala	Ser	Cys	Ala	Ala	Leu	Val	Ile	Gln	Ser
				85				90						95	
Leu	Ala	Ala	Asn	Leu	Gly	Val	Val	Thr	Gly	Lys	His	Leu	Ala	Glu	Gln
			100					105						110	
Cys	Arg	Ala	Glu	Tyr	Ser	Lys	Val	Pro	Asn	Phe	Met	Leu	Trp	Val	Val
			115					120				125			
Ala	Glu	Ile	Ala	Val	Val	Ala	Cys	Asp	Ile	Pro	Glu	Val	Ile	Gly	Thr
			130					135				140			
Ala	Phe	Ala	Leu	Asn	Met	Leu	Phe	Ser	Ile	Pro	Val	Trp	Ile	Gly	Val
145								150				155			160
Leu	Leu	Thr	Gly	Leu	Ser	Thr	Leu	Ile	Leu	Leu	Ala	Leu	Gln	Lys	Tyr
				165				170						175	
Gly	Val	Arg	Lys	Leu	Glu	Phe	Leu	Ile	Ala	Phe	Leu	Val	Phe	Thr	Ile
			180					185						190	
Ala	Ile	Cys	Phe	Phe	Val	Glu	Leu	His	Tyr	Ser	Lys	Pro	Asp	Pro	Gly
			195					200					205		
Glu	Val	Leu	His	Gly	Leu	Phe	Val	Pro	Gln	Leu	Lys	Gly	Asn	Gly	Ala
			210					215				220			
Thr	Gly	Leu	Ala	Ile	Ser	Leu	Leu	Gly	Ala	Met	Val	Met	Pro	His	Asn
225								230				235			240
Leu	Phe	Leu	His	Ser	Ala	Leu	Val	Leu	Ser	Arg	Lys	Ile	Pro	Arg	Ser
				245				250						255	
Ala	Ser	Gly	Ile	Lys	Glu	Ala	Cys	Arg	Phe	Tyr	Leu	Ile	Glu	Ser	Gly
			260					265					270		
Leu	Ala	Leu	Met	Val	Ala	Phe	Leu	Ile	Asn	Val	Ser	Val	Ile	Ser	Val
			275					280					285		
Ser	Gly	Ala	Val	Cys	Asn	Ala	Pro	Asn	Leu	Ser	Pro	Glu	Asp	Arg	Ala
			290					295					300		

Asn Cys Glu Asp Leu Asp Leu Asn Lys Ala Ser Phe Leu Leu Arg Asn
305 310 315 320
Val Val Gly Lys Trp Ser Ser Lys Leu Phe Ala Ile Ala Leu Leu Ala
325 330 335
Ser Gly Gln Ser Ser Thr Ile Thr Gly Thr Tyr Ala Gly Gln Tyr Val
340 345 350
Met Gln Gly Phe Leu Asp Leu Arg Leu Glu Pro Trp Leu Arg Asn Leu
355 360 365
Leu Thr Arg Cys Leu Ala Ile Ile Pro Ser Leu Ile Val Ala Leu Ile
370 375 380
Gly Gly Ser Ala Gly Ala Gly Lys Leu Ile Ile Ile Ala Ser Met Ile
385 390 395 400
Leu Ser Phe Glu Leu Pro Phe Ala Leu Val Pro Leu Leu Lys Phe Thr
405 410 415
Ser Cys Lys Thr Lys Met Gly Ser His Val Asn Pro Met Ala Ile Thr
420 425 430
Ala Leu Thr Trp Val Ile Gly Gly Leu Ile Met Gly Ile Asn Ile Tyr
435 440 445
Tyr Leu Val Ser Ser Phe Ile Lys Leu Leu Ile His Ser His Met Lys
450 455 460
Leu Ile Leu Val Val Phe Cys Gly Ile Leu Gly Phe Ala Gly Ile Ala
465 470 475 480
Leu Tyr Leu Ala Ala Ile Ala Tyr Leu Val Phe Arg Lys Asn Arg Val
485 490 495
Ala Thr Ser Leu Leu Ile Ser Arg Asp Ser Gln Asn Val Glu Thr Leu
500 505 510
Pro Arg Gln Asp Ile Val Asn Met Gln Leu Pro Cys Arg Val Ser Thr
515 520 525
Ser Asp Val Gly
530

(2) INFORMATION FOR SEQ ID NO:1219:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 409 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..409

(D) OTHER INFORMATION: / Ceres Seq. ID 1499878

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1219:

Met Leu Trp Val Val Ala Glu Ile Ala Val Val Ala Cys Asp Ile Pro
1 5 10 15
Glu Val Ile Gly Thr Ala Phe Ala Leu Asn Met Leu Phe Ser Ile Pro
20 25 30
Val Trp Ile Gly Val Leu Leu Thr Gly Leu Ser Thr Leu Ile Leu Leu
35 40 45
Ala Leu Gln Lys Tyr Gly Val Arg Lys Leu Glu Phe Leu Ile Ala Phe
50 55 60
Leu Val Phe Thr Ile Ala Ile Cys Phe Phe Val Glu Leu His Tyr Ser
65 70 75 80
Lys Pro Asp Pro Gly Glu Val Leu His Gly Leu Phe Val Pro Gln Leu
85 90 95
Lys Gly Asn Gly Ala Thr Gly Leu Ala Ile Ser Leu Leu Gly Ala Met
100 105 110
Val Met Pro His Asn Leu Phe Leu His Ser Ala Leu Val Leu Ser Arg
115 120 125
Lys Ile Pro Arg Ser Ala Ser Gly Ile Lys Glu Ala Cys Arg Phe Tyr
130 135 140
Leu Ile Glu Ser Gly Leu Ala Leu Met Val Ala Phe Leu Ile Asn Val

145	Ser	Val	Ile	Ser	Val	Ser	Gly	Ala	Val	Cys	Asn	Ala	Pro	Asn	Leu	Ser
				165	Ala	Asn	Cys	Glu	Asp	Leu	Asp	Leu	Asn	Lys	Ala	Ser
Pro	Glu	Asp	Arg													
			180	Asn	Val	Val	Gly	Lys	Trp	Ser	Ser	Lys	Leu	Phe	Ala	
Phe	Leu	Leu	Arg													
			195				200						205			
Ile	Ala	Leu	Leu	Ala	Ser	Gly	Gln	Ser	Ser	Thr	Ile	Thr	Gly	Thr	Tyr	
			210				215					220				
Ala	Gly	Gln	Tyr	Val	Met	Gln	Gly	Phe	Leu	Asp	Leu	Arg	Leu	Glu	Pro	
225					230					235					240	
Trp	Leu	Arg	Asn	Leu	Leu	Thr	Arg	Cys	Leu	Ala	Ile	Ile	Pro	Ser	Leu	
				245					250						255	
Ile	Val	Ala	Leu	Ile	Gly	Gly	Ser	Ala	Gly	Ala	Gly	Lys	Leu	Ile	Ile	
			260					265					270			
Ile	Ala	Ser	Met	Ile	Leu	Ser	Phe	Glu	Leu	Pro	Phe	Ala	Leu	Val	Pro	
			275				280					285				
Leu	Leu	Lys	Phe	Thr	Ser	Cys	Lys	Thr	Lys	Met	Gly	Ser	His	Val	Asn	
			290			295					300					
Pro	Met	Ala	Ile	Thr	Ala	Leu	Thr	Trp	Val	Ile	Gly	Gly	Leu	Ile	Met	
305					310					315					320	
Gly	Ile	Asn	Ile	Tyr	Tyr	Leu	Val	Ser	Ser	Phe	Ile	Lys	Leu	Leu	Ile	
				325					330					335		
His	Ser	His	Met	Lys	Leu	Ile	Leu	Val	Val	Phe	Cys	Gly	Ile	Leu	Gly	
			340					345					350			
Phe	Ala	Gly	Ile	Ala	Leu	Tyr	Leu	Ala	Ala	Ile	Ala	Tyr	Leu	Val	Phe	
			355				360					365				
Arg	Lys	Asn	Arg	Val	Ala	Thr	Ser	Leu	Leu	Ile	Ser	Arg	Asp	Ser	Gln	
			370			375					380					
Asn	Val	Glu	Thr	Leu	Pro	Arg	Gln	Asp	Ile	Val	Asn	Met	Gln	Leu	Pro	
385					390					395					400	
Cys	Arg	Val	Ser	Thr	Ser	Asp	Val	Gly								
					405											

(2) INFORMATION FOR SEQ ID NO:1220:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 700 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..700
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499899

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1220:

acttgttctc	atattagttt	gttatacaac	tcacttagaa	taatgtagat	tacatttcag	60
ccaaattcat	attcttgaga	gaaaagaaat	cgaagatggc	aacaaaatcc	accggaggta	120
ccgagaaaac	caagtcgata	gaagtgaaga	agaaactaat	caacgtgttg	atcgtcgatg	180
atgatccatt	aaaccgtaga	ctccacgaga	tgatcatcaa	aacgaticgga	ggaattttctc	240
agactgcaaa	gaatggcgag	gaggcagtga	tcctccaccg	tgacggcgaa	gcattctttcg	300
accttattct	aatggataag	gaaatgcctg	agagggatgg	agtttcgaca	actaagaagc	360
taagagaaat	gaaagtgcg	tcaatgatcg	ttggggtaac	gtcagtagct	gaccaagaag	420
aagagcgtaa	ggcttttatg	gaagctgggc	tcaaccattg	cttggaaaaa	cccttaacca	480
aggccaagat	cttcccgcgc	attagccacc	tcttcgatgc	ttgatggatg	aaggctcatt	540
aatgtatcta	tattttcaat	catgaaatca	cctacacgtg	tatttgacac	aaaaatctgc	600
atttgttgtg	atatagggtt	tctcatatct	atgtttgatt	tattttctta	tcgtccgagg	660
taaaatcatg	caagtcattt	cttttggtta	ataaaatatt			

(2) INFORMATION FOR SEQ ID NO:1221:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 142 amino acids
- (B) TYPE: amino acid

(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..142
(D) OTHER INFORMATION: / Ceres Seq. ID 1499900
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1221:
Met Ala Thr Lys Ser Thr Gly Gly Thr Glu Lys Thr Lys Ser Ile Glu
1 5 10 15
Val Lys Lys Lys Leu Ile Asn Val Leu Ile Val Asp Asp Asp Pro Leu
20 25 30
Asn Arg Arg Leu His Glu Met Ile Ile Lys Thr Ile Gly Gly Ile Ser
35 40 45
Gln Thr Ala Lys Asn Gly Glu Glu Ala Val Ile Leu His Arg Asp Gly
50 55 60
Glu Ala Ser Phe Asp Leu Ile Leu Met Asp Lys Glu Met Pro Glu Arg
65 70 75 80
Asp Gly Val Ser Thr Thr Lys Lys Leu Arg Glu Met Lys Val Thr Ser
85 90 95
Met Ile Val Gly Val Thr Ser Val Ala Asp Gln Glu Glu Glu Arg Lys
100 105 110
Ala Phe Met Glu Ala Gly Leu Asn His Cys Leu Glu Lys Pro Leu Thr
115 120 125
Lys Ala Lys Ile Phe Pro Leu Ile Ser His Leu Phe Asp Ala
130 135 140

(2) INFORMATION FOR SEQ ID NO:1222:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 104 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide
(B) LOCATION: 1..104

(D) OTHER INFORMATION: / Ceres Seq. ID 1499901

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1222:

Met Ile Ile Lys Thr Ile Gly Gly Ile Ser Gln Thr Ala Lys Asn Gly
1 5 10 15
Glu Glu Ala Val Ile Leu His Arg Asp Gly Glu Ala Ser Phe Asp Leu
20 25 30
Ile Leu Met Asp Lys Glu Met Pro Glu Arg Asp Gly Val Ser Thr Thr
35 40 45
Lys Lys Leu Arg Glu Met Lys Val Thr Ser Met Ile Val Gly Val Thr
50 55 60
Ser Val Ala Asp Gln Glu Glu Glu Arg Lys Ala Phe Met Glu Ala Gly
65 70 75 80
Leu Asn His Cys Leu Glu Lys Pro Leu Thr Lys Ala Lys Ile Phe Pro
85 90 95
Leu Ile Ser His Leu Phe Asp Ala
100

(2) INFORMATION FOR SEQ ID NO:1223:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 520 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..520

(D) OTHER INFORMATION: / Ceres Seq. ID 1499902

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1223:

aaggtgtcgg	atcttgatga	agcttcgaag	attcttgtgc	cggagtctgt	gaaaaagctc	60
cgggaactta	tgggttacat	attttacaaa	ccggcgttgg	caagactggt	tcctacttgt	120
cttctccatg	atttcacga	acatgctttg	acaagagata	atatggaaga	gaagagagaa	180
ctgattaaag	ccataccaaa	agacagaata	atctcagaga	ttccaaagct	caaacaacca	240
acattgataa	tatgggggga	gcatgatcaa	gtgttcccat	tggagatggg	caagagactt	300
gagaagcatg	taggagataa	tgggaaactc	gttatcatca	agagaactgg	tcatatcttt	360
aacttcgaga	aacctaaaaa	gtttatcaaa	cttctcaaat	cttttcttct	agagactagt	420
aaaccacaga	ttcctgtctc	taatgtttga	ttcttagtca	tcgttttgaa	gacacctca	480
taastaattt	ccaaggatta	ataacatata	tatcattttc			

(2) INFORMATION FOR SEQ ID NO:1224:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 149 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..149

(D) OTHER INFORMATION: / Ceres Seq. ID 1499903

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1224:

Lys	Val	Ser	Asp	Leu	Asp	Glu	Ala	Ser	Lys	Ile	Leu	Val	Pro	Glu	Ser	
1				5				10						15		
Val	Lys	Lys	Leu	Arg	Glu	Leu	Met	Gly	Tyr	Ile	Phe	Tyr	Lys	Pro	Ala	
			20					25					30			
Leu	Ala	Arg	Leu	Val	Pro	Thr	Cys	Leu	Leu	His	Asp	Phe	Ile	Glu	His	
		35					40					45				
Ala	Leu	Thr	Arg	Asp	Asn	Met	Glu	Glu	Lys	Arg	Glu	Leu	Ile	Lys	Ala	
		50				55					60					
Ile	Pro	Lys	Asp	Arg	Ile	Ile	Ser	Glu	Ile	Pro	Lys	Leu	Lys	Gln	Pro	
65				70						75				80		
Thr	Leu	Ile	Ile	Trp	Gly	Glu	His	Asp	Gln	Val	Phe	Pro	Leu	Glu	Met	
			85					90						95		
Gly	Lys	Arg	Leu	Glu	Lys	His	Val	Gly	Asp	Asn	Gly	Lys	Leu	Val	Ile	
			100					105					110			
Ile	Lys	Arg	Thr	Gly	His	Ile	Phe	Asn	Phe	Glu	Lys	Pro	Lys	Lys	Phe	
		115				120					125					
Ile	Lys	Leu	Leu	Lys	Ser	Phe	Leu	Leu	Glu	Thr	Ser	Lys	Pro	Gln	Ile	
		130				135					140					
Pro	Val	Ser	Asn	Val												
145																

(2) INFORMATION FOR SEQ ID NO:1225:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 126 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..126

(D) OTHER INFORMATION: / Ceres Seq. ID 1499904

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1225:

Met	Gly	Tyr	Ile	Phe	Tyr	Lys	Pro	Ala	Leu	Ala	Arg	Leu	Val	Pro	Thr	
1				5				10						15		
Cys	Leu	Leu	His	Asp	Phe	Ile	Glu	His	Ala	Leu	Thr	Arg	Asp	Asn	Met	
			20					25					30			
Glu	Glu	Lys	Arg	Glu	Leu	Ile	Lys	Ala	Ile	Pro	Lys	Asp	Arg	Ile	Ile	

35 40 45
Ser Glu Ile Pro Lys Leu Lys Gln Pro Thr Leu Ile Ile Trp Gly Glu
50 55 60
His Asp Gln Val Phe Pro Leu Glu Met Gly Lys Arg Leu Glu Lys His
65 70 75 80
Val Gly Asp Asn Gly Lys Leu Val Ile Ile Lys Arg Thr Gly His Ile
85 90 95
Phe Asn Phe Glu Lys Pro Lys Lys Phe Ile Lys Leu Leu Lys Ser Phe
100 105 110
Leu Leu Glu Thr Ser Lys Pro Gln Ile Pro Val Ser Asn Val
115 120 125

(2) INFORMATION FOR SEQ ID NO:1226:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 95 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..95

(D) OTHER INFORMATION: / Ceres Seq. ID 1499905

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1226:

Met Glu Glu Lys Arg Glu Leu Ile Lys Ala Ile Pro Lys Asp Arg Ile
1 5 10 15
Ile Ser Glu Ile Pro Lys Leu Lys Gln Pro Thr Leu Ile Ile Trp Gly
20 25 30
Glu His Asp Gln Val Phe Pro Leu Glu Met Gly Lys Arg Leu Glu Lys
35 40 45
His Val Gly Asp Asn Gly Lys Leu Val Ile Ile Lys Arg Thr Gly His
50 55 60
Ile Phe Asn Phe Glu Lys Pro Lys Lys Phe Ile Lys Leu Leu Lys Ser
65 70 75 80
Phe Leu Leu Glu Thr Ser Lys Pro Gln Ile Pro Val Ser Asn Val
85 90 95

(2) INFORMATION FOR SEQ ID NO:1227:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 982 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..982

(D) OTHER INFORMATION: / Ceres Seq. ID 1499906

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1227:

agaacacaaa caaaaacaca ttgtaacatt agtttaagca ttaagcttct ttatgtcgaa 60
taataataat tctccgacca ccgtgaatca agaaacgacg acgtctcgtg aagtctcaat 120
cacattgcct actgatcaat ctccctcaaac ctcaccagga tcattcttctt ctccctcacc 180
gagaccttcc ggtggatcac cggcgagaag aacggcgact ggattatccg gcaagcactc 240
tatttttcagg gggattcgac tacgtaacgg aaaatgggta tcggagatta gagagccacg 300
taaaacgaca agaatttggc tcgggactta tccgggtaccg gagatggctg ccgccgctta 360
cgacgtggct gcgttagctt taaaaggacc aggccgtttt gaattttcctt gggtttagct 420
ttgacttacg tggctccggt ttcaaaactct gctgcggata taagagcggc tgctagtaga 480
gcagcggaga tgaagcaacc ggatcagggt ggggatgaga aggtattgga accggttcaa 540
cccggcaaaag aggaagaatt agaagaagtg tcgtgtaact cgtgttcgtt ggagtttatg 600
gatgaggaag cgatgttgaa tatgccgact ttgttgacgg agatggctga agggatgttg 660
atgagtccac cgagaatgat gatacatccg acgatggaag atgattcgcc ggagaatcat 720
gaaggagata atctttggag ttataaatga atccattgaa gctgctctct tttttattgt 780
tttccggtcg aatgagattt tccccctttt tttttctttt tgggtcgctg ttatggaaag 840

tcaaataagggt tattaatatg atctattaat atttttgaaa cataatgagt ttgaatttga 900
atttttccat ttttatataa atatggttta tatgaggga aaatagatac atacgaaga 960
tataagaatt gtttttctgc tt

(2) INFORMATION FOR SEQ ID NO:1228:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 121 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..121

(D) OTHER INFORMATION: / Ceres Seq. ID 1499907

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1228:

Met	Ser	Asn	Asn	Asn	Asn	Ser	Pro	Thr	Thr	Val	Asn	Gln	Glu	Thr	Thr
1			5						10					15	
Thr	Ser	Arg	Glu	Val	Ser	Ile	Thr	Leu	Pro	Thr	Asp	Gln	Ser	Pro	Gln
		20						25				30			
Thr	Ser	Pro	Gly	Ser	Ser	Ser	Ser	Pro	Ser	Pro	Arg	Pro	Ser	Gly	Gly
		35					40				45				
Ser	Pro	Ala	Arg	Arg	Thr	Ala	Thr	Gly	Leu	Ser	Gly	Lys	His	Ser	Ile
	50					55					60				
Phe	Arg	Gly	Ile	Arg	Leu	Arg	Asn	Gly	Lys	Trp	Val	Ser	Glu	Ile	Arg
65				70					75					80	
Glu	Pro	Arg	Lys	Thr	Thr	Arg	Ile	Trp	Leu	Gly	Thr	Tyr	Pro	Val	Pro
			85					90					95		
Glu	Met	Ala	Ala	Ala	Tyr	Asp	Val	Ala	Ala	Leu	Ala	Leu	Lys	Gly	
		100					105					110			
Pro	Gly	Arg	Phe	Glu	Phe	Ser	Trp	Val							
	115						120								

(2) INFORMATION FOR SEQ ID NO:1229:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 86 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..86

(D) OTHER INFORMATION: / Ceres Seq. ID 1499908

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1229:

Met	Lys	Gln	Pro	Asp	Gln	Gly	Gly	Asp	Glu	Lys	Val	Leu	Glu	Pro	Val
1			5					10						15	
Gln	Pro	Gly	Lys	Glu	Glu	Glu	Leu	Glu	Glu	Val	Ser	Cys	Asn	Ser	Cys
		20					25					30			
Ser	Leu	Glu	Phe	Met	Asp	Glu	Glu	Ala	Met	Leu	Asn	Met	Pro	Thr	Leu
	35					40					45				
Leu	Thr	Glu	Met	Ala	Glu	Gly	Met	Leu	Met	Ser	Pro	Pro	Arg	Met	Met
	50					55				60					
Ile	His	Pro	Thr	Met	Glu	Asp	Asp	Ser	Pro	Glu	Asn	His	Glu	Gly	Asp
65				70					75					80	
Asn	Leu	Trp	Ser	Tyr	Lys										
		85													

(2) INFORMATION FOR SEQ ID NO:1230:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 932 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..932

(D) OTHER INFORMATION: / Ceres Seq. ID 1499909

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1230:

aactgtttga	tttctgagga	gaatccattg	tttccattcg	aagaaaactc	taactttctc	60
gttgaagctt	tgagctctct	acctctttat	ctccggagat	gtataataac	atgggacctc	120
aaccggggat	gccaagacct	ccaggaaacc	ctgagcctgg	tccattttgt	aatcctttca	180
ctggagctgg	ctcgggtttt	atccgtggtg	gtttgggagc	gtatggggag	agaattttag	240
gatcgartc	tgagtatgtt	cagagcaata	taagccgta	cttctctgat	ccgcaatact	300
atttccaagt	gaatgatcaa	tatgtgagga	ataaactgaa	ggttgttctg	tttcctttcc	360
tacaccgggg	acactggacc	agaatatctg	aaccagtgg	tggtaggctc	tcatacaagc	420
ctccaatata	tgatatcaat	gctcccagac	ttgtacattc	cctttatggc	atttggtacc	480
tacgttggtc	ttgctggtct	ttcattggga	cttaatggaa	agtttacacc	ggaagctttg	540
aattggctgt	ttgtgaaagg	attggttgg	tggtttttgc	aagtaatgct	cctgaaagta	600
acactttctat	cacttggtag	tggagaggca	ccattactag	atattgtggc	atacggagg	660
tatgcttttt	ctggctctgt	tcttgccggc	tttgccaaaa	taatgtgggg	atactcgtac	720
tacgcgttga	tgccatggac	ttgtctatgc	actgggattt	tcttggtgaa	gacgatgaaa	780
cgtgttctgt	ttgctgaagt	aagaagttac	gattcgagca	aacatcacta	ccttcttctg	840
tttttagcct	tggtccagtt	cccacttttg	atatggcttg	gtaacattag	tgtaattgg	900
cttctttgaa	atgaaaaaag	acgtttttgt	gt			

(2) INFORMATION FOR SEQ ID NO:1231:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 159 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..159

(D) OTHER INFORMATION: / Ceres Seq. ID 1499910

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1231:

Met	Ile	Ser	Met	Leu	Pro	Asp	Leu	Tyr	Ile	Pro	Phe	Met	Ala	Phe	Gly
1			5					10						15	
Thr	Tyr	Val	Val	Leu	Ala	Gly	Leu	Ser	Leu	Gly	Leu	Asn	Gly	Lys	Phe
			20					25					30		
Thr	Pro	Glu	Ala	Leu	Asn	Trp	Leu	Phe	Val	Lys	Gly	Leu	Val	Gly	Trp
			35					40					45		
Phe	Leu	Gln	Val	Met	Leu	Leu	Lys	Val	Thr	Leu	Leu	Ser	Leu	Gly	Ser
			50				55				60				
Gly	Glu	Ala	Pro	Leu	Leu	Asp	Ile	Val	Ala	Tyr	Gly	Gly	Tyr	Ala	Phe
65					70				75					80	
Ala	Gly	Leu	Cys	Leu	Ala	Gly	Phe	Ala	Lys	Ile	Met	Trp	Gly	Tyr	Ser
			85						90					95	
Tyr	Tyr	Ala	Leu	Met	Pro	Trp	Thr	Cys	Leu	Cys	Thr	Gly	Ile	Phe	Leu
			100					105					110		
Val	Lys	Thr	Met	Lys	Arg	Val	Leu	Phe	Ala	Glu	Val	Arg	Ser	Tyr	Asp
			115				120					125			
Ser	Ser	Lys	His	His	Tyr	Leu	Leu	Phe	Leu	Ala	Leu	Val	Gln	Phe	
			130			135				140					
Pro	Leu	Leu	Ile	Trp	Leu	Gly	Asn	Ile	Ser	Val	Asn	Trp	Leu	Leu	
145					150					155					

(2) INFORMATION FOR SEQ ID NO:1232:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 156 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..156

(D) OTHER INFORMATION: / Ceres Seq. ID 1499911

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1232:

```
Met Leu Pro Asp Leu Tyr Ile Pro Phe Met Ala Phe Gly Thr Tyr Val
1      5      10      15
Val Leu Ala Gly Leu Ser Leu Gly Leu Asn Gly Lys Phe Thr Pro Glu
      20      25      30
Ala Leu Asn Trp Leu Phe Val Lys Gly Leu Val Gly Trp Phe Leu Gln
      35      40      45
Val Met Leu Leu Lys Val Thr Leu Leu Ser Leu Gly Ser Gly Glu Ala
      50      55      60
Pro Leu Leu Asp Ile Val Ala Tyr Gly Gly Tyr Ala Phe Ala Gly Leu
65      70      75      80
Cys Leu Ala Gly Phe Ala Lys Ile Met Trp Gly Tyr Ser Tyr Tyr Ala
      85      90      95
Leu Met Pro Trp Thr Cys Leu Cys Thr Gly Ile Phe Leu Val Lys Thr
      100     105     110
Met Lys Arg Val Leu Phe Ala Glu Val Arg Ser Tyr Asp Ser Ser Lys
      115     120     125
His His Tyr Leu Leu Leu Phe Leu Ala Leu Val Gln Phe Pro Leu Leu
      130     135     140
Ile Trp Leu Gly Asn Ile Ser Val Asn Trp Leu Leu
145      150      155
```

(2) INFORMATION FOR SEQ ID NO:1233:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 147 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..147

(D) OTHER INFORMATION: / Ceres Seq. ID 1499912

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1233:

```
Met Ala Phe Gly Thr Tyr Val Val Leu Ala Gly Leu Ser Leu Gly Leu
1      5      10      15
Asn Gly Lys Phe Thr Pro Glu Ala Leu Asn Trp Leu Phe Val Lys Gly
      20      25      30
Leu Val Gly Trp Phe Leu Gln Val Met Leu Leu Lys Val Thr Leu Leu
      35      40      45
Ser Leu Gly Ser Gly Glu Ala Pro Leu Leu Asp Ile Val Ala Tyr Gly
      50      55      60
Gly Tyr Ala Phe Ala Gly Leu Cys Leu Ala Gly Phe Ala Lys Ile Met
65      70      75      80
Trp Gly Tyr Ser Tyr Tyr Ala Leu Met Pro Trp Thr Cys Leu Cys Thr
      85      90      95
Gly Ile Phe Leu Val Lys Thr Met Lys Arg Val Leu Phe Ala Glu Val
      100     105     110
Arg Ser Tyr Asp Ser Ser Lys His His Tyr Leu Leu Leu Phe Leu Ala
      115     120     125
Leu Val Gln Phe Pro Leu Leu Ile Trp Leu Gly Asn Ile Ser Val Asn
130      135      140
Trp Leu Leu
145
```

(2) INFORMATION FOR SEQ ID NO:1234:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 619 base pairs

(B) TYPE: nucleic acid

```

      (C) STRANDEDNESS: single
      (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
      (A) NAME/KEY: -
      (B) LOCATION: 1..619
      (D) OTHER INFORMATION: / Ceres Seq. ID 1499924

```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1234:							
atttccggcg	actgtgaatt	atgtggtcgg	cgacgttatc	tttcccttct	tttgtggctt		60
cttcattctt	tctaccta	tacaggaacc	gtaggtttcc	aaagattaaa	gcttcgctct		120
ttaattaccc	tctagcgcgc	aaaatcatgg	tcagaaattt	accgttttct	mcaagtgaag		180
atttttctaaa	gagagagt	tcagcttttg	gagagatagc	tgaagtgaa	cttatcaaa		240
attaggcaat	gcagagatca	aaaggttatg	ctttttattca	attcacgtct	caagatgatg		300
cttttcttgc	catagagacc	atggaccgtc	ggatgtacaa	tggaagaatg	atttatatatg		360
acattgcgaa	acccggtaaa	cgtgatttcc	aaggactacc	gaggacttct	gggtccccctg		420
agaagtcgga	tgtgccagaa	gaagccgcta	atgatgaggt	tgctgattgc	tggtattagt		480
tgttagtatc	aagctcacca	aactgtaact	gaacttgcat	aaatcagatg	tcaaattatg		540
cttcttatta	ggaatttgat	caatgtgaag	aatggtgttt	actgataaac	aattattgac		600
acggttccag	ttacagctc						

(2) INFORMATION FOR SEQ ID NO:1235:

```
(i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 152 amino acids
    (B) TYPE: amino acid
    (C) STRANDEDNESS:
    (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
    (A) NAME/KEY: peptide
    (B) LOCATION: 1..152
    (D) OTHER INFORMATION: / Ceres Seq. ID 1499925
```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1235:

[illegible]

(2) INFORMATION FOR SEQ ID NO:1236:

```

(i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 110 amino acids
    (B) TYPE: amino acid
    (C) STRANDEDNESS:
    (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
    (A) NAME/KEY: peptide
    (B) LOCATION: 1..110

```


(D) OTHER INFORMATION: / Ceres Seq. ID 1499926

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1236:

Met Val Arg Asn Leu Pro Phe Ser Xaa Ser Glu Asp Phe Leu Lys Arg
1 5 10 15
Glu Phe Ser Ala Phe Gly Glu Ile Ala Glu Val Lys Leu Ile Lys Asp
20 25 30
Glu Ala Met Gln Arg Ser Lys Gly Tyr Ala Phe Ile Gln Phe Thr Ser
35 40 45
Gln Asp Asp Ala Phe Leu Ala Ile Glu Thr Met Asp Arg Arg Met Tyr
50 55 60
Asn Gly Arg Met Ile Tyr Ile Asp Ile Ala Lys Pro Gly Lys Arg Asp
65 70 75 80
Phe Gln Gly Leu Pro Arg Thr Ser Gly Pro Pro Glu Lys Ser Asp Val
85 90 95
Pro Glu Glu Ala Ala Asn Asp Glu Val Ala Asp Cys Trp Tyr
100 105 110

(2) INFORMATION FOR SEQ ID NO:1237:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 76 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..76

(D) OTHER INFORMATION: / Ceres Seq. ID 1499927

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1237:

Met Gln Arg Ser Lys Gly Tyr Ala Phe Ile Gln Phe Thr Ser Gln Asp
1 5 10 15
Asp Ala Phe Leu Ala Ile Glu Thr Met Asp Arg Arg Met Tyr Asn Gly
20 25 30
Arg Met Ile Tyr Ile Asp Ile Ala Lys Pro Gly Lys Arg Asp Phe Gln
35 40 45
Gly Leu Pro Arg Thr Ser Gly Pro Pro Glu Lys Ser Asp Val Pro Glu
50 55 60
Glu Ala Ala Asn Asp Glu Val Ala Asp Cys Trp Tyr
65 70 75

(2) INFORMATION FOR SEQ ID NO:1238:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 622 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..622

(D) OTHER INFORMATION: / Ceres Seq. ID 1499928

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1238:

acttcaaatac	cataatcgct	ctacttctct	ctctctcttag	attcgaaaaa	atggcgaaac	60
tggatgatgtt	gttggttctc	tgtatcttac	cggcgatagc	catggcgagg	aggaggggaa	120
atatttgaaa	gaatacaatg	gtggttcaag	gtagcaccta	ctgtgacatt	tgcaaattcg	180
gcttcgagac	tcctgaatcc	tcctacttca	tccccgggtg	aacgggtgaag	ctatcatgca	240
aagacaggaa	gacaatggaa	gaggttttaca	cagacaaaag	tgtatcagac	aaagaaggaa	300
agtataagtt	cattgtccac	gacgatcaga	catgctaaca	acatgggatt	tgagaaagaa	360
gtgagtgtatg	tgttctgctc	tgttttgttt	cagaagtata	tggttgatga	agatgaggat	420
gatattaaaa	accatctcta	atctctctgt	ttaatcttat	gatctgctgt	tttcttcatt	480
aatgagtttc	gagttatgga	agagatatat	tctgtatttg	tttgattact	tatttggtgt	540
ctttagagat	gttgactctg	gtgatcggat	aactatctgt	ttgtgtaagc	ttcttatata	600
ttgatgtgtc	atttccttgc	tt				

(2) INFORMATION FOR SEQ ID NO:1239:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 111 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..111
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499929

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1239:

Phe	Lys	Ser	Ile	Ile	Ala	Leu	Leu	Leu	Ser	Arg	Phe	Glu	Lys
1				5				10				15	
Met	Ala	Lys	Leu	Val	Met	Leu	Leu	Val	Cys	Ile	Leu	Pro	Ala
			20					25				30	Ile
Ala	Met	Ala	Ala	Arg	Arg	Gly	Asn	Ile	Gly	Lys	Asn	Thr	Met
			35				40				45	Val	Val
Gln	Gly	Ser	Thr	Tyr	Cys	Asp	Ile	Cys	Lys	Phe	Gly	Phe	Glu
			50			55				60		Thr	Pro
Glu	Ser	Ser	Tyr	Phe	Ile	Pro	Gly	Ala	Thr	Val	Lys	Leu	Ser
65					70					75			Cys
Asp	Arg	Lys	Thr	Met	Glu	Glu	Val	Tyr	Thr	Asp	Lys	Ala	Val
				85					90				Ser
												95	Asp
Lys	Glu	Gly	Lys	Tyr	Lys	Phe	Ile	Val	His	Asp	Asp	Gln	Thr
								100					Cys
									105				
												110	

(2) INFORMATION FOR SEQ ID NO:1240:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 95 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..95
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499930

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1240:

Met	Ala	Lys	Leu	Val	Met	Leu	Leu	Val	Leu	Cys	Ile	Leu	Pro	Ala	Ile
1					5				10					15	
Ala	Met	Ala	Ala	Arg	Arg	Gly	Asn	Ile	Gly	Lys	Asn	Thr	Met	Val	Val
			20					25					30		
Gln	Gly	Ser	Thr	Tyr	Cys	Asp	Ile	Cys	Lys	Phe	Gly	Phe	Glu	Thr	Pro
			35				40					45			
Glu	Ser	Ser	Tyr	Phe	Ile	Pro	Gly	Ala	Thr	Val	Lys	Leu	Ser	Cys	Lys
			50				55				60				
Asp	Arg	Lys	Thr	Met	Glu	Glu	Val	Tyr	Thr	Asp	Lys	Ala	Val	Ser	Asp
65					70					75				80	
Lys	Glu	Gly	Lys	Tyr	Lys	Phe	Ile	Val	His	Asp	Asp	Gln	Thr	Cys	
					85				90					95	

(2) INFORMATION FOR SEQ ID NO:1241:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 90 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..90
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499931

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1241:

Met Leu Leu Val Leu Cys Ile Leu Pro Ala Ile Ala Met Ala Ala Arg
1 5 10 15
Arg Gly Asn Ile Gly Lys Asn Thr Met Val Val Gln Gly Ser Thr Tyr
20 25 30
Cys Asp Ile Cys Lys Phe Gly Phe Glu Thr Pro Glu Ser Ser Tyr Phe
35 40 45
Ile Pro Gly Ala Thr Val Lys Leu Ser Cys Lys Asp Arg Lys Thr Met
50 55 60
Glu Glu Val Tyr Thr Asp Lys Ala Val Ser Asp Lys Glu Gly Lys Tyr
65 70 75 80
Lys Phe Ile Val His Asp Asp Gln Thr Cys
85 90

(2) INFORMATION FOR SEQ ID NO:1242:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1010 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1010
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499935

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1242:

acaatcaaaag atgacactag ctagacattt tcgtttttcat ctccccacga atcaaaaagat 60
ggctttttgcc attgcttctg ctctcacttc cacactcaca ttatccacga gcagagtcaca 120
aaatcctacc cagagaagac cacatgtagc gtccacatca tccaccgggtg gaagattaat 180
gagagagcgc ttggtggttg ttcgtgccgg caaagaagtt tctagcgtct gtgaaccact 240
tcctccggag cgctccttat ggttccttgg tagctctcca cctgaatggc tcgatggcag 300
cttacctggt gatttcggtt tcgatacctct cggtttaggg tctggatccg gacaccctca 360
aatggtttgc acaagctgag cttatacata gccggtgggc aatgctggcc gtgaccggta 420
tcataatacc agaatgtmhh cgagcggwta ggtttcattg aaaatttctc atggtatgac 480
gcagggtctc gtgagtactt bgcggattcc actacgctgt ttgtggctca aatggtttta 540
atgggctggg cagaaggtak aagatgggct gatttgatta aaccgggggtc tgttgacata 600
gaaccaaagt acccgcataa agtaaatcct aaaccggatg ttggttacc tggaggtttg 660
tggttcgatt ttatgatgtg ggggagaggt tctcctgaac cggtaatggt tttgaggact 720
aaagagatta agaacggacg gctcgcgatg cttgctttcc ttgggttctg tttccaagct 780
acctacacta gccaaatcc aattgagaat ctcatggctc atctggctga tcttggtcat 840
tgcaacgtct tttcggcatt tacatcacat taatgaggat tagcttgggg cgaatataat 900
attttttata tatttatgga tgttgaactt ttgtatagtg tcaactcgccg ttgttacaac 960
ttctgcttac ttaattaaca tgtaaaatat attatatata tatgtagaag

(2) INFORMATION FOR SEQ ID NO:1243:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 125 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..125
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499936

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1243:

Gln Ser Lys Met Thr Leu Ala Arg His Phe Arg Phe His Leu Pro Thr
1 5 10 15
Asn Gln Lys Met Ala Phe Ala Ile Ala Ser Ala Leu Thr Ser Thr Leu
20 25 30
Thr Leu Ser Thr Ser Arg Val Gln Asn Pro Thr Gln Arg Arg Pro His
35 40 45
Val Ala Ser Thr Ser Ser Thr Gly Gly Arg Leu Met Arg Glu Arg Leu

50	55	60
Val Val Val Arg Ala Gly Lys Glu Val Ser Ser Val Cys Glu Pro Leu		
65	70	75
Pro Pro Asp Arg Pro Leu Trp Phe Pro Gly Ser Ser Pro Pro Glu Trp		80
	85	90
Leu Asp Gly Ser Leu Pro Gly Asp Phe Gly Phe Asp Pro Leu Gly Leu		95
	100	105
Gly Ser Gly Ser Gly His Pro Gln Met Val Cys Thr Ser		110
	115	120
		125

(2) INFORMATION FOR SEQ ID NO:1244:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 122 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..122

(D) OTHER INFORMATION: / Ceres Seq. ID 1499937

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1244:

Met Thr Leu Ala Arg His Phe Arg Phe His Leu Pro Thr Asn Gln Lys		
1	5	10
		15
Met Ala Phe Ala Ile Ala Ser Ala Leu Thr Ser Thr Leu Thr Leu Ser		
	20	25
		30
Thr Ser Arg Val Gln Asn Pro Thr Gln Arg Arg Pro His Val Ala Ser		
	35	40
		45
Thr Ser Ser Thr Gly Gly Arg Leu Met Arg Glu Arg Leu Val Val Val		
	50	55
		60
Arg Ala Gly Lys Glu Val Ser Ser Val Cys Glu Pro Leu Pro Pro Asp		
65	70	75
		80
Arg Pro Leu Trp Phe Pro Gly Ser Ser Pro Pro Glu Trp Leu Asp Gly		
	85	90
		95
Ser Leu Pro Gly Asp Phe Gly Phe Asp Pro Leu Gly Leu Gly Ser Gly		
	100	105
		110
Ser Gly His Pro Gln Met Val Cys Thr Ser		
	115	120

(2) INFORMATION FOR SEQ ID NO:1245:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 113 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..113

(D) OTHER INFORMATION: / Ceres Seq. ID 1499938

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1245:

Met Val Leu Met Gly Trp Ala Glu Gly Xaa Arg Trp Ala Asp Leu Ile		
1	5	10
		15
Lys Pro Gly Ser Val Asp Ile Glu Pro Lys Tyr Pro His Lys Val Asn		
	20	25
		30
Pro Lys Pro Asp Val Gly Tyr Pro Gly Gly Leu Trp Phe Asp Phe Met		
	35	40
		45
Met Trp Gly Arg Gly Ser Pro Glu Pro Val Met Val Leu Arg Thr Lys		
	50	55
		60
Glu Ile Lys Asn Gly Arg Leu Ala Met Leu Ala Phe Leu Gly Phe Cys		
65	70	75
		80
Phe Gln Ala Thr Tyr Thr Ser Gln Asp Pro Ile Glu Asn Leu Met Ala		
	85	90
		95

His Leu Ala Asp Pro Gly His Cys Asn Val Phe Ser Ala Phe Thr Ser
100 105 110
His

(2) INFORMATION FOR SEQ ID NO:1246:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 568 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..568
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499939

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1246:

acggatccac	cggagagatc	tggctgcca	ttccctcgct	ccttcccgtg	aaccacaaac	60
ctaacgcgga	rmggcgcggg	ccggcmrccg	ggcgaggtgc	gcgtagctgc	cgctgattgt	120
cgccggatcc	atccaccatg	ggcggtggca	acggccagaa	gtccaagatg	gcccgcgagc	180
gcaacttgga	gaagaacaag	ggggccaag	ggagccagct	cgagaccaac	aagaaggcca	240
tgagcatcca	gtgcaaagt	tgcattgcaa	cattcatgtg	taccacgayt	gaagtgaagt	300
gccgggagca	cgccgaggcc	aagcatccca	agacagacgt	gtaccagtgc	ttccccatc	360
tgaagaagt	aaaggcctga	acttagcaac	cagtgtctgt	ttggctacta	cgatcggggc	420
agggggcggt	ccttgtgttg	aggggtgttc	ttccgtgtta	tcttcccgtc	agtcatgcgt	480
cctgtcctat	gttaacctac	ataagaaagc	gatgtggtgt	ccacttctag	tgaactact	540
gtctgtgtgt	aaaacctggt	tggtttcg				

(2) INFORMATION FOR SEQ ID NO:1247:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 122 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..122
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499940

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1247:

Gly	Ser	Thr	Gly	Glu	Ile	Trp	Ser	Ala	Ile	Pro	Ser	Leu	Leu	Pro	Val
1			5					10					15		
Asn	His	Lys	Pro	Asn	Ala	Xaa	Xaa	Arg	Gly	Pro	Xaa	Xaa	Gly	Arg	Gly
		20						25					30		
Ala	Arg	Ser	Cys	Arg	Arg	Leu	Ser	Pro	Asp	Pro	Ser	Thr	Met	Gly	Gly
		35					40					45			
Gly	Asn	Gly	Gln	Lys	Ser	Lys	Met	Ala	Arg	Glu	Arg	Asn	Leu	Glu	Lys
		50				55					60				
Asn	Lys	Gly	Ala	Lys	Gly	Ser	Gln	Leu	Glu	Thr	Asn	Lys	Lys	Ala	Met
65				70					75					80	
Ser	Ile	Gln	Cys	Lys	Val	Cys	Met	Gln	Thr	Phe	Met	Cys	Thr	Thr	Xaa
		85						90						95	
Glu	Val	Lys	Cys	Arg	Glu	His	Ala	Glu	Ala	Lys	His	Pro	Lys	Thr	Asp
		100					105						110		
Val	Tyr	Gln	Cys	Phe	Pro	His	Leu	Lys	Lys						
		115					120								

(2) INFORMATION FOR SEQ ID NO:1248:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 77 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

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(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..77

(D) OTHER INFORMATION: / Ceres Seq. ID 1499941

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1248:

```
Met Gly Gly Gly Asn Gly Gln Lys Ser Lys Met Ala Arg Glu Arg Asn
1          5          10          15
Leu Glu Lys Asn Lys Gly Ala Lys Gly Ser Gln Leu Glu Thr Asn Lys
20          25          30
Lys Ala Met Ser Ile Gln Cys Lys Val Cys Met Gln Thr Phe Met Cys
35          40          45
Thr Thr Xaa Glu Val Lys Cys Arg Glu His Ala Glu Ala Lys His Pro
50          55          60
Lys Thr Asp Val Tyr Gln Cys Phe Pro His Leu Lys Lys
65          70          75
```

(2) INFORMATION FOR SEQ ID NO:1249:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 67 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..67

(D) OTHER INFORMATION: / Ceres Seq. ID 1499942

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1249:

```
Met Ala Arg Glu Arg Asn Leu Glu Lys Asn Lys Gly Ala Lys Gly Ser
1          5          10          15
Gln Leu Glu Thr Asn Lys Lys Ala Met Ser Ile Gln Cys Lys Val Cys
20          25          30
Met Gln Thr Phe Met Cys Thr Thr Xaa Glu Val Lys Cys Arg Glu His
35          40          45
Ala Glu Ala Lys His Pro Lys Thr Asp Val Tyr Gln Cys Phe Pro His
50          55          60
Leu Lys Lys
65
```

(2) INFORMATION FOR SEQ ID NO:1250:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 531 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..531

(D) OTHER INFORMATION: / Ceres Seq. ID 1499943

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1250:

```
aacaacattc aaaagctatt agcgattctt cttctctctg attcaatctt cttcatagtt      60
tctaagctct caaattcttg acgaagcaat ggctcgtagc aagcaaactg caagaaaatc      120
acacggagga aaagctccga ggactctgct cgctaccaag gcggcgagga aatctgcgcc      180
gactactgga ggagtcaaga aacctcaccg ttaccgtccc ggaaccgtcg ctcttcgtga      240
gattcgtaaa taccagaaga gcacagagtt gttgatccgt aaacttcctt ttcaacgtct      300
tgttcgtgaa atcgctcaag attacaagac ggatctgaga ttccagagcc atgcgntggt      360
agctcttcaa gaagctgctg aagcatatct gggttggttg tttgaagata caaatctgtg      420
tgccattcat gccaaagagg ttacgatcat gcctaaagat gttcaattgg cagaaggatt      480
cgtggagagc gtgcttagat tcgaattaaa atcatcaact attattctat t
```

(2) INFORMATION FOR SEQ ID NO:1251:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 147 amino acids

(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..147
(D) OTHER INFORMATION: / Ceres Seq. ID 1499944
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1251:
Met Ala Arg Thr Lys Gln Thr Ala Arg Lys Ser His Gly Gly Lys Ala
1 5 10 15
Pro Arg Thr Leu Leu Ala Thr Lys Ala Ala Arg Lys Ser Ala Pro Thr
20 25 30
Thr Gly Gly Val Lys Lys Pro His Arg Tyr Arg Pro Gly Thr Val Ala
35 40 45
Leu Arg Glu Ile Arg Lys Tyr Gln Lys Ser Thr Glu Leu Leu Ile Arg
50 55 60
Lys Leu Pro Phe Gln Arg Leu Val Arg Glu Ile Ala Gln Asp Tyr Lys
65 70 75 80
Thr Asp Leu Arg Phe Gln Ser His Ala Xaa Leu Ala Leu Gln Glu Ala
85 90 95
Ala Glu Ala Tyr Leu Val Gly Leu Phe Glu Asp Thr Asn Leu Cys Ala
100 105 110
Ile His Ala Lys Arg Val Thr Ile Met Pro Lys Asp Val Gln Leu Ala
115 120 125
Glu Gly Phe Val Glu Ser Val Leu Arg Phe Glu Leu Lys Ser Ser Thr
130 135 140
Ile Ile Leu
145

(2) INFORMATION FOR SEQ ID NO:1252:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1308 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -
(B) LOCATION: 1..1308
(D) OTHER INFORMATION: / Ceres Seq. ID 1499960

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1252:

atattttcat	ataaataaac	ctctcaacct	ccacactttc	tcacccatca	cacaatcctc	60
aaaacagagt	aacccaaaaa	acagagcaat	ctctaaaaaa	tctcaagaaa	cctcactaaa	120
atgggttcaa	cggcggagac	acaattaact	ccggtgcaag	tcaccgacga	cgaagctgcc	180
ctcttcgcca	tgcaactagc	cagtgccttc	gttcttccga	tggttttaaa	atccgcctta	240
gagcttgacc	ttcttgagat	tatggccaag	aatggttctc	ccatgtctcc	taccgagatc	300
gcttctaaac	ttccgaccaa	aaacctgaa	gctccggtca	tgctcgaccg	tatcctccgt	360
cttcttacgt	cttactccgt	cttaacctgc	tccaaccgta	aactttccgg	tgatggcggt	420
gaacggattt	acgggcttgg	tccggtttgc	aagtatttga	ccaagaacga	agatgggtgt	480
tccattgctg	ctctttgtct	tatgaaccaa	gacaaggttc	tcattggaaag	ctggtaccat	540
ttgaaggatg	caattcttga	tggtgggatt	ccattcaaca	aggcttatgg	aatgagcgcg	600
ttcgagtacc	acgggactga	cctagatttc	aacaaggctc	ttaacaatgg	aatgtctaac	660
cattccacaa	tcaccatgaa	gaagattctt	gagacctata	agggttttga	agggttgact	720
tctttgggtg	atgttggtgg	tggcattggg	gctacactca	aaatgattgt	ctccaagtac	780
cctaattctta	aaggcatcaa	ctttgatctc	ccacatgtca	ttgaagatgc	tccttctcat	840
cctggtattg	agcatgttgg	aggagatatg	tttgtaagtg	tccctaaagg	tgatgccata	900
ttcatgaagt	ggatatgtca	tgactggagt	gacgaacatt	gcgtgaaatt	cttgaaaaac	960
tgctacagat	cacttcacga	ggatggaaaa	gtgatattag	cagagtgtat	acttccagag	1020
acaccagact	caagcctctc	aaccaaacaa	gtagtccatg	tcgattgcat	tatgttggct	1080
cacaatcccg	gaggcaaaga	acgaaccgag	aaagagtttg	aggcattagc	caaagcatca	1140
ggcttcaagg	gcatacaagt	tgtctgcgac	gcttttggtg	ttaaccttat	tgagttactc	1200

aagaagctct aaaaacaaac aatgttccta tgaagatgat ttatatgtaa acattatctc 1260
atatctcctt ccacggttcc aaaactatgc tgtttaataa tgggtttt

(2) INFORMATION FOR SEQ ID NO:1253:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 363 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..363
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499961

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1253:

Met	Gly	Ser	Thr	Ala	Glu	Thr	Gln	Leu	Thr	Pro	Val	Gln	Val	Thr	Asp
1				5				10					15		
Asp	Glu	Ala	Ala	Leu	Phe	Ala	Met	Gln	Leu	Ala	Ser	Ala	Ser	Val	Leu
			20					25					30		
Pro	Met	Ala	Leu	Lys	Ser	Ala	Leu	Glu	Leu	Asp	Leu	Leu	Glu	Ile	Met
			35					40					45		
Ala	Lys	Asn	Gly	Ser	Pro	Met	Ser	Pro	Thr	Glu	Ile	Ala	Ser	Lys	Leu
			50					55				60			
Pro	Thr	Lys	Asn	Pro	Glu	Ala	Pro	Val	Met	Leu	Asp	Arg	Ile	Leu	Arg
65					70					75				80	
Leu	Leu	Thr	Ser	Tyr	Ser	Val	Leu	Thr	Cys	Ser	Asn	Arg	Lys	Leu	Ser
				85						90				95	
Gly	Asp	Gly	Val	Glu	Arg	Ile	Tyr	Gly	Leu	Gly	Pro	Val	Cys	Lys	Tyr
			100					105					110		
Leu	Thr	Lys	Asn	Glu	Asp	Gly	Val	Ser	Ile	Ala	Ala	Leu	Cys	Leu	Met
			115					120					125		
Asn	Gln	Asp	Lys	Val	Leu	Met	Glu	Ser	Trp	Tyr	His	Leu	Lys	Asp	Ala
			130					135				140			
Ile	Leu	Asp	Gly	Gly	Ile	Pro	Phe	Asn	Lys	Ala	Tyr	Gly	Met	Ser	Ala
145					150					155				160	
Phe	Glu	Tyr	His	Gly	Thr	Asp	Pro	Arg	Phe	Asn	Lys	Val	Phe	Asn	Asn
				165						170				175	
Gly	Met	Ser	Asn	His	Ser	Thr	Ile	Thr	Met	Lys	Lys	Ile	Leu	Glu	Thr
			180					185					190		
Tyr	Lys	Gly	Phe	Glu	Gly	Leu	Thr	Ser	Leu	Val	Asp	Val	Gly	Gly	Gly
			195					200				205			
Ile	Gly	Ala	Thr	Leu	Lys	Met	Ile	Val	Ser	Lys	Tyr	Pro	Asn	Leu	Lys
			210					215				220			
Gly	Ile	Asn	Phe	Asp	Leu	Pro	His	Val	Ile	Glu	Asp	Ala	Pro	Ser	His
225					230					235				240	
Pro	Gly	Ile	Glu	His	Val	Gly	Gly	Asp	Met	Phe	Val	Ser	Val	Pro	Lys
				245						250				255	
Gly	Asp	Ala	Ile	Phe	Met	Lys	Trp	Ile	Cys	His	Asp	Trp	Ser	Asp	Glu
			260					265					270		
His	Cys	Val	Lys	Phe	Leu	Lys	Asn	Cys	Tyr	Glu	Ser	Leu	Pro	Glu	Asp
			275					280					285		
Gly	Lys	Val	Ile	Leu	Ala	Glu	Cys	Ile	Leu	Pro	Glu	Thr	Pro	Asp	Ser
			290					295				300			
Ser	Leu	Ser	Thr	Lys	Gln	Val	Val	His	Val	Asp	Cys	Ile	Met	Leu	Ala
305					310					315				320	
His	Asn	Pro	Gly	Gly	Lys	Glu	Arg	Thr	Glu	Lys	Glu	Phe	Glu	Ala	Leu
				325						330				335	
Ala	Lys	Ala	Ser	Gly	Phe	Lys	Gly	Ile	Lys	Val	Val	Cys	Asp	Ala	Phe
			340					345					350		
Gly	Val	Asn	Leu	Ile	Glu	Leu	Leu	Lys	Lys	Leu					
			355					360							

(2) INFORMATION FOR SEQ ID NO:1254:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 340 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..340
 (D) OTHER INFORMATION: / Ceres Seq. ID 1499962
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1254:

Met Gln Leu Ala Ser Ala Ser Val Leu Pro Met Ala Leu Lys Ser Ala
1 5 10 15
Leu Glu Leu Asp Leu Leu Glu Ile Met Ala Lys Asn Gly Ser Pro Met
 20 25 30
Ser Pro Thr Glu Ile Ala Ser Lys Leu Pro Thr Lys Asn Pro Glu Ala
 35 40 45
Pro Val Met Leu Asp Arg Ile Leu Arg Leu Leu Thr Ser Tyr Ser Val
 50 55 60
Leu Thr Cys Ser Asn Arg Lys Leu Ser Gly Asp Gly Val Glu Arg Ile
65 70 75 80
Tyr Gly Leu Gly Pro Val Cys Lys Tyr Leu Thr Lys Asn Glu Asp Gly
 85 90 95
Val Ser Ile Ala Ala Leu Cys Leu Met Asn Gln Asp Lys Val Leu Met
 100 105 110
Glu Ser Trp Tyr His Leu Lys Asp Ala Ile Leu Asp Gly Gly Ile Pro
 115 120 125
Phe Asn Lys Ala Tyr Gly Met Ser Ala Phe Glu Tyr His Gly Thr Asp
130 135 140
Pro Arg Phe Asn Lys Val Phe Asn Asn Gly Met Ser Asn His Ser Thr
145 150 155 160
Ile Thr Met Lys Lys Ile Leu Glu Thr Tyr Lys Gly Phe Glu Gly Leu
 165 170 175
Thr Ser Leu Val Asp Val Gly Gly Gly Ile Gly Ala Thr Leu Lys Met
 180 185 190
Ile Val Ser Lys Tyr Pro Asn Leu Lys Gly Ile Asn Phe Asp Leu Pro
 195 200 205
His Val Ile Glu Asp Ala Pro Ser His Pro Gly Ile Glu His Val Gly
210 215 220
Gly Asp Met Phe Val Ser Val Pro Lys Gly Asp Ala Ile Phe Met Lys
225 230 235 240
Trp Ile Cys His Asp Trp Ser Asp Glu His Cys Val Lys Phe Leu Lys
 245 250 255
Asn Cys Tyr Glu Ser Leu Pro Glu Asp Gly Lys Val Ile Leu Ala Glu
 260 265 270
Cys Ile Leu Pro Glu Thr Pro Asp Ser Ser Leu Ser Thr Lys Gln Val
 275 280 285
Val His Val Asp Cys Ile Met Leu Ala His Asn Pro Gly Gly Lys Glu
290 295 300
Arg Thr Glu Lys Glu Phe Glu Ala Leu Ala Lys Ala Ser Gly Phe Lys
305 310 315 320
Gly Ile Lys Val Val Cys Asp Ala Phe Gly Val Asn Leu Ile Glu Leu
 325 330 335
Leu Lys Lys Leu
 340

(2) INFORMATION FOR SEQ ID NO:1255:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 330 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..330

(D) OTHER INFORMATION: / Ceres Seq. ID 1499963

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1255:

Met	Ala	Leu	Lys	Ser	Ala	Leu	Glu	Leu	Asp	Leu	Leu	Glu	Ile	Met	Ala	
1				5				10						15		
Lys	Asn	Gly	Ser	Pro	Met	Ser	Pro	Thr	Glu	Ile	Ala	Ser	Lys	Leu	Pro	
			20					25					30			
Thr	Lys	Asn	Pro	Glu	Ala	Pro	Val	Met	Leu	Asp	Arg	Ile	Leu	Arg	Leu	
			35				40						45			
Leu	Thr	Ser	Tyr	Ser	Val	Leu	Thr	Cys	Ser	Asn	Arg	Lys	Leu	Ser	Gly	
	50					55					60					
Asp	Gly	Val	Glu	Arg	Ile	Tyr	Gly	Leu	Gly	Pro	Val	Cys	Lys	Tyr	Leu	
65					70					75					80	
Thr	Lys	Asn	Glu	Asp	Gly	Val	Ser	Ile	Ala	Ala	Leu	Cys	Leu	Met	Asn	
				85					90					95		
Gln	Asp	Lys	Val	Leu	Met	Glu	Ser	Trp	Tyr	His	Leu	Lys	Asp	Ala	Ile	
			100					105					110			
Leu	Asp	Gly	Gly	Ile	Pro	Phe	Asn	Lys	Ala	Tyr	Gly	Met	Ser	Ala	Phe	
		115					120					125				
Glu	Tyr	His	Gly	Thr	Asp	Pro	Arg	Phe	Asn	Lys	Val	Phe	Asn	Asn	Gly	
	130					135					140					
Met	Ser	Asn	His	Ser	Thr	Ile	Thr	Met	Lys	Lys	Ile	Leu	Glu	Thr	Tyr	
145					150					155					160	
Lys	Gly	Phe	Glu	Gly	Leu	Thr	Ser	Leu	Val	Asp	Val	Gly	Gly	Gly	Ile	
			165						170					175		
Gly	Ala	Thr	Leu	Lys	Met	Ile	Val	Ser	Lys	Tyr	Pro	Asn	Leu	Lys	Gly	
			180					185					190			
Ile	Asn	Phe	Asp	Leu	Pro	His	Val	Ile	Glu	Asp	Ala	Pro	Ser	His	Pro	
		195					200					205				
Gly	Ile	Glu	His	Val	Gly	Gly	Asp	Met	Phe	Val	Ser	Val	Pro	Lys	Gly	
	210					215					220					
Asp	Ala	Ile	Phe	Met	Lys	Trp	Ile	Cys	His	Asp	Trp	Ser	Asp	Glu	His	
225					230					235					240	
Cys	Val	Lys	Phe	Leu	Lys	Asn	Cys	Tyr	Glu	Ser	Leu	Pro	Glu	Asp	Gly	
			245						250					255		
Lys	Val	Ile	Leu	Ala	Glu	Cys	Ile	Leu	Pro	Glu	Thr	Pro	Asp	Ser	Ser	
			260					265					270			
Leu	Ser	Thr	Lys	Gln	Val	Val	His	Val	Asp	Cys	Ile	Met	Leu	Ala	His	
	275						280					285				
Asn	Pro	Gly	Gly	Lys	Glu	Arg	Thr	Glu	Lys	Glu	Phe	Glu	Ala	Leu	Ala	
	290					295					300					
Lys	Ala	Ser	Gly	Phe	Lys	Gly	Ile	Lys	Val	Val	Cys	Asp	Ala	Phe	Gly	
305					310					315					320	
Val	Asn	Leu	Ile	Glu	Leu	Leu	Lys	Lys	Leu							
				325					330							

(2) INFORMATION FOR SEQ ID NO:1256:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 916 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..916

(D) OTHER INFORMATION: / Ceres Seq. ID 1499964

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1256:

acgaaagaag agaacaaaga agaaattttg aaaatagtga aaatggtaac cgtaagccaa

agtcacacga	cgacgtttct	cttcttcacc	acattttctct	tgatattcgg	atcaatctca	120
gccgtccgtt	tgcttccacg	accaaacact	acaacaacca	acgatctaga	tttcatccga	180
acaagctgca	acgtactctt	atatccagac	gtctgcttca	cgtcactctc	cggtacgcc	240
tctgccgttc	aagacagtcc	ggcgaggcta	gccaaagctcg	caatcggcgt	ttcactttaa	300
caagccaaat	ccactgcggc	ttttctctcc	aaactctcac	gctctgccgc	taaatactcc	360
ggtgatggcc	accaaacagc	ttccgccgta	atccgagact	gcgtttcgaa	cgtcgaagac	420
gcgngtggac	gagatgagag	gatctctccg	tcaactacgc	gacatgaacg	gcagaggagg	480
cggcacggca	gctcggagg	cggtagaaac	gtttagggtt	cagatgagta	acgtgcagac	540
gtggatgagt	gcagcattga	cggatgagga	cacgtgtacg	aatggatttg	aagatatgga	600
cgaaggagga	ttgattaaga	cgaccgtttg	tgatcggctc	gaggaagtga	agaggctaac	660
gagtaatgct	cttgcccttg	tcaacactta	cgccaacaat	ggagctccat	gaccatgaga	720
ccatgagacc	atgaggagtt	ttacttttga	tttaagtgtc	tctttatata	atttaataca	780
ttgtgggggt	taagttagag	ttatgtgtcg	atttcatcat	gttttacatt	tgtttttgta	840
tcacccgagt	ttcttatggt	taaagggttc	agagagatgt	tgtatctttg	atttactaat	900
caaactgcac	gatgat					

(2) INFORMATION FOR SEQ ID NO:1257:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 99 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..99
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499965

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1257:

Thr	Lys	Glu	Glu	Asn	Lys	Glu	Glu	Ile	Leu	Lys	Ile	Val	Lys	Met	Val
1				5				10						15	
Thr	Val	Ser	Gln	Ser	His	Thr	Thr	Thr	Phe	Leu	Phe	Phe	Thr	Thr	Phe
			20					25					30		
Leu	Leu	Ile	Phe	Gly	Ser	Ile	Ser	Ala	Val	Arg	Leu	Leu	Pro	Arg	Pro
			35					40					45		
Asn	Thr	Thr	Thr	Thr	Asn	Asp	Leu	Asp	Phe	Ile	Arg	Thr	Ser	Cys	Asn
			50			55				60					
Ala	Thr	Leu	Tyr	Pro	Asp	Val	Cys	Phe	Thr	Ser	Leu	Ser	Gly	Tyr	Ala
65					70					75				80	
Ser	Ala	Val	Gln	Asp	Ser	Pro	Ala	Arg	Leu	Ala	Lys	Leu	Ala	Ile	Gly
			85					90						95	
Val	Ser	Leu													

(2) INFORMATION FOR SEQ ID NO:1258:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 116 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..116
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499966

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1258:

Glu	Arg	Arg	Glu	Gln	Arg	Arg	Asn	Phe	Glu	Asn	Ser	Glu	Asn	Gly	Asn
1				5				10						15	
Arg	Lys	Pro	Lys	Ser	His	Asp	Asp	Val	Ser	Leu	Leu	His	His	Ile	Ser
			20					25					30		
Leu	Asp	Ile	Arg	Ile	Asn	Leu	Ser	Arg	Pro	Phe	Ala	Ser	Thr	Thr	Lys
			35					40					45		
His	Tyr	Asn	Asn	Gln	Arg	Ser	Arg	Phe	His	Pro	Asn	Lys	Leu	Gln	Arg
50						55					60				

Tyr Ser Ile Ser Arg Arg Leu Leu His Val Thr Leu Arg Leu Arg Leu
65 70 75 80
Cys Arg Ser Arg Gln Ser Gly Glu Ala Ser Gln Ala Arg Asn Arg Arg
85 90 95
Phe Thr Leu Thr Ser Gln Ile His Cys Gly Phe Ser Leu Gln Thr Leu
100 105 110
Thr Leu Cys Arg
115

(2) INFORMATION FOR SEQ ID NO:1259:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 92 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..92
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499967

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1259:

Met Arg Gly Ser Leu Arg Gln Leu Arg Asp Met Asn Gly Arg Gly Gly
1 5 10 15
Gly Thr Ala Ala Arg Arg Ser Val Glu Thr Phe Arg Phe Gln Met Ser
20 25 30
Asn Val Gln Thr Trp Met Ser Ala Ala Leu Thr Asp Glu Asp Thr Cys
35 40 45
Thr Asn Gly Phe Glu Asp Met Asp Glu Gly Gly Leu Ile Lys Thr Thr
50 55 60
Val Cys Asp Arg Leu Glu Glu Val Lys Arg Leu Thr Ser Asn Ala Leu
65 70 75 80
Ala Leu Val Asn Thr Tyr Ala Asn Asn Gly Ala Pro
85 90

(2) INFORMATION FOR SEQ ID NO:1260:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 257 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..257
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499968

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1260:

ctattgtgtt tgatcaggtt accaaatcca ttgaaggact gcttcctttg ccaaagatcc 60
ataacccaaa tgaccctcgg agaatcgagt ttaaagagct tgaagctgaa aaggcagtga 120
tcgatgtgaa agtcacact ttggtgcgag agctttgggc tggctcgggt tacttgatcc 180
tacagactgc ggggttcattg aggctaactg tttgggaact ctcgtgggac gtgatggagc 240
caatctggtt ctatgtc

(2) INFORMATION FOR SEQ ID NO:1261:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 85 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..85
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499969

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1261:

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Ile Val Phe Asp Gln Val Thr Lys Ser Ile Glu Gly Leu Leu Pro Leu
1 5 10 15
Pro Lys Ile His Asn Pro Asn Asp Pro Arg Arg Ile Glu Phe Lys Glu
20 25 30
Leu Glu Ala Glu Lys Ala Val Ile Asp Val Lys Ala His Thr Leu Val
35 40 45
Arg Glu Leu Trp Ala Gly Leu Gly Tyr Leu Ile Leu Gln Thr Ala Gly
50 55 60
Phe Met Arg Leu Thr Phe Trp Glu Leu Ser Trp Asp Val Met Glu Pro
65 70 75 80
Ile Cys Phe Tyr Val
85

(2) INFORMATION FOR SEQ ID NO:1262:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 573 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..573

(D) OTHER INFORMATION: / Ceres Seq. ID 1499970

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1262:

ggagaagacg tcgtgattat ccgagtagta gctcagattc cgaatcagaa tcggagtcgg	60
aatattctga ttctgaggag agtgagagtg aagatgagag aagaaggaag aagaggaaga	120
gaaaggagag ggaagaggaa gagaaagaga ggaagagaag gagaagagag aaagataaga	180
agaagaggaa caagtctgat aaagatggag ataagaagag gaaggagaag aagaagaaga	240
agtctgagaa agtgaagaaa ggagctgtta ctgaatcatg gggcaagtat ggaatcatca	300
gagaaactga tatgtggaat aaacgtccag agttcacagc atggttgctt gaagtaaaga	360
aggttaattt ggaaagcttg ccaccttggg aagagaagaa aatgtttaaa gattttatgg	420
aggatcataa tactggtaca tttacctcga aaaaatacta tgacattgat ggttactata	480
gacttaagtt ggaaaaagag atgaaaaagg gtttgaagaa agctgggatt agtgaacgta	540
ctgtgttcaa tgatgaggaa caacgccgac tgg	

(2) INFORMATION FOR SEQ ID NO:1263:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 190 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..190

(D) OTHER INFORMATION: / Ceres Seq. ID 1499971

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1263:

Arg Arg Arg Arg Asp Tyr Pro Ser Ser Ser Ser Asp Ser Glu Ser Glu
1 5 10 15
Ser Glu Ser Glu Tyr Ser Asp Ser Glu Ser Glu Ser Glu Asp Glu
20 25 30
Arg Arg Arg Lys Lys Arg Lys Arg Lys Glu Arg Glu Glu Glu Glu Lys
35 40 45
Glu Arg Lys Arg Arg Arg Arg Glu Lys Asp Lys Lys Lys Arg Asn Lys
50 55 60
Ser Asp Lys Asp Gly Asp Lys Lys Arg Lys Glu Lys Lys Lys Lys Lys
65 70 75 80
Ser Glu Lys Val Lys Lys Gly Ala Val Thr Glu Ser Trp Gly Lys Tyr
85 90 95
Gly Ile Ile Arg Glu Thr Asp Met Trp Asn Lys Arg Pro Glu Phe Thr
100 105 110
Ala Trp Leu Leu Glu Val Lys Lys Val Asn Leu Glu Ser Leu Pro Pro

115	120	125
Trp Glu Lys Lys Met Phe Lys Asp Phe Met Glu Asp His Asn Thr		
130	135	140
Gly Thr Phe Thr Ser Lys Lys Tyr Tyr Asp Ile Asp Gly Tyr Tyr Arg		
145	150	155
Leu Lys Leu Glu Lys Glu Met Lys Lys Gly Leu Lys Lys Ala Gly Ile		
165	170	175
Ser Glu Arg Thr Val Phe Asn Asp Glu Glu Gln Arg Arg Leu		
180	185	190

(2) INFORMATION FOR SEQ ID NO:1264:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1770 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1770
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499972

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1264:

atcactagtc	actatacacc	aatcttagat	ccgggaagct	aatttctctt	ctccgatcgg	60
tgaatgcagt	tacattgacc	tcggatctaa	ccaagctctt	ctggtttcca	gctctctgga	120
attcaaaaaa	atggaggaga	aatccaagtc	aagaggttgg	tgcggttggt	tcatcgccat	180
tattgtgcta	gcttctgtta	tcctcgccgt	cgtttacct	gttaaattga	gaacgaagaa	240
atccggtgac	gatgacggtg	gctgtcccgt	tcctggacct	cccggcgcca	ttgataagaa	300
atacgccgac	gctcttaagc	tcgctttgca	gttcttcgat	atccagaaat	ctggtaaatt	360
ggagaacaat	aagatacctt	ggagaggaga	ttcaggtctt	aaagatggaa	gtgaagataa	420
tctggatctt	tccaaaggct	tatatgatgc	tggagatcat	ataaagtttg	gttttccaat	480
ggctttcact	gctacagttt	tgtcatggtc	gattcttgag	tatggtgatc	aaatgaatgc	540
agtcacaacaa	ttggatcctg	ctaaagactc	tctccggtgg	atcactgact	atcttatcaa	600
agctcatcct	tctgacaatg	tcctctatat	ccaggtggga	gatccaaaag	tagatcatcc	660
atgctgggag	agaccagagg	atatgaaaga	gaagagacca	cttactaaaa	ttgatgtaga	720
tactccaggg	acagagggtg	ctgctgaaac	tgctgcagct	atggcttcag	cgtctttggt	780
gtttaaggat	agtgatccta	catattcagc	aacgcttctg	aaacatgcga	agcagttggt	840
tgattttgca	gatacaaaga	gaggctctta	cagtgttaac	atacctgagg	ttcagaagtt	900
ttacaattcg	actggatatg	gtgatgagct	actatgggca	gctagttggt	tgtatcatgc	960
aacagaggat	aaaacttacc	ttgattatgt	gtctaatacat	ggaaaagaat	ttgctagtgt	1020
tggaaatcct	acttggttta	gttgggacaa	caagcttgca	ggaacacagg	tactattatc	1080
aagattactc	ttctttaaga	aagatttatc	aggaagcaag	ggacttggaa	attacaggaa	1140
cacagctaaa	gctgtcatgt	gtggacttct	accaaagtct	ccaacatcta	cagctagtag	1200
aacaaacggt	ggtcttatat	gggttagtga	atggaactcg	atgcaacaat	ccgtttcgtc	1260
agcgttttta	gctcgcgttt	tcagtgtatta	catgctcact	tcccgtatcc	ataaaaatct	1320
ttgcgacggg	aaaactttca	aagcaacaga	gcttagagat	ttcgccaaat	cgcaggctga	1380
ttacatgctg	gggaagaatc	cgttgggaac	gagcttcgtg	gtgggttatg	gagacaaata	1440
cccacaattt	gtgcatcata	gaggagcttc	gatcccgcca	gatgcaacaa	cgggttgctt	1500
agatggattc	aaatggttta	actcaacgaa	accaaaccga	aacatagcat	atggtgcact	1560
cgtaggtggg	cctttcttca	atgagacgtt	cactgactca	cagagagaacc	caatgcagaa	1620
cgagccaacc	acttacaaca	atgcactcct	cgttgggtctc	ttgtctagtc	ttgtcactac	1680
atcttctact	ttacagtcgt	tgaagtgagc	tttgcggtgtt	ttagccttct	tattgaaaat	1740
cacattgctt	cattttttatt	tgtaattttc				

(2) INFORMATION FOR SEQ ID NO:1265:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 525 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..525

(D) OTHER INFORMATION: / Ceres Seq. ID 1499973

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1265:

Met	Glu	Glu	Lys	Ser	Lys	Ser	Arg	Gly	Trp	Cys	Gly	Trp	Phe	Ile	Ala	
1				5				10						15		
Ile	Ile	Val	Leu	Ala	Ser	Val	Ile	Leu	Ala	Val	Val	Tyr	Thr	Val	Lys	
			20					25					30			
Leu	Arg	Thr	Lys	Lys	Ser	Gly	Asp	Asp	Gly	Gly	Cys	Pro	Val	Pro		
			35				40				45					
Gly	Pro	Pro	Gly	Ala	Ile	Asp	Lys	Lys	Tyr	Ala	Asp	Ala	Leu	Lys	Leu	
	50					55				60						
Ala	Leu	Gln	Phe	Phe	Asp	Ile	Gln	Lys	Ser	Gly	Lys	Leu	Glu	Asn	Asn	
65					70					75				80		
Lys	Ile	Pro	Trp	Arg	Gly	Asp	Ser	Gly	Leu	Lys	Asp	Gly	Ser	Glu	Asp	
				85				90					95			
Asn	Leu	Asp	Leu	Ser	Lys	Gly	Leu	Tyr	Asp	Ala	Gly	Asp	His	Ile	Lys	
			100					105					110			
Phe	Gly	Phe	Pro	Met	Ala	Phe	Thr	Ala	Thr	Val	Leu	Ser	Trp	Ser	Ile	
			115				120					125				
Leu	Glu	Tyr	Gly	Asp	Gln	Met	Asn	Ala	Val	Asn	Gln	Leu	Asp	Pro	Ala	
	130					135				140						
Lys	Asp	Ser	Leu	Arg	Trp	Ile	Thr	Asp	Tyr	Leu	Ile	Lys	Ala	His	Pro	
145					150					155					160	
Ser	Asp	Asn	Val	Leu	Tyr	Ile	Gln	Val	Gly	Asp	Pro	Lys	Val	Asp	His	
				165					170					175		
Pro	Cys	Trp	Glu	Arg	Pro	Glu	Asp	Met	Lys	Glu	Lys	Arg	Pro	Leu	Thr	
			180					185					190			
Lys	Ile	Asp	Val	Asp	Thr	Pro	Gly	Thr	Glu	Val	Ala	Ala	Glu	Thr	Ala	
	195						200					205				
Ala	Ala	Met	Ala	Ser	Ala	Ser	Leu	Val	Phe	Lys	Asp	Ser	Asp	Pro	Thr	
	210					215				220						
Tyr	Ser	Ala	Thr	Leu	Leu	Lys	His	Ala	Lys	Gln	Leu	Phe	Asp	Phe	Ala	
225					230					235					240	
Asp	Thr	Lys	Arg	Gly	Ser	Tyr	Ser	Val	Asn	Ile	Pro	Glu	Val	Gln	Lys	
				245					250					255		
Phe	Tyr	Asn	Ser	Thr	Gly	Tyr	Gly	Asp	Glu	Leu	Leu	Trp	Ala	Ala	Ser	
			260					265					270			
Trp	Leu	Tyr	His	Ala	Thr	Glu	Asp	Lys	Thr	Tyr	Leu	Asp	Tyr	Val	Ser	
			275				280					285				
Asn	His	Gly	Lys	Glu	Phe	Ala	Ser	Phe	Gly	Asn	Pro	Thr	Trp	Phe	Ser	
	290					295				300						
Trp	Asp	Asn	Lys	Leu	Ala	Gly	Thr	Gln	Val	Leu	Leu	Ser	Arg	Leu	Leu	
305					310					315					320	
Phe	Phe	Lys	Lys	Asp	Leu	Ser	Gly	Ser	Lys	Gly	Leu	Gly	Asn	Tyr	Arg	
				325					330					335		
Asn	Thr	Ala	Lys	Ala	Val	Met	Cys	Gly	Leu	Leu	Pro	Lys	Ser	Pro	Thr	
			340					345					350			
Ser	Thr	Ala	Ser	Arg	Thr	Asn	Gly	Gly	Leu	Ile	Trp	Val	Ser	Glu	Trp	
			355				360					365				
Asn	Ser	Met	Gln	Gln	Ser	Val	Ser	Ser	Ala	Phe	Leu	Ala	Ser	Leu	Phe	
	370					375					380					
Ser	Asp	Tyr	Met	Leu	Thr	Ser	Arg	Ile	His	Lys	Ile	Ser	Cys	Asp	Gly	
385					390					395					400	
Lys	Ile	Phe	Lys	Ala	Thr	Glu	Leu	Arg	Asp	Phe	Ala	Lys	Ser	Gln	Ala	
				405					410					415		
Asp	Tyr	Met	Leu	Gly	Lys	Asn	Pro	Leu	Gly	Thr	Ser	Phe	Val	Val	Gly	
			420					425					430			
Tyr	Gly	Asp	Lys	Tyr	Pro	Gln	Phe	Val	His	His	Arg	Gly	Ala	Ser	Ile	
			435				440					445				
Pro	Ala	Asp	Ala	Thr	Thr	Gly	Cys	Leu	Asp	Gly	Phe	Lys	Trp	Phe	Asn	
	450					455					460					
Ser	Thr	Lys	Pro	Asn	Pro	Asn	Ile	Ala	Tyr	Gly	Ala	Leu	Val	Gly	Gly	

465		470		475		480									
Pro	Phe	Phe	Asn	Glu	Thr	Phe	Thr	Asp	Ser	Arg	Glu	Asn	Pro	Met	Gln
			485						490					495	
Asn	Glu	Pro	Thr	Thr	Tyr	Asn	Asn	Ala	Leu	Leu	Val	Gly	Leu	Leu	Ser
			500					505					510		
Ser	Leu	Val	Thr	Thr	Ser	Ser	Thr	Leu	Gln	Ser	Leu	Lys			
		515					520					525			

(2) INFORMATION FOR SEQ ID NO:1266:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 409 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..409
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499974

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1266:

Met	Ala	Phe	Thr	Ala	Thr	Val	Leu	Ser	Trp	Ser	Ile	Leu	Glu	Tyr	Gly
1			5					10					15		
Asp	Gln	Met	Asn	Ala	Val	Asn	Gln	Leu	Asp	Pro	Ala	Lys	Asp	Ser	Leu
			20					25					30		
Arg	Trp	Ile	Thr	Asp	Tyr	Leu	Ile	Lys	Ala	His	Pro	Ser	Asp	Asn	Val
		35					40					45			
Leu	Tyr	Ile	Gln	Val	Gly	Asp	Pro	Lys	Val	Asp	His	Pro	Cys	Trp	Glu
	50				55					60					
Arg	Pro	Glu	Asp	Met	Lys	Glu	Lys	Arg	Pro	Leu	Thr	Lys	Ile	Asp	Val
65				70				75						80	
Asp	Thr	Pro	Gly	Thr	Glu	Val	Ala	Ala	Glu	Thr	Ala	Ala	Ala	Met	Ala
			85					90						95	
Ser	Ala	Ser	Leu	Val	Phe	Lys	Asp	Ser	Asp	Pro	Thr	Tyr	Ser	Ala	Thr
			100					105					110		
Leu	Leu	Lys	His	Ala	Lys	Gln	Leu	Phe	Asp	Phe	Ala	Asp	Thr	Lys	Arg
		115				120						125			
Gly	Ser	Tyr	Ser	Val	Asn	Ile	Pro	Glu	Val	Gln	Lys	Phe	Tyr	Asn	Ser
	130					135					140				
Thr	Gly	Tyr	Gly	Asp	Glu	Leu	Leu	Trp	Ala	Ala	Ser	Trp	Leu	Tyr	His
145				150					155					160	
Ala	Thr	Glu	Asp	Lys	Thr	Tyr	Leu	Asp	Tyr	Val	Ser	Asn	His	Gly	Lys
			165					170						175	
Glu	Phe	Ala	Ser	Phe	Gly	Asn	Pro	Thr	Trp	Phe	Ser	Trp	Asp	Asn	Lys
		180						185					190		
Leu	Ala	Gly	Thr	Gln	Val	Leu	Leu	Ser	Arg	Leu	Leu	Phe	Phe	Lys	Lys
		195				200						205			
Asp	Leu	Ser	Gly	Ser	Lys	Gly	Leu	Gly	Asn	Tyr	Arg	Asn	Thr	Ala	Lys
	210					215					220				
Ala	Val	Met	Cys	Gly	Leu	Leu	Pro	Lys	Ser	Pro	Thr	Ser	Thr	Ala	Ser
225				230						235				240	
Arg	Thr	Asn	Gly	Gly	Leu	Ile	Trp	Val	Ser	Glu	Trp	Asn	Ser	Met	Gln
			245					250						255	
Gln	Ser	Val	Ser	Ser	Ala	Phe	Leu	Ala	Ser	Leu	Phe	Ser	Asp	Tyr	Met
		260						265					270		
Leu	Thr	Ser	Arg	Ile	His	Lys	Ile	Ser	Cys	Asp	Gly	Lys	Ile	Phe	Lys
		275					280					285			
Ala	Thr	Glu	Leu	Arg	Asp	Phe	Ala	Lys	Ser	Gln	Ala	Asp	Tyr	Met	Leu
	290					295					300				
Gly	Lys	Asn	Pro	Leu	Gly	Thr	Ser	Phe	Val	Val	Gly	Tyr	Gly	Asp	Lys
305				310						315				320	
Tyr	Pro	Gln	Phe	Val	His	His	Arg	Gly	Ala	Ser	Ile	Pro	Ala	Asp	Ala
			325					330						335	

Thr Thr Gly Cys Leu Asp Gly Phe Lys Trp Phe Asn Ser Thr Lys Pro
340 345 350
Asn Pro Asn Ile Ala Tyr Gly Ala Leu Val Gly Gly Pro Phe Phe Asn
355 360 365
Glu Thr Phe Thr Asp Ser Arg Glu Asn Pro Met Gln Asn Glu Pro Thr
370 375 380
Thr Tyr Asn Asn Ala Leu Val Gly Leu Leu Ser Ser Leu Val Thr
385 390 395 400
Thr Ser Ser Thr Leu Gln Ser Leu Lys
405

(2) INFORMATION FOR SEQ ID NO:1267:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 391 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..391

(D) OTHER INFORMATION: / Ceres Seq. ID 1499975

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1267:

Met Asn Ala Val Asn Gln Leu Asp Pro Ala Lys Asp Ser Leu Arg Trp
1 5 10 15
Ile Thr Asp Tyr Leu Ile Lys Ala His Pro Ser Asp Asn Val Leu Tyr
20 25 30
Ile Gln Val Gly Asp Pro Lys Val Asp His Pro Cys Trp Glu Arg Pro
35 40 45
Glu Asp Met Lys Glu Lys Arg Pro Leu Thr Lys Ile Asp Val Asp Thr
50 55 60
Pro Gly Thr Glu Val Ala Ala Glu Thr Ala Ala Ala Met Ala Ser Ala
65 70 75 80
Ser Leu Val Phe Lys Asp Ser Asp Pro Thr Tyr Ser Ala Thr Leu Leu
85 90 95
Lys His Ala Lys Gln Leu Phe Asp Phe Ala Asp Thr Lys Arg Gly Ser
100 105 110
Tyr Ser Val Asn Ile Pro Glu Val Gln Lys Phe Tyr Asn Ser Thr Gly
115 120 125
Tyr Gly Asp Glu Leu Leu Trp Ala Ala Ser Trp Leu Tyr His Ala Thr
130 135 140
Glu Asp Lys Thr Tyr Leu Asp Tyr Val Ser Asn His Gly Lys Glu Phe
145 150 155 160
Ala Ser Phe Gly Asn Pro Thr Trp Phe Ser Trp Asp Asn Lys Leu Ala
165 170 175
Gly Thr Gln Val Leu Leu Ser Arg Leu Leu Phe Phe Lys Lys Asp Leu
180 185 190
Ser Gly Ser Lys Gly Leu Gly Asn Tyr Arg Asn Thr Ala Lys Ala Val
195 200 205
Met Cys Gly Leu Leu Pro Lys Ser Pro Thr Ser Thr Ala Ser Arg Thr
210 215 220
Asn Gly Gly Leu Ile Trp Val Ser Glu Trp Asn Ser Met Gln Gln Ser
225 230 235 240
Val Ser Ser Ala Phe Leu Ala Ser Leu Phe Ser Asp Tyr Met Leu Thr
245 250 255
Ser Arg Ile His Lys Ile Ser Cys Asp Gly Lys Ile Phe Lys Ala Thr
260 265 270
Glu Leu Arg Asp Phe Ala Lys Ser Gln Ala Asp Tyr Met Leu Gly Lys
275 280 285
Asn Pro Leu Gly Thr Ser Phe Val Val Gly Tyr Gly Asp Lys Tyr Pro
290 295 300
Gln Phe Val His His Arg Gly Ala Ser Ile Pro Ala Asp Ala Thr Thr

305 310 315 320
Gly Cys Leu Asp Gly Phe Lys Trp Phe Asn Ser Thr Lys Pro Asn Pro
 325 330 335
Asn Ile Ala Tyr Gly Ala Leu Val Gly Gly Pro Phe Phe Asn Glu Thr
 340 345 350
Phe Thr Asp Ser Arg Glu Asn Pro Met Gln Asn Glu Pro Thr Thr Tyr
 355 360 365
Asn Asn Ala Leu Leu Val Gly Leu Leu Ser Ser Leu Val Thr Thr Ser
 370 375 380
Ser Thr Leu Gln Ser Leu Lys
385 390

(2) INFORMATION FOR SEQ ID NO:1268:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 883 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..883
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499976

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1268:

aagtgtgtaa	tttctcttct	tcgtaatcta	atthtgtttg	tttactgttg	atthtgtgtc	60
ttttctgttt	cgtggaccct	tttggaatcc	atcaatttta	gggtttcatt	cttcttcgtg	120
tgtgggtttt	gatttcttct	tcttctctcg	agaaaaaat	gggtcaagct	ttgggttgta	180
ttcaagttga	tcagtcgaat	gtagcaatca	aagagacttt	tgggaagttt	gacgaattct	240
tgagccgggt	tgctactgtt	tgccatgggt	tttgggaagt	caagtcgctg	gtcacctttc	300
tttacgtgtt	caacagctcg	atgttcgctg	cgagacaaag	actaaggata	atgtgtttgt	360
cacggttggt	gcttccattc	aataccgtgc	cttagcggag	agtgtctcaag	atgcttttta	420
caagctcagc	aacacaagga	atcagattca	agcttatgtc	tttgatgtga	tccgagcaag	480
tgtacctaa	ctggatctag	actctacctt	tgagcaaaa	aatgacattg	caaaaaccgt	540
tgagactgag	ctcgaaaagg	ctatgtcgca	ttacggatat	gagattgttc	agacactgat	600
tgtggatgag	gagcctgatg	tgcatgtcaa	gagggcaatg	aatgagatca	atgctgtctc	660
tagaatgaga	gaggcagcga	gtgagaaagc	tgagttagta	atttcaaaca	ggaaagaaac	720
tcagcaacaa	agtgcagtga	agatgcagaa	gaagaggatc	gagaatcatt	ttggtggctt	780
taaagctctg	aaagtgaag	ggctaataaa	gccgtaacgt	gacagcttca	agtttctctc	840
taactacaat	tcttttaaat	tggtgatct	ctaacaatac	agg		

(2) INFORMATION FOR SEQ ID NO:1269:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 78 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..78
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499977

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1269:

Met	Gly	Gln	Ala	Leu	Gly	Cys	Ile	Gln	Val	Asp	Gln	Ser	Asn	Val	Ala
1				5				10					15		
Ile	Lys	Glu	Thr	Phe	Gly	Lys	Phe	Asp	Glu	Phe	Leu	Ser	Arg	Val	Val
			20					25					30		
Thr	Val	Cys	His	Gly	Val	Trp	Glu	Val	Lys	Ser	Leu	Val	Thr	Phe	Leu
		35					40					45			
Tyr	Val	Phe	Asn	Ser	Ser	Met	Phe	Ala	Ala	Arg	Gln	Arg	Leu	Arg	Ile
		50				55				60					
Met	Cys	Leu	Ser	Arg	Leu	Leu	Pro	Phe	Asn	Thr	Val	Pro			
65					70				75						

(2) INFORMATION FOR SEQ ID NO:1270:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 84 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..84
 (D) OTHER INFORMATION: / Ceres Seq. ID 1499978
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1270:
Met Ser His Tyr Gly Tyr Glu Ile Val Gln Thr Leu Ile Val Asp Ile
1 5 10 15
Glu Pro Asp Val His Val Lys Arg Ala Met Asn Glu Ile Asn Ala Ala
 20 25 30
Ser Arg Met Arg Glu Ala Ala Ser Glu Lys Ala Glu Leu Val Ile Ser
 35 40 45
Asn Arg Lys Glu Thr Gln Gln Gln Ser Asp Val Lys Met Gln Lys Lys
 50 55 60
Arg Ile Glu Asn His Phe Gly Gly Phe Lys Arg Leu Lys Val Lys Gly
65 70 75 80
Leu Ile Lys Pro

(2) INFORMATION FOR SEQ ID NO:1271:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 59 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: peptide
 (ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..59
 (D) OTHER INFORMATION: / Ceres Seq. ID 1499979
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1271:
Met Asn Glu Ile Asn Ala Ala Ser Arg Met Arg Glu Ala Ala Ser Glu
1 5 10 15
Lys Ala Glu Leu Val Ile Ser Asn Arg Lys Glu Thr Gln Gln Gln Ser
 20 25 30
Asp Val Lys Met Gln Lys Lys Arg Ile Glu Asn His Phe Gly Gly Phe
 35 40 45
Lys Arg Leu Lys Val Lys Gly Leu Ile Lys Pro
50 55

(2) INFORMATION FOR SEQ ID NO:1272:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1178 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: DNA (genomic)
 (ix) FEATURE:
 (A) NAME/KEY: -
 (B) LOCATION: 1..1178
 (D) OTHER INFORMATION: / Ceres Seq. ID 1499984
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1272:
ctcaaccttt tgggtgaaaa aaccagaaaa tggggttgca tccaatttcc gacgccaatg 60
aacacaatcc cttcggctct ctcaccgccg acgaattcta cgccaaacat tccgttagcc 120
actcctccgc ttcatcacc aaccctcgcg gtctcaaact cttcactcaa tgggtggtcac 180
cactccctcc aactaaacca atcggtatca tcgctgtcgt tcatggcttc accggcgaat 240
ccagttgggt ccttcagctc acatcaatcc tcttcgctaa atccggtttc ataacctgcg 300
caattgatca ccaaggccat ggattctccg atggactcat cgctcatatc cctgacatca 360

```
atcccgctcgt cgatgactgt atctctttct tcgatgactt ccgtagccgt caaacaccgt      420
cagatctgcc  gtgttttctc tactctgaat ccctaggcgg cgcgattgct ctctacatct      480
cgcttcgtca  gagaggtgtt tgggatggac ttatcctcaa cggagctatg tgtggaatca      540
gcgataaatt  caaacgcggc tggccgttgg agcatttgct attcgtcgtc gcgaatctta      600
tccctacttg  gcgcgttatc cccactcgcg gatctattcc cgatgtttcg ttcaaggagc      660
cgtggaagag  gaagcttgcc atggctagcc caaggaggac ggtggcgaaa ccacgggccc      720
ctactgctta  tgagctgatt cgtgtttgta aggatctgca ggggaggttt gaggaagtgg      780
aggttccgct  tctgattgtg cacggcggag gtgatgttgt atgcgacgta gcgtgtgttg      840
aggagcttca  tcggagagcg attagtggag ataagacgat caagatctac cctgagttgt      900
ggcatcagat  gattggggaa tcggaggaga aagtcgatct ggtttacggg gatatgctga      960
gctggctcaa  gagtcgagct gaaaggaagg cacgcgccgc cgttgatgga ggagcagctt     1020
agagtccctt  ttgagtcttt ggggtgttga ttgtagtcca ataggactgt gccatctggc     1080
aagaaactat  ttatggtttt actgtttcgt aatcgtagca catggtttac agttaaacca     1140
atacctttgg  gtatcatcaa taatataaaa aatcgttg
```

(2) INFORMATION FOR SEQ ID NO:1273:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 339 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..339
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499985

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1273:

```
Gln Pro Phe Gly Gly Lys Asn Gln Lys Met Gly Leu His Pro Ile Ser
1          5          10          15
Asp Ala Asn Glu His Asn Pro Phe Gly Ser Leu Thr Ala Asp Glu Phe
          20          25          30
Tyr Ala Lys His Ser Val Ser His Ser Ser Ala Phe Ile Thr Asn Pro
          35          40          45
Arg Gly Leu Lys Leu Phe Thr Gln Trp Trp Ser Pro Leu Pro Pro Thr
          50          55          60
Lys Pro Ile Gly Ile Ile Ala Val Val His Gly Phe Thr Gly Glu Ser
65          70          75          80
Ser Trp Phe Leu Gln Leu Thr Ser Ile Leu Phe Ala Lys Ser Gly Phe
          85          90          95
Ile Thr Cys Ala Ile Asp His Gln Gly His Gly Phe Ser Asp Gly Leu
          100          105          110
Ile Ala His Ile Pro Asp Ile Asn Pro Val Val Asp Asp Cys Ile Ser
          115          120          125
Phe Phe Asp Asp Phe Arg Ser Arg Gln Thr Pro Ser Asp Leu Pro Cys
          130          135          140
Phe Leu Tyr Ser Glu Ser Leu Gly Gly Ala Ile Ala Leu Tyr Ile Ser
145          150          155          160
Leu Arg Gln Arg Gly Val Trp Asp Gly Leu Ile Leu Asn Gly Ala Met
          165          170          175
Cys Gly Ile Ser Asp Lys Phe Lys Pro Pro Trp Pro Leu Glu His Leu
          180          185          190
Leu Phe Val Val Ala Asn Leu Ile Pro Thr Trp Arg Val Ile Pro Thr
          195          200          205
Arg Gly Ser Ile Pro Asp Val Ser Phe Lys Glu Pro Trp Lys Arg Lys
          210          215          220
Leu Ala Met Ala Ser Pro Arg Arg Thr Val Ala Lys Pro Arg Ala Ala
225          230          235          240
Thr Ala Tyr Glu Leu Ile Arg Val Cys Lys Asp Leu Gln Gly Arg Phe
          245          250          255
Glu Glu Val Glu Val Pro Leu Leu Ile Val His Gly Gly Gly Asp Val
          260          265          270
Val Cys Asp Val Ala Cys Val Glu Glu Leu His Arg Arg Ala Ile Ser
```

275 280 285
Glu Asp Lys Thr Ile Lys Ile Tyr Pro Glu Leu Trp His Gln Met Ile
290 295 300
Gly Glu Ser Glu Glu Lys Val Asp Leu Val Tyr Gly Asp Met Leu Ser
305 310 315 320
Trp Leu Lys Ser Arg Ala Glu Arg Lys Ala Arg Ala Ala Val Asp Gly
325 330 335
Gly Ala Ala

(2) INFORMATION FOR SEQ ID NO:1274:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 330 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..330

(D) OTHER INFORMATION: / Ceres Seq. ID 1499986

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1274:

Met Gly Leu His Pro Ile Ser Asp Ala Asn Glu His Asn Pro Phe Gly
1 5 10 15
Ser Leu Thr Ala Asp Glu Phe Tyr Ala Lys His Ser Val Ser His Ser
20 25 30
Ser Ala Phe Ile Thr Asn Pro Arg Gly Leu Lys Leu Phe Thr Gln Trp
35 40 45
Trp Ser Pro Leu Pro Pro Thr Lys Pro Ile Gly Ile Ile Ala Val Val
50 55 60
His Gly Phe Thr Gly Glu Ser Ser Trp Phe Leu Gln Leu Thr Ser Ile
65 70 75 80
Leu Phe Ala Lys Ser Gly Phe Ile Thr Cys Ala Ile Asp His Gln Gly
85 90 95
His Gly Phe Ser Asp Gly Leu Ile Ala His Ile Pro Asp Ile Asn Pro
100 105 110
Val Val Asp Asp Cys Ile Ser Phe Phe Asp Asp Phe Arg Ser Arg Gln
115 120 125
Thr Pro Ser Asp Leu Pro Cys Phe Leu Tyr Ser Glu Ser Leu Gly Gly
130 135 140
Ala Ile Ala Leu Tyr Ile Ser Leu Arg Gln Arg Gly Val Trp Asp Gly
145 150 155 160
Leu Ile Leu Asn Gly Ala Met Cys Gly Ile Ser Asp Lys Phe Lys Pro
165 170 175
Pro Trp Pro Leu Glu His Leu Leu Phe Val Val Ala Asn Leu Ile Pro
180 185 190
Thr Trp Arg Val Ile Pro Thr Arg Gly Ser Ile Pro Asp Val Ser Phe
195 200 205
Lys Glu Pro Trp Lys Arg Lys Leu Ala Met Ala Ser Pro Arg Arg Thr
210 215 220
Val Ala Lys Pro Arg Ala Ala Thr Ala Tyr Glu Leu Ile Arg Val Cys
225 230 235 240
Lys Asp Leu Gln Gly Arg Phe Glu Glu Val Glu Val Pro Leu Leu Ile
245 250 255
Val His Gly Gly Asp Val Val Cys Asp Val Ala Cys Val Glu Glu
260 265 270
Leu His Arg Arg Ala Ile Ser Glu Asp Lys Thr Ile Lys Ile Tyr Pro
275 280 285
Glu Leu Trp His Gln Met Ile Gly Glu Ser Glu Glu Lys Val Asp Leu
290 295 300
Val Tyr Gly Asp Met Leu Ser Trp Leu Lys Ser Arg Ala Glu Arg Lys
305 310 315 320

Ala Arg Ala Ala Val Asp Gly Gly Ala Ala
325 330

(2) INFORMATION FOR SEQ ID NO:1275:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1591 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1591
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499989

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1275:

```
ctcttgtctt ttgtctctcc accaattttt tcttgttctt tctctctcca ccacataaaa      60
aaaaaaaaac ctagctttgt cccctcaact cactgattga actgcttgat ttctgattga      120
tcattctgggt ggttttgat cgaagagtat tgttgtatta gtggctgggt gctctccaaa      180
agagtaaggc cggagagaga aatcaatggc ctctggcggc ggagaggcgg ataaatcact      240
tgaaatcggg tccgggaccg cggatcccaa aataggcggg actgggagca ggagcgccgg      300
agaagaacga tacttcaggg cagatacact ggatttcagt aaatgggatt tgcatatggg      360
tcaaacctct actagcagcg tcctcaccac ttccgcttcc acgagcgctc ccgcaccggc      420
gatgcaggaa tgggagattg acctctccaa actcgatatg aagcacgtcc tcgctcacgg      480
tacttacggc actgtctacc gcggtgtcta cgccggccaa agctgaaact acaactctcc gtgcttcctt      600
agattgggga gaagatgggt acgccacacc agctgaaact acaactctcc gtgcttcctt      600
cgagcaagag gtcgcccgtct ggcagaagct cgatcatccc aacgttacca agttcatagg      660
agcatccatg ggaacctctg atctgcggat ccctcctgct ggtgatactg gcggacgtgg      720
taacggtgca catcctgcga gggcctgttg tgttggtggt gaatatgttg ccggaggcac      780
gcttaagaag ttctctcatca agaaatatag ggccaaacta cccatcaagg atgtcattca      840
gctcgtcttg gatctcgcta gagggcttag ttacctccac tccaaggcga ttgtacatag      900
ggacgtgaag tcagagaaca tgctgttaca gcctaacaag acgctgaaga tcgctgattt      960
cggggtagct agagttgaag ctcaagaacc tcaagacatg acgggtggaa ctggaacact      1020
tggatacatg gcaccagagg ttcttgaagg aaagccttac aacaggaaat gcgatgtcta      1080
tagctttggg gtatgcctct gggaaatata ctgctgtgac atgccctatg ctgactgtag      1140
ttttgctgag atctctcacg ccgttggtca taggaatctg agaccagaga ttccgaaatg      1200
ctgcccgcag gcagtggcaa acatcatgaa gagatgctgg gaccggaatc cagacaggcg      1260
tccggagatg gaggaggtgg tgaagctgct tgaagccata gacacaagca aaggtgggtg      1320
aatgatagct ccggaccagt ttcagggggt cctctgtttc ttcaaaccctc gaggccctg      1380
aatctctctc cctctctttc ctttttgctc cgtgtctgat atattcttga gagctgcgtg      1440
attctttgga ttttgtattt actttgagct atgggagttg gattgggtgtg ggttttgtca      1500
taagaatctt tctgcgctct atgtatttat atacttaaca cagtcgtgta taattcgatt      1560
aagctttatt ttattttttg atgttgattc c
```

(2) INFORMATION FOR SEQ ID NO:1276:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 391 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..391
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499990

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1276:

```
Met Ala Ser Gly Gly Gly Glu Ala Asp Lys Ser Leu Glu Ile Gly Ser
1      5      10      15
Gly Thr Ala Asp Pro Lys Ile Gly Gly Thr Gly Ser Arg Ser Ala Gly
20      25      30
Glu Glu Arg Tyr Phe Arg Ala Asp Thr Leu Asp Phe Ser Lys Trp Asp
35      40      45
Leu His Met Gly Gln Thr Ser Thr Ser Ser Val Leu Thr Asn Ser Ala
50      55      60
```

Ser Thr Ser Ala Pro Ala Pro Ala Met Gln Glu Trp Glu Ile Asp Leu
65 70 75 80
Ser Lys Leu Asp Met Lys His Val Leu Ala His Gly Thr Tyr Gly Thr
85 90 95
Val Tyr Arg Gly Val Tyr Ala Gly Gln Glu Val Ala Val Lys Val Leu
100 105 110
Asp Trp Gly Glu Asp Gly Tyr Ala Thr Pro Ala Glu Thr Thr Thr Leu
115 120 125
Arg Ala Ser Phe Glu Gln Glu Val Ala Val Trp Gln Lys Leu Asp His
130 135 140
Pro Asn Val Thr Lys Phe Ile Gly Ala Ser Met Gly Thr Ser Asp Leu
145 150 155 160
Arg Ile Pro Pro Ala Gly Asp Thr Gly Gly Arg Gly Asn Gly Ala His
165 170 175
Pro Ala Arg Ala Cys Cys Val Val Val Glu Tyr Val Ala Gly Gly Thr
180 185 190
Leu Lys Lys Phe Leu Ile Lys Lys Tyr Arg Ala Lys Leu Pro Ile Lys
195 200 205
Asp Val Ile Gln Leu Ala Leu Asp Leu Ala Arg Gly Leu Ser Tyr Leu
210 215 220
His Ser Lys Ala Ile Val His Arg Asp Val Lys Ser Glu Asn Met Leu
225 230 235 240
Leu Gln Pro Asn Lys Thr Leu Lys Ile Ala Asp Phe Gly Val Ala Arg
245 250 255
Val Glu Ala Gln Asn Pro Gln Asp Met Thr Gly Gly Thr Gly Thr Leu
260 265 270
Gly Tyr Met Ala Pro Glu Val Leu Glu Gly Lys Pro Tyr Asn Arg Lys
275 280 285
Cys Asp Val Tyr Ser Phe Gly Val Cys Leu Trp Glu Ile Tyr Cys Cys
290 295 300
Asp Met Pro Tyr Ala Asp Cys Ser Phe Ala Glu Ile Ser His Ala Val
305 310 315 320
Val His Arg Asn Leu Arg Pro Glu Ile Pro Lys Cys Cys Pro His Ala
325 330 335
Val Ala Asn Ile Met Lys Arg Cys Trp Asp Pro Asn Pro Asp Arg Arg
340 345 350
Pro Glu Met Glu Glu Val Val Lys Leu Leu Glu Ala Ile Asp Thr Ser
355 360 365
Lys Gly Gly Gly Met Ile Ala Pro Asp Gln Phe Gln Gly Cys Leu Cys
370 375 380
Phe Phe Lys Pro Arg Gly Pro
385 390

(2) INFORMATION FOR SEQ ID NO:1277:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 341 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..341
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499991

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1277:

Met Gly Gln Thr Ser Thr Ser Ser Val Leu Thr Asn Ser Ala Ser Thr
1 5 10 15
Ser Ala Pro Ala Pro Ala Met Gln Glu Trp Glu Ile Asp Leu Ser Lys
20 25 30
Leu Asp Met Lys His Val Leu Ala His Gly Thr Tyr Gly Thr Val Tyr
35 40 45
Arg Gly Val Tyr Ala Gly Gln Glu Val Ala Val Lys Val Leu Asp Trp

50	55	60
Gly Glu Asp Gly Tyr Ala Thr Pro Ala Glu Thr Thr Thr Leu Arg Ala		
65	70	75
Ser Phe Glu Gln Glu Val Ala Val Trp Gln Lys Leu Asp His Pro Asn		80
	85	90
Val Thr Lys Phe Ile Gly Ala Ser Met Gly Thr Ser Asp Leu Arg Ile		95
	100	105
Pro Pro Ala Gly Asp Thr Gly Gly Arg Gly Asn Gly Ala His Pro Ala		110
	115	120
Arg Ala Cys Cys Val Val Val Glu Tyr Val Ala Gly Gly Thr Leu Lys		125
	130	135
Lys Phe Leu Ile Lys Lys Tyr Arg Ala Lys Leu Pro Ile Lys Asp Val		140
145	150	155
Ile Gln Leu Ala Leu Asp Leu Ala Arg Gly Leu Ser Tyr Leu His Ser		160
	165	170
Lys Ala Ile Val His Arg Asp Val Lys Ser Glu Asn Met Leu Leu Gln		175
	180	185
Pro Asn Lys Thr Leu Lys Ile Ala Asp Phe Gly Val Ala Arg Val Glu		190
	195	200
Ala Gln Asn Pro Gln Asp Met Thr Gly Gly Thr Gly Thr Leu Gly Tyr		205
	210	215
Met Ala Pro Glu Val Leu Glu Gly Lys Pro Tyr Asn Arg Lys Cys Asp		220
225	230	235
Val Tyr Ser Phe Gly Val Cys Leu Trp Glu Ile Tyr Cys Cys Asp Met		240
	245	250
Pro Tyr Ala Asp Cys Ser Phe Ala Glu Ile Ser His Ala Val Val His		255
	260	265
Arg Asn Leu Arg Pro Glu Ile Pro Lys Cys Cys Pro His Ala Val Ala		270
	275	280
Asn Ile Met Lys Arg Cys Trp Asp Pro Asn Pro Asp Arg Arg Pro Glu		285
	290	295
Met Glu Glu Val Val Lys Leu Leu Glu Ala Ile Asp Thr Ser Lys Gly		300
305	310	315
Gly Gly Met Ile Ala Pro Asp Gln Phe Gln Gly Cys Leu Cys Phe Phe		320
	325	330
Lys Pro Arg Gly Pro		335
	340	

(2) INFORMATION FOR SEQ ID NO:1278:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 319 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..319
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499992

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1278:

Met Gln Glu Trp Glu Ile Asp Leu Ser Lys Leu Asp Met Lys His Val	
1	5
Leu Ala His Gly Thr Tyr Gly Thr Val Tyr Arg Gly Val Tyr Ala Gly	10
	20
Gln Glu Val Ala Val Lys Val Leu Asp Trp Gly Glu Asp Gly Tyr Ala	25
	30
Thr Pro Ala Glu Thr Thr Thr Leu Arg Ala Ser Phe Glu Gln Glu Val	35
	40
Ala Val Trp Gln Lys Leu Asp His Pro Asn Val Thr Lys Phe Ile Gly	45
65	50
Ala Ser Met Gly Thr Ser Asp Leu Arg Ile Pro Pro Ala Gly Asp Thr	55
	60
	70
	75
	80
	85
	90
	95

Gly Gly Arg Gly Asn Gly Ala His Pro Ala Arg Ala Cys Cys Val Val
100 105 110
Val Glu Tyr Val Ala Gly Gly Thr Leu Lys Lys Phe Leu Ile Lys Lys
115 120 125
Tyr Arg Ala Lys Leu Pro Ile Lys Asp Val Ile Gln Leu Ala Leu Asp
130 135 140
Leu Ala Arg Gly Leu Ser Tyr Leu His Ser Lys Ala Ile Val His Arg
145 150 155 160
Asp Val Lys Ser Glu Asn Met Leu Leu Gln Pro Asn Lys Thr Leu Lys
165 170 175
Ile Ala Asp Phe Gly Val Ala Arg Val Glu Ala Gln Asn Pro Gln Asp
180 185 190
Met Thr Gly Gly Thr Gly Thr Leu Gly Tyr Met Ala Pro Glu Val Leu
195 200 205
Glu Gly Lys Pro Tyr Asn Arg Lys Cys Asp Val Tyr Ser Phe Gly Val
210 215 220
Cys Leu Trp Glu Ile Tyr Cys Cys Asp Met Pro Tyr Ala Asp Cys Ser
225 230 235 240
Phe Ala Glu Ile Ser His Ala Val Val His Arg Asn Leu Arg Pro Glu
245 250 255
Ile Pro Lys Cys Cys Pro His Ala Val Ala Asn Ile Met Lys Arg Cys
260 265 270
Trp Asp Pro Asn Pro Asp Arg Arg Pro Glu Met Glu Glu Val Val Lys
275 280 285
Leu Leu Glu Ala Ile Asp Thr Ser Lys Gly Gly Gly Met Ile Ala Pro
290 295 300
Asp Gln Phe Gln Gly Cys Leu Cys Phe Phe Lys Pro Arg Gly Pro
305 310 315

(2) INFORMATION FOR SEQ ID NO:1279:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 576 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..576
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499993

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1279:

aattaaccgt cacgagctac atgctctgta tcttcagatt tcctaaatac ttacaattcc	60
cattccaatt ctgatttggt taatccaaaa caaaaaaaaaa ggaaactttc ttttacccta	120
aatctataaa aacgaaaccc ttcttcacaa atctttgttc ttcgtaatct ctcttaaaag	180
cttttgtttc aatttcaatg gagtgggttc gaggagaaac aattgggttc ggaaccttct	240
ctactgtcag tacagcgaca aagtctagaa actccggcga ctttctctgca cttatcgctg	300
tgaagtcgac gggttcttac ggcgcgcgtt cactctccaa cgagaaatcg gtgttggtt	360
cactccgtga ttgtcctgag atcatacggg gttacggcga ggattcaact gtggagaacg	420
gagaagagat gcataacttg ttcttagagt acgcttcgag aggaagctta gcgaggtaca	480
tgaagaaact tggcgggtgar gggttaccgg agtccaccgt acgtcgctac acaggatcgg	540
tgcttcgagg gttacgtcat attcacgcta aagggt	

(2) INFORMATION FOR SEQ ID NO:1280:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 126 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..126
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499994

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1280:

Met Glu Trp Val Arg Gly Glu Thr Ile Gly Phe Gly Thr Phe Ser Thr
1 5 10 15
Val Ser Thr Ala Thr Lys Ser Arg Asn Ser Gly Asp Phe Pro Ala Leu
20 25 30
Ile Ala Val Lys Ser Thr Gly Ser Tyr Gly Ala Ala Ser Leu Ser Asn
35 40 45
Glu Lys Ser Val Leu Asp Ser Leu Arg Asp Cys Pro Glu Ile Ile Arg
50 55 60
Cys Tyr Gly Glu Asp Ser Thr Val Glu Asn Gly Glu Glu Met His Asn
65 70 75 80
Leu Phe Leu Glu Tyr Ala Ser Arg Gly Ser Leu Ala Arg Tyr Met Lys
85 90 95
Lys Leu Gly Gly Xaa Gly Leu Pro Glu Ser Thr Val Arg Arg Tyr Thr
100 105 110
Gly Ser Val Leu Arg Gly Leu Arg His Ile His Ala Lys Gly
115 120 125

(2) INFORMATION FOR SEQ ID NO:1281:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 461 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..461
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499995

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1281:

atcatcacta acaaaacaca catcaaaaac gattttacaa gaaaaaata tcagaaaaaa 60
tgtcagagac caacaagaat gccttccaag ccggtcaggc cgctggcaaa gctgaggaga 120
agagcaatgt tctgctggac aaggccaagg atgctgctgc tgcagctgga gcttccgcgc 180
aacaggcggg aaagagtata tcggatgcgg cagtgggagg tgtaacttc gtgaaggaca 240
agaccggcct gaacaagtag cgatccgagt caactttggg agttataatt tcccttttct 300
aattaattgt tgggattttc aaataaaaatt tgggagtcac aattgattct cgtactcatc 360
gtacttggtt ttgttttttag tggtgtaagt tttaaatggt tcttctccct ttagatgtac 420
tacgtattgg aactttaagt ttaatcaaca aaatctagtt t

(2) INFORMATION FOR SEQ ID NO:1282:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 77 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..77
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499996

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1282:

Ile Ile Thr Asn Lys Thr His Ile Lys Asn Asp Phe Thr Arg Lys Lys
1 5 10 15
Tyr Gln Lys Lys Cys Gln Arg Pro Thr Arg Met Pro Ser Lys Pro Val
20 25 30
Arg Pro Leu Ala Lys Leu Arg Arg Arg Ala Met Phe Cys Trp Thr Arg
35 40 45
Pro Arg Met Leu Leu Leu Gln Leu Glu Leu Pro Arg Asn Arg Arg Glu
50 55 60
Arg Val Tyr Arg Met Arg Gln Trp Glu Val Leu Thr Ser
65 70 75

(2) INFORMATION FOR SEQ ID NO:1283:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 66 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..66
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1499997

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1283:

```
Met Ser Glu Thr Asn Lys Asn Ala Phe Gln Ala Gly Gln Ala Ala Gly
1           5           10          15
Lys Ala Glu Glu Lys Ser Asn Val Leu Asp Lys Ala Lys Asp Ala
20          25          30
Ala Ala Ala Ala Gly Ala Ser Ala Gln Gln Ala Gly Lys Ser Ile Ser
35          40          45
Asp Ala Ala Val Gly Gly Val Asn Phe Val Lys Asp Lys Thr Gly Leu
50          55          60
Asn Lys
65
```

(2) INFORMATION FOR SEQ ID NO:1284:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 51 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..51
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499998

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1284:

```
Met Pro Ser Lys Pro Val Arg Pro Leu Ala Lys Leu Arg Arg Ala
1           5           10          15
Met Phe Cys Trp Thr Arg Pro Arg Met Leu Leu Gln Leu Glu Leu
20          25          30
Pro Arg Asn Arg Arg Glu Arg Val Tyr Arg Met Arg Gln Trp Glu Val
35          40          45
Leu Thr Ser
50
```

(2) INFORMATION FOR SEQ ID NO:1285:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 515 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..515
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499999

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1285:

```
acgtttctat ctagagagaa cacaacacat cgaaccatgg agaaatcaac aagaacccta      60
ttcataacca tcgtgataac ctccatgttg ctagggtttg gaaactctga tcttgctcag      120
gacagagagg agtgtacgaa ccagctcata gaactatcca cgtgtattcc gtacgttgga      180
ggagacgcca aggctccaac aaaagattgt tgtgcagggt ttggccaagt tataagaaag      240
agtgagaagt gtgttttgc attttggtctc tgaccaatat gcaaacacac ttctggactc      300
tttcttcctc catcatttgt gctttttttc ttcttgtggt ttgtctttaa gacttggtat      360
atttcttaca atatgtttgt tatgttctct ggtgtgtggt ttgttttttt tggattact      420
ttcatatttt ttctgtcgaa gaggacttgt attcgacaat gtcgcttcaa ttttgttgtt      480
tccttagaaa ctaaataaat attggtttat attgg
```

(2) INFORMATION FOR SEQ ID NO:1286:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 90 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..90

(D) OTHER INFORMATION: / Ceres Seq. ID 1500000

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1286:

Thr	Phe	Leu	Ser	Arg	Glu	Asn	Thr	Thr	His	Arg	Thr	Met	Glu	Lys	Ser
1				5					10					15	
Thr	Arg	Thr	Leu	Phe	Ile	Thr	Ile	Val	Ile	Thr	Ser	Met	Leu	Leu	Gly
			20					25					30		
Phe	Gly	Asn	Ser	Asp	Leu	Ala	Gln	Asp	Arg	Glu	Glu	Cys	Thr	Asn	Gln
		35				40						45			
Leu	Ile	Glu	Leu	Ser	Thr	Cys	Ile	Pro	Tyr	Val	Gly	Gly	Asp	Ala	Lys
	50					55					60				
Ala	Pro	Thr	Lys	Asp	Cys	Cys	Ala	Gly	Phe	Gly	Gln	Val	Ile	Arg	Lys
65				70					75						80
Ser	Glu	Lys	Cys	Val	Cys	Ile	Phe	Gly	Leu						
				85					90						

(2) INFORMATION FOR SEQ ID NO:1287:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 78 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..78

(D) OTHER INFORMATION: / Ceres Seq. ID 1500001

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1287:

Met	Glu	Lys	Ser	Thr	Arg	Thr	Leu	Phe	Ile	Thr	Ile	Val	Ile	Thr	Ser
1				5					10					15	
Met	Leu	Leu	Gly	Phe	Gly	Asn	Ser	Asp	Leu	Ala	Gln	Asp	Arg	Glu	Glu
		20						25					30		
Cys	Thr	Asn	Gln	Leu	Ile	Glu	Leu	Ser	Thr	Cys	Ile	Pro	Tyr	Val	Gly
		35				40						45			
Gly	Asp	Ala	Lys	Ala	Pro	Thr	Lys	Asp	Cys	Cys	Ala	Gly	Phe	Gly	Gln
	50					55					60				
Val	Ile	Arg	Lys	Ser	Glu	Lys	Cys	Val	Cys	Ile	Phe	Gly	Leu		
65				70						75					

(2) INFORMATION FOR SEQ ID NO:1288:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 62 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..62

(D) OTHER INFORMATION: / Ceres Seq. ID 1500002

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1288:

Met	Leu	Leu	Gly	Phe	Gly	Asn	Ser	Asp	Leu	Ala	Gln	Asp	Arg	Glu	Glu
1				5					10					15	
Cys	Thr	Asn	Gln	Leu	Ile	Glu	Leu	Ser	Thr	Cys	Ile	Pro	Tyr	Val	Gly

20 25 30
Gly Asp Ala Lys Ala Pro Thr Lys Asp Cys Cys Ala Gly Phe Gly Gln
35 40 45
Val Ile Arg Lys Ser Glu Lys Cys Val Cys Ile Phe Gly Leu
50 55 60

(2) INFORMATION FOR SEQ ID NO:1289:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1413 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
(B) LOCATION: 1..1413
(D) OTHER INFORMATION: / Ceres Seq. ID 1500003

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1289:

```
agttgttttt ttctttttct ttcttcgac taaagctctc ttctttctct tcaaacggag 60
ctctcttctt cttcttcaac ctttggtctt cgatctctgt cttttttttt tttatctctt 120
cttcgattgt aagaaaagt ttacgtctaa gaaatctggg tttaagtgtg tttgaaattg 180
tggatcgatt catagattct cgataccaat aggatgtggt gatacgtttg taatctctgtg 240
ccatatcttt ggtttgtcaa agagagtgtg ttttaatgtc aatttctggg taaccaagtt 300
tgagcttatt ccttttgatt ctgcccggct ctctgatttt ttaagtgtg gacgacaagt 360
gatgaaaaga tagagacaaa gaaaggcttc aagtttggtg ataactgctg tctaaagagt 420
tcgttccctt gagagattct cactctgaca taagagttcc cccaaccgga agagaaattc 480
aaagatcaga aaacggtgaa agatgcgacg acgaccagga attggaggat taaaaaggc 540
cgcagctgct agggatcagt accggttact aggagaaaaa gtagccaagg ttacggactg 600
atatgatgaa rgaacagctc tccacgttcc gttcccagct tgaagagttc gctcgtaaac 660
acaagaatga cattcgtaag aatcctgcct tcagggtctc gttccatgaa atgtgtgcta 720
acattggtgt ggatcctctt gcttctaaca agggtttctg ggctgagctc cttggtattg 780
gtgacttcta ctatgaactt ggagttcaga ttattgaagt ttgcatgctt acaagatcac 840
ataatggagg tttgatcagc ttgcaagagc tctgcaacca tcttcgtcag agaaggaaga 900
aagaccgtga agctgtgact gaagatgatt gtcttcgagc tattagcaag cttaaaggat 960
tgggtagcgg atttgagggt atcactattg gcaagaaaaa gcttgctcgt tcagtaccca 1020
cagagctgaa caaagaccat aaccagattt tggagttggc tcagggccaa ggctttgtga 1080
ttgtggaaga ggtacaaaga cgctctctat ggacatctgg tcgctgtata gatgctctcg 1140
aaactttgtt agaggagggc cttgccatga tcgacaatgg ccataaagac ggaaagtgtc 1200
ggtagctggt tccctgtgtt tcttcgggtt actcatccat cgggatctga tacttaaatg 1260
gtacatgctc agttgttttg cttgttttta tacagtatta aatacagtca cactcgttac 1320
atataaatta cgaagaaatc ttttcagtat attactgaaa ttttcttgta catgtatcac 1380
tctgtaaaaa aaatatttat gcttggttgt tgt
```

(2) INFORMATION FOR SEQ ID NO:1290:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 215 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..215
(D) OTHER INFORMATION: / Ceres Seq. ID 1500004

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1290:

```
Met Met Xaa Glu Gln Leu Ser Thr Phe Arg Ser Gln Leu Glu Glu Phe
1 5 10 15
Ala Arg Lys His Lys Asn Asp Ile Arg Lys Asn Pro Ala Phe Arg Ala
20 25 30
Gln Phe His Glu Met Cys Ala Asn Ile Gly Val Asp Pro Leu Ala Ser
35 40 45
Asn Lys Gly Phe Trp Ala Glu Leu Leu Gly Ile Gly Asp Phe Tyr Tyr
50 55 60
```

Glu Leu Gly Val Gln Ile Ile Glu Val Cys Met Leu Thr Arg Ser His
65 70 75 80
Asn Gly Gly Leu Ile Ser Leu Gln Glu Leu Cys Asn His Leu Arg Gln
85 90 95
Arg Arg Lys Lys Asp Arg Glu Ala Val Thr Glu Asp Asp Cys Leu Arg
100 105 110
Ala Ile Ser Lys Leu Lys Val Leu Gly Ser Gly Phe Glu Val Ile Thr
115 120 125
Ile Gly Lys Lys Lys Leu Val Arg Ser Val Pro Thr Glu Leu Asn Lys
130 135 140
Asp His Asn Gln Ile Leu Glu Leu Ala Gln Gly Gln Gly Phe Val Ile
145 150 155 160
Val Glu Glu Val Gln Arg Arg Leu Ser Trp Thr Ser Gly Arg Val Ile
165 170 175
Asp Ala Leu Glu Thr Leu Leu Glu Glu Gly Leu Ala Met Ile Asp Asn
180 185 190
Gly His Lys Asp Gly Lys Cys Arg Tyr Trp Phe Pro Cys Val Ser Ser
195 200 205
Val Tyr Ser Ser Ile Gly Ile
210 215

(2) INFORMATION FOR SEQ ID NO:1291:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 214 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..214

(D) OTHER INFORMATION: / Ceres Seq. ID 1500005

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1291:

Met Xaa Glu Gln Leu Ser Thr Phe Arg Ser Gln Leu Glu Glu Phe Ala
1 5 10 15
Arg Lys His Lys Asn Asp Ile Arg Lys Asn Pro Ala Phe Arg Ala Gln
20 25 30
Phe His Glu Met Cys Ala Asn Ile Gly Val Asp Pro Leu Ala Ser Asn
35 40 45
Lys Gly Phe Trp Ala Glu Leu Leu Gly Ile Gly Asp Phe Tyr Tyr Glu
50 55 60
Leu Gly Val Gln Ile Ile Glu Val Cys Met Leu Thr Arg Ser His Asn
65 70 75 80
Gly Gly Leu Ile Ser Leu Gln Glu Leu Cys Asn His Leu Arg Gln Arg
85 90 95
Arg Lys Lys Asp Arg Glu Ala Val Thr Glu Asp Asp Cys Leu Arg Ala
100 105 110
Ile Ser Lys Leu Lys Val Leu Gly Ser Gly Phe Glu Val Ile Thr Ile
115 120 125
Gly Lys Lys Lys Leu Val Arg Ser Val Pro Thr Glu Leu Asn Lys Asp
130 135 140
His Asn Gln Ile Leu Glu Leu Ala Gln Gly Gln Gly Phe Val Ile Val
145 150 155 160
Glu Glu Val Gln Arg Arg Leu Ser Trp Thr Ser Gly Arg Val Ile Asp
165 170 175
Ala Leu Glu Thr Leu Leu Glu Glu Gly Leu Ala Met Ile Asp Asn Gly
180 185 190
His Lys Asp Gly Lys Cys Arg Tyr Trp Phe Pro Cys Val Ser Ser Val
195 200 205
Tyr Ser Ser Ile Gly Ile
210

(2) INFORMATION FOR SEQ ID NO:1292:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 179 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..179
 (D) OTHER INFORMATION: / Ceres Seq. ID 1500006
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1292:

Met Cys Ala Asn Ile Gly Val Asp Pro Leu Ala Ser Asn Lys Gly Phe
1 5 10 15
Trp Ala Glu Leu Leu Gly Ile Gly Asp Phe Tyr Tyr Glu Leu Gly Val
 20 25 30
Gln Ile Ile Glu Val Cys Met Leu Thr Arg Ser His Asn Gly Gly Leu
 35 40 45
Ile Ser Leu Gln Glu Leu Cys Asn His Leu Arg Gln Arg Arg Lys Lys
50 55 60
Asp Arg Glu Ala Val Thr Glu Asp Asp Cys Leu Arg Ala Ile Ser Lys
65 70 75 80
Leu Lys Val Leu Gly Ser Gly Phe Glu Val Ile Thr Ile Gly Lys Lys
 85 90 95
Lys Leu Val Arg Ser Val Pro Thr Glu Leu Asn Lys Asp His Asn Gln
 100 105 110
Ile Leu Glu Leu Ala Gln Gly Gln Gly Phe Val Ile Val Glu Glu Val
115 120 125
Gln Arg Arg Leu Ser Trp Thr Ser Gly Arg Val Ile Asp Ala Leu Glu
130 135 140
Thr Leu Leu Glu Glu Gly Leu Ala Met Ile Asp Asn Gly His Lys Asp
145 150 155 160
Gly Lys Cys Arg Tyr Trp Phe Pro Cys Val Ser Ser Val Tyr Ser Ser
 165 170 175
Ile Gly Ile

- (2) INFORMATION FOR SEQ ID NO:1293:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1653 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: DNA (genomic)
 (ix) FEATURE:
 (A) NAME/KEY: -
 (B) LOCATION: 1..1653
 (D) OTHER INFORMATION: / Ceres Seq. ID 1500007
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1293:

accaaaatag	atctaaaaca	tggaaccaa	aaccctaatt	ttctcaattc	tcgtcgttgt	60
tctttctctc	atttacttaa	ttggaaaact	caagcgaaag	ccaaatctac	ctccgagtcc	120
ggcatgggtg	ttaccggtga	ttggtcacct	ccgtcttctc	aaaccaccga	ttcatcgcac	180
attcctctcc	ctctctcaat	ccctaaacaa	tgctccgatc	ttctccctcc	gactcggtaa	240
ccgactcggt	ttcgtgaact	cgtcacactc	gatcgccgag	gaatgtttca	ccaaaaacga	300
cgtcgtactg	gcgaacagac	caaacttcat	cctcgctaaa	cacgttgctg	acgattacac	360
aacctatgat	gcagcttcc	acggtgacca	ctggcgtaac	ctccgccgca	tcggctccgt	420
cgagatatcc	tccaaccacc	gtctcaatag	ctttctgtct	attcgtaaa	acgagatccg	480
acgacttggt	tttcgtcttt	cacgtaactt	ttcacaagag	tttgtgaagg	tggatatgaa	540
atcaatgtta	tctgacttaa	cattcaacaa	cattataaga	atgggtggccg	gaaaacgtta	600
ctacggagac	ggtgttgagg	atgatccgga	ggctaaacgt	gtccggcagc	ttatagcga	660
tgtggtggct	tgtgctgggt	ctggaaacgc	tggtgattac	ttaccggttt	tgcggttggt	720
ttcagattac	gaaacacggg	ttaagaagtt	agcgggtagg	ctcgacgagt	tcttgcaagg	780
attggttgat	gagaaacgag	acgctaagga	gaaaggaac	actatgattg	atcacttgct	840

tactctgcaa	gaatcacaa	cggattactt	cactgatcgt	atcatcaaag	gaaacatgct	900
tgctttgata	ctagcagga	cgcacacatc	agcggttacg	ttagaatggg	cattgtcgaa	960
cgtgttgaa	cattcggagg	tattgaacaa	ggcgagagat	gaaatcgata	gaaagatcgg	1020
tttagacagg	cttatggatg	aatcagatat	ctcaaacctg	ccttatctcc	aaaacattgt	1080
gtctgaaacg	ttgcgctttt	atcctgcggc	tcccatgctt	cttcctcacg	ttgcctcgga	1140
agattgtaaa	gttgcaggat	atgatatgcc	gcgtggcacg	atactattga	ccaatgtgtg	1200
ggctatacac	agagatcctc	agctatggga	tgatccaatg	agcttcaagc	cagagaggtt	1260
tgagaaggaa	ggagaagctc	agaagcttat	gccgtttggg	ttaggaagaa	ggcgtgtcc	1320
tggttctgga	ctggctcacc	ggcttataaa	cctgactctt	ggatcattga	ttcagtgttt	1380
ggaatgggag	aagattggag	aagaagtgga	tatgagtga	ggcaaagggtg	ttacaatgcc	1440
taaagccaag	cctttagaag	ccatgtgcag	agcacgtccc	tctgttggtta	aaatcttcaa	1500
ctagtccgct	tgacgttttag	tcttttagta	atggctatgt	atacactaga	taactaatta	1560
tgtttgtatg	ttttcttttt	tttttgggtga	aaatattatg	tttgtatggt	atatgagaat	1620
attttacc	aaatattatg	tttgtatggt	atatgagaat			

(2) INFORMATION FOR SEQ ID NO:1294:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 494 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..494

(D) OTHER INFORMATION: / Ceres Seq. ID 1500008

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1294:

Met	Glu	Thr	Lys	Thr	Leu	Ile	Phe	Ser	Ile	Leu	Val	Val	Val	Leu	Ser
1			5					10						15	
Leu	Ile	Tyr	Leu	Ile	Gly	Lys	Leu	Lys	Arg	Lys	Pro	Asn	Leu	Pro	Pro
			20					25					30		
Ser	Pro	Ala	Trp	Ser	Leu	Pro	Val	Ile	Gly	His	Leu	Arg	Leu	Leu	Lys
		35					40					45			
Pro	Pro	Ile	His	Arg	Thr	Phe	Leu	Ser	Leu	Ser	Gln	Ser	Leu	Asn	Asn
		50				55					60				
Ala	Pro	Ile	Phe	Ser	Leu	Arg	Leu	Gly	Asn	Arg	Leu	Val	Phe	Val	Asn
65					70				75						80
Ser	Ser	His	Ser	Ile	Ala	Glu	Glu	Cys	Phe	Thr	Lys	Asn	Asp	Val	Val
			85					90					95		
Leu	Ala	Asn	Arg	Pro	Asn	Phe	Ile	Leu	Ala	Lys	His	Val	Ala	Tyr	Asp
			100					105					110		
Tyr	Thr	Thr	Met	Ile	Ala	Ala	Ser	Tyr	Gly	Asp	His	Trp	Arg	Asn	Leu
		115					120					125			
Arg	Arg	Ile	Gly	Ser	Val	Glu	Ile	Phe	Ser	Asn	His	Arg	Leu	Asn	Ser
			130				135					140			
Phe	Leu	Ser	Ile	Arg	Lys	Xaa	Glu	Ile	Arg	Arg	Leu	Val	Phe	Arg	Leu
145					150				155						160
Ser	Arg	Asn	Phe	Ser	Gln	Glu	Phe	Val	Lys	Val	Asp	Met	Lys	Ser	Met
			165					170					175		
Leu	Ser	Asp	Leu	Thr	Phe	Asn	Asn	Ile	Arg	Met	Val	Ala	Gly	Lys	
			180					185					190		
Arg	Tyr	Tyr	Gly	Asp	Gly	Val	Glu	Asp	Asp	Pro	Glu	Ala	Lys	Arg	Val
		195					200					205			
Arg	Gln	Leu	Ile	Ala	Asp	Val	Val	Ala	Cys	Ala	Gly	Ala	Gly	Asn	Ala
		210				215					220				
Val	Asp	Tyr	Leu	Pro	Val	Leu	Arg	Leu	Val	Ser	Asp	Tyr	Glu	Thr	Arg
225					230				235						240
Val	Lys	Lys	Leu	Ala	Gly	Arg	Leu	Asp	Glu	Phe	Leu	Gln	Gly	Leu	Val
			245					250					255		
Asp	Glu	Lys	Arg	Asp	Ala	Lys	Glu	Lys	Gly	Asn	Thr	Met	Ile	Asp	His
			260				265					270			
Leu	Leu	Thr	Leu	Gln	Glu	Ser	Gln	Pro	Asp	Tyr	Phe	Thr	Asp	Arg	Ile

275					280					285					
Ile	Lys	Gly	Asn	Met	Leu	Ala	Leu	Ile	Leu	Ala	Gly	Thr	Asp	Thr	Ser
290						295					300				
Ala	Val	Thr	Leu	Glu	Trp	Ala	Leu	Ser	Asn	Val	Leu	Asn	His	Ser	Glu
305					310					315					320
Val	Leu	Asn	Lys	Ala	Arg	Asp	Glu	Ile	Asp	Arg	Lys	Ile	Gly	Leu	Asp
				325					330					335	
Arg	Leu	Met	Asp	Glu	Ser	Asp	Ile	Ser	Asn	Leu	Pro	Tyr	Leu	Gln	Asn
			340					345					350		
Ile	Val	Ser	Glu	Thr	Leu	Arg	Leu	Tyr	Pro	Ala	Ala	Pro	Met	Leu	Leu
		355					360					365			
Pro	His	Val	Ala	Ser	Glu	Asp	Cys	Lys	Val	Ala	Gly	Tyr	Asp	Met	Pro
		370				375					380				
Arg	Gly	Thr	Ile	Leu	Leu	Thr	Asn	Val	Trp	Ala	Ile	His	Arg	Asp	Pro
385					390					395					400
Gln	Leu	Trp	Asp	Asp	Pro	Met	Ser	Phe	Lys	Pro	Glu	Arg	Phe	Glu	Lys
				405					410					415	
Glu	Gly	Glu	Ala	Gln	Lys	Leu	Met	Pro	Phe	Gly	Leu	Gly	Arg	Arg	Ala
			420					425					430		
Cys	Pro	Gly	Ser	Gly	Leu	Ala	His	Arg	Leu	Ile	Asn	Leu	Thr	Leu	Gly
		435					440					445			
Ser	Leu	Ile	Gln	Cys	Leu	Glu	Trp	Glu	Lys	Ile	Gly	Glu	Glu	Val	Asp
		450				455					460				
Met	Ser	Glu	Gly	Lys	Gly	Val	Thr	Met	Pro	Lys	Ala	Lys	Pro	Leu	Glu
465					470					475					480
Ala	Met	Cys	Arg	Ala	Arg	Pro	Ser	Val	Val	Lys	Ile	Phe	Asn		
				485				490							

(2) INFORMATION FOR SEQ ID NO:1295:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 379 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..379

(D) OTHER INFORMATION: / Ceres Seq. ID 1500009

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1295:

Met	Ile	Ala	Ala	Ser	Tyr	Gly	Asp	His	Trp	Arg	Asn	Leu	Arg	Arg	Ile
1				5					10					15	
Gly	Ser	Val	Glu	Ile	Phe	Ser	Asn	His	Arg	Leu	Asn	Ser	Phe	Leu	Ser
		20						25					30		
Ile	Arg	Lys	Xaa	Glu	Ile	Arg	Arg	Leu	Val	Phe	Arg	Leu	Ser	Arg	Asn
		35					40					45			
Phe	Ser	Gln	Glu	Phe	Val	Lys	Val	Asp	Met	Lys	Ser	Met	Leu	Ser	Asp
		50				55				60					
Leu	Thr	Phe	Asn	Asn	Ile	Ile	Arg	Met	Val	Ala	Gly	Lys	Arg	Tyr	Tyr
65					70					75				80	
Gly	Asp	Gly	Val	Glu	Asp	Asp	Pro	Glu	Ala	Lys	Arg	Val	Arg	Gln	Leu
			85						90					95	
Ile	Ala	Asp	Val	Val	Ala	Cys	Ala	Gly	Ala	Gly	Asn	Ala	Val	Asp	Tyr
		100						105					110		
Leu	Pro	Val	Leu	Arg	Leu	Val	Ser	Asp	Tyr	Glu	Thr	Arg	Val	Lys	Lys
		115						120					125		
Leu	Ala	Gly	Arg	Leu	Asp	Glu	Phe	Leu	Gln	Gly	Leu	Val	Asp	Glu	Lys
		130				135					140				
Arg	Asp	Ala	Lys	Glu	Lys	Gly	Asn	Thr	Met	Ile	Asp	His	Leu	Leu	Thr
145					150					155					160
Leu	Gln	Glu	Ser	Gln	Pro	Asp	Tyr	Phe	Thr	Asp	Arg	Ile	Ile	Lys	Gly
				165					170					175	

Asn Met Leu Ala Leu Ile Leu Ala Gly Thr Asp Thr Ser Ala Val Thr
180 185 190
Leu Glu Trp Ala Leu Ser Asn Val Leu Asn His Ser Glu Val Leu Asn
195 200 205
Lys Ala Arg Asp Glu Ile Asp Arg Lys Ile Gly Leu Asp Arg Leu Met
210 215 220
Asp Glu Ser Asp Ile Ser Asn Leu Pro Tyr Leu Gln Asn Ile Val Ser
225 230 235 240
Glu Thr Leu Arg Leu Tyr Pro Ala Ala Pro Met Leu Leu Pro His Val
245 250 255
Ala Ser Glu Asp Cys Lys Val Ala Gly Tyr Asp Met Pro Arg Gly Thr
260 265 270
Ile Leu Leu Thr Asn Val Trp Ala Ile His Arg Asp Pro Gln Leu Trp
275 280 285
Asp Asp Pro Met Ser Phe Lys Pro Glu Arg Phe Glu Lys Glu Gly Glu
290 295 300
Ala Gln Lys Leu Met Pro Phe Gly Leu Gly Arg Arg Ala Cys Pro Gly
305 310 315 320
Ser Gly Leu Ala His Arg Leu Ile Asn Leu Thr Leu Gly Ser Leu Ile
325 330 335
Gln Cys Leu Glu Trp Glu Lys Ile Gly Glu Glu Val Asp Met Ser Glu
340 345 350
Gly Lys Gly Val Thr Met Pro Lys Ala Lys Pro Leu Glu Ala Met Cys
355 360 365
Arg Ala Arg Pro Ser Val Val Lys Ile Phe Asn
370 375

(2) INFORMATION FOR SEQ ID NO:1296:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 322 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..322

(D) OTHER INFORMATION: / Ceres Seq. ID 1500010

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1296:

Met Lys Ser Met Leu Ser Asp Leu Thr Phe Asn Asn Ile Ile Arg Met
1 5 10 15
Val Ala Gly Lys Arg Tyr Tyr Gly Asp Gly Val Glu Asp Asp Pro Glu
20 25 30
Ala Lys Arg Val Arg Gln Leu Ile Ala Asp Val Val Ala Cys Ala Gly
35 40 45
Ala Gly Asn Ala Val Asp Tyr Leu Pro Val Leu Arg Leu Val Ser Asp
50 55 60
Tyr Glu Thr Arg Val Lys Lys Leu Ala Gly Arg Leu Asp Glu Phe Leu
65 70 75 80
Gln Gly Leu Val Asp Glu Lys Arg Asp Ala Lys Glu Lys Gly Asn Thr
85 90 95
Met Ile Asp His Leu Leu Thr Leu Gln Glu Ser Gln Pro Asp Tyr Phe
100 105 110
Thr Asp Arg Ile Ile Lys Gly Asn Met Leu Ala Leu Ile Leu Ala Gly
115 120 125
Thr Asp Thr Ser Ala Val Thr Leu Glu Trp Ala Leu Ser Asn Val Leu
130 135 140
Asn His Ser Glu Val Leu Asn Lys Ala Arg Asp Glu Ile Asp Arg Lys
145 150 155 160
Ile Gly Leu Asp Arg Leu Met Asp Glu Ser Asp Ile Ser Asn Leu Pro
165 170 175
Tyr Leu Gln Asn Ile Val Ser Glu Thr Leu Arg Leu Tyr Pro Ala Ala

	180		185		190										
Pro	Met	Leu	Pro	His	Val	Ala	Ser	Glu	Asp	Cys	Lys	Val	Ala	Gly	
	195					200					205				
Tyr	Asp	Met	Pro	Arg	Gly	Thr	Ile	Leu	Leu	Thr	Asn	Val	Trp	Ala	Ile
	210					215					220				
His	Arg	Asp	Pro	Gln	Leu	Trp	Asp	Asp	Pro	Met	Ser	Phe	Lys	Pro	Glu
	225				230					235					240
Arg	Phe	Glu	Lys	Glu	Gly	Glu	Ala	Gln	Lys	Leu	Met	Pro	Phe	Gly	Leu
			245						250					255	
Gly	Arg	Arg	Ala	Cys	Pro	Gly	Ser	Gly	Leu	Ala	His	Arg	Leu	Ile	Asn
			260					265					270		
Leu	Thr	Leu	Gly	Ser	Leu	Ile	Gln	Cys	Leu	Glu	Trp	Glu	Lys	Ile	Gly
	275						280					285			
Glu	Glu	Val	Asp	Met	Ser	Glu	Gly	Lys	Gly	Val	Thr	Met	Pro	Lys	Ala
	290					295					300				
Lys	Pro	Leu	Glu	Ala	Met	Cys	Arg	Ala	Arg	Pro	Ser	Val	Val	Lys	Ile
	305				310					315					320
Phe	Asn														

(2) INFORMATION FOR SEQ ID NO:1297:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1465 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1465
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500011

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1297:

gcagtgaggaga	gagagcatgt	gaataaaaag	cgtgaagcct	tttgatatct	ctttctcttc	60
ctcttccttt	ctcctccgat	agatttcgcc	ggcgatggcg	gtggactcct	tagaaacgga	120
gattgacacg	gcgggtgcgtg	ttgtccacct	cgcttcttct	ctctgtgtta	aagttcaaga	180
gaagcttcat	cttcctaacg	gtgggtcacgt	taagtctaaa	gacgatgatt	cccctgtcac	240
cgtcgctgat	tttggtgtac	aagcaattgt	gagctgggtt	ttagctgaag	tgtttggtga	300
tcaaaacctt	tcaattgttg	ctgaagaaga	cactgagaca	ctctctgagg	ctgattcttt	360
aggctcttta	ggagctgtgt	cgaatgcggt	taatgaagca	ttgtccgaag	ctcagaacta	420
cgggcttccg	aagccagtta	agccattggg	gtctagtga	attcttaagg	ctattagtag	480
atgtaactct	gttgaggagac	ctaaaggaag	gcattgggtt	cttgatcctg	ttgatggaac	540
gttaggggtt	gttcgtgggg	atcagtatgc	tggtgcttta	gctttgatag	agaatggtaa	600
agttcttttg	ggtgtactag	gatgtcctaa	ttatccgggt	aagaaagaat	gtttaagtaa	660
tggttgtaac	caagctatga	agacgaaagc	tggtgctggt	tcagtatcga	aaggatgtgt	720
tatgtatgca	aagagaggta	gtgggtcaagc	ttggatgcaa	cctttgatcg	ttggaggaat	780
accagaatct	gcaacacttc	ttaaggtttc	ttcagttgat	gatccgggtt	tagctacagt	840
ttgtgagcca	gtagagagag	caaactcaaa	ccacttggtc	actgcaggac	ttgccaatag	900
catgggagtt	agaaagcagc	ctatgcgagt	gtatagcatg	gtgaaatag	cagcgattgc	960
acgtggagac	gctgaagtgt	ttatgaagtt	tgcacagtca	agttacaaag	agaagatatg	1020
ggatcacgca	gctggagttg	ttattgtgga	agaagctggt	ggtgtggtga	ctgatgcggg	1080
agggagaaac	ttagacttct	cgaagggtgt	ttacttgga	ggtcttgacc	gtggaatcat	1140
cgcatgttct	ggtcaagttt	tacatgagaa	gattataggt	gctgtttatg	ctagttggga	1200
atcttccagt	ctctgaaaaa	gcttatccac	aatccgtagt	ttggtgcagc	atcatcgagc	1260
caaagcaaag	gaggaacaag	ggccattacg	gtttaggatg	agcaagggcc	agtttcaatg	1320
aatgtgaatg	gcggagaagt	aaatatagtc	gaggaagcag	cggtaaaagt	aagaatctag	1380
tttatttacc	tatctaagag	taataaagct	gctgcatttc	acgaaccctt	atgttctatg	1440
atctttaatg	gatgatata	ca ttttt				

(2) INFORMATION FOR SEQ ID NO:1298:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 373 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:

- (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..373
 (D) OTHER INFORMATION: / Ceres Seq. ID 1500012

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1298:

Met	Ala	Val	Asp	Ser	Leu	Glu	Thr	Glu	Ile	Asp	Thr	Ala	Val	Arg	Val
1				5					10					15	
Val	His	Leu	Ala	Ser	Ser	Leu	Cys	Val	Lys	Val	Gln	Glu	Lys	Leu	His
			20				25						30		
Leu	Pro	Asn	Gly	Gly	His	Val	Lys	Ser	Lys	Asp	Asp	Asp	Ser	Pro	Val
			35				40					45			
Thr	Val	Ala	Asp	Phe	Gly	Val	Gln	Ala	Ile	Val	Ser	Trp	Val	Leu	Ala
	50				55					60					
Glu	Val	Phe	Gly	Asp	Gln	Asn	Leu	Ser	Ile	Val	Ala	Glu	Glu	Asp	Thr
65					70					75				80	
Glu	Thr	Leu	Ser	Glu	Ala	Asp	Ser	Leu	Gly	Leu	Leu	Gly	Ala	Val	Ser
				85					90					95	
Asn	Ala	Val	Asn	Glu	Ala	Leu	Ser	Glu	Ala	Gln	Asn	Tyr	Gly	Leu	Pro
			100					105					110		
Lys	Pro	Val	Lys	Pro	Leu	Gly	Ser	Glu	Ile	Leu	Lys	Ala	Ile	Ser	
			115				120					125			
Arg	Cys	Asn	Ser	Val	Gly	Gly	Pro	Lys	Gly	Arg	His	Trp	Val	Leu	Asp
	130					135					140				
Pro	Val	Asp	Gly	Thr	Leu	Gly	Phe	Val	Arg	Gly	Asp	Gln	Tyr	Ala	Val
145					150					155				160	
Ala	Leu	Ala	Leu	Ile	Glu	Asn	Gly	Lys	Val	Leu	Leu	Gly	Val	Leu	Gly
				165					170					175	
Cys	Pro	Asn	Tyr	Pro	Val	Lys	Lys	Glu	Cys	Leu	Ser	Asn	Gly	Cys	Asn
			180					185					190		
Gln	Ala	Met	Lys	Thr	Lys	Ala	Val	Ala	Gly	Ser	Val	Ser	Lys	Gly	Cys
		195					200					205			
Val	Met	Tyr	Ala	Lys	Arg	Gly	Ser	Gly	Gln	Ala	Trp	Met	Gln	Pro	Leu
	210					215					220				
Ile	Val	Gly	Gly	Ile	Pro	Glu	Ser	Ala	Thr	Leu	Leu	Lys	Val	Ser	Ser
225					230					235				240	
Val	Asp	Asp	Pro	Val	Leu	Ala	Thr	Val	Cys	Glu	Pro	Val	Glu	Arg	Ala
				245					250					255	
Asn	Ser	Asn	His	Leu	Phe	Thr	Ala	Gly	Leu	Ala	Asn	Ser	Met	Gly	Val
			260					265					270		
Arg	Lys	Gln	Pro	Met	Arg	Val	Tyr	Ser	Met	Val	Lys	Tyr	Ala	Ala	Ile
		275					280					285			
Ala	Arg	Gly	Asp	Ala	Glu	Val	Phe	Met	Lys	Phe	Ala	Gln	Ser	Ser	Tyr
	290					295					300				
Lys	Glu	Lys	Ile	Trp	Asp	His	Ala	Ala	Gly	Val	Val	Ile	Val	Glu	Glu
305					310					315				320	
Ala	Gly	Gly	Val	Val	Thr	Asp	Ala	Gly	Gly	Arg	Asn	Leu	Asp	Phe	Ser
			325					330						335	
Lys	Gly	Val	Tyr	Leu	Glu	Gly	Leu	Asp	Arg	Gly	Ile	Ile	Ala	Cys	Ser
		340					345						350		
Gly	Gln	Val	Leu	His	Glu	Lys	Ile	Ile	Gly	Ala	Val	Tyr	Ala	Ser	Trp
		355					360					365			
Glu	Ser	Ser	Ser	Leu											
															370

(2) INFORMATION FOR SEQ ID NO:1299:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1472 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1472

(D) OTHER INFORMATION: / Ceres Seq. ID 1500017

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1299:

```
aaaaaagtca atcatatcaa atcccaaata ctcccagatg tttttatcat cttcttcttc      60
ctgaagattt gatttcatTT tctctctttt cagatcccta ttctcatggc ttctggatct      120
tactggtgct atagttgtag ccgattcgtt tgggtttccg attcaatctc ttgccctgat      180
tgcgacggtg gtttcctcga actcatccaa gagcctctcg atttcacacc ttccgattcc      240
ttcaccacca ccaccaccac tcaacatcgc agccccactc gcttccctcc tcttcttctt      300
tcttcttcca ccccatccgc ttctatgcac gccgataaca gtccccactcc taccatcggt      360
actcgtacac gaagcaatcg atctcctaata ccagttattg ttctccgtgg atctgctgct      420
gctccttctt ctgatgttgt ttccgaaggt ttagatcgat ctgcttttca gatgtattac      480
gatgatggtg ctgattctgg tcttagacct ttaccaccga gtatgactga gtttttggtt      540
ggttctggat ttgatcgttt gttagatcag atctctcaga tcgagcttaa caccaatcgg      600
aatcttctgt cttgtgaaca tccaccggct tctaaatcgg ccattgaagc ttgcctctg      660
attgaaatcg atccgactca tctcttatcg gattctcaat ctcatcgcg tggttgcaaa      720
gagaatttctg ttttgaaatc atctgctcgc gagatgcctt gtaatcacat ctatcatcct      780
gattgtattc ttcttggctg tgcgattcgt aactcttgct cggtttgccg tcatgagcta      840
ccggcgaggg atctcaccga cggaaccggg gctgctttga ctgctgttac cgctactgca      900
gaggaagagg aagactcagc tgcgggggta acgatttgga ggttaccagg tggaggattc      960
gctgtaggga gaatccctgg tggttgagga ggtggagata gaatgatgcc ggtgggttac      1020
acggagggtg atggtggtag atcgggtgat gagagacttc cgagaagagt agcttggggg      1080
tcgagaagag gtggaagaga tgggtggagg agtagagagc agaggtgggt gctttgcggg      1140
tcggatcatg aggccttttc gatgttttag tggatcatct ggatccattg ctgctgctgc      1200
tgctgcatca tccgggtccg ggtccagaat tcgggttact cgtagaacca ggtcgttctc      1260
tatgttcagt acggcgctcg cttcgtcaag gagacgaaat tggctagcgt gattactaga      1320
attaccaagc tctcttctca ggtgaaaact aaacacgaaa gaacacactc ttcttctggt      1380
taaatttttc ctatgttctt tattaagttt ttgtctattt cagtgtaatg attatattca      1440
ttcttaaaat ttgaatctat gcgagtaaat tg
```

(2) INFORMATION FOR SEQ ID NO:1300:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 354 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..354

(D) OTHER INFORMATION: / Ceres Seq. ID 1500018

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1300:

```
Met Ala Ser Gly Ser Tyr Trp Cys Tyr Ser Cys Ser Arg Phe Val Trp
1      5      10      15
Val Ser Asp Ser Ile Ser Cys Pro Asp Cys Asp Gly Gly Phe Leu Glu
20     25     30
Leu Ile Gln Glu Pro Leu Asp Phe Thr Pro Ser Asp Ser Phe Thr Thr
35     40     45
Thr Thr Thr Thr Gln His Arg Ser Pro Thr Arg Phe Pro Pro Pro Ser
50     55     60
Ser Ser Ser Ser Thr Pro Ser Ala Ser Met His Ala Asp Asn Ser Pro
65     70     75     80
Thr Pro Thr Ile Val Thr Arg Thr Arg Ser Asn Arg Ser Pro Asn Pro
85     90     95
Val Ile Val Leu Arg Gly Ser Ala Ala Ala Pro Ser Ser Asp Val Val
100    105    110
Ser Glu Gly Leu Asp Arg Ser Ala Phe Gln Met Tyr Tyr Asp Asp Gly
115    120    125
Thr Asp Ser Gly Leu Arg Pro Leu Pro Pro Ser Met Thr Glu Phe Leu
130    135    140
```

Leu Gly Ser Gly Phe Asp Arg Leu Leu Asp Gln Ile Ser Gln Ile Glu
145 150 155 160
Leu Asn Thr Asn Arg Asn Leu Arg Ser Cys Glu His Pro Pro Ala Ser
165 170 175
Lys Ser Ala Ile Glu Ala Leu Pro Leu Ile Glu Ile Asp Pro Thr His
180 185 190
Leu Leu Ser Asp Ser Gln Ser His Cys Ala Val Cys Lys Glu Asn Phe
195 200 205
Val Leu Lys Ser Ser Ala Arg Glu Met Pro Cys Asn His Ile Tyr His
210 215 220
Pro Asp Cys Ile Leu Pro Trp Leu Ala Ile Arg Asn Ser Cys Pro Val
225 230 235 240
Cys Arg His Glu Leu Pro Ala Glu Asp Leu Thr Asp Gly Thr Gly Ala
245 250 255
Ala Leu Thr Ala Val Thr Ala Thr Ala Glu Glu Glu Glu Asp Ser Ala
260 265 270
Ala Gly Leu Thr Ile Trp Arg Leu Pro Gly Gly Gly Phe Ala Val Gly
275 280 285
Arg Ile Pro Gly Gly Trp Arg Gly Gly Asp Arg Met Met Pro Val Val
290 295 300
Tyr Thr Glu Val Asp Gly Gly Arg Leu Gly Asp Glu Arg Leu Pro Arg
305 310 315 320
Arg Val Ala Trp Gly Ser Arg Arg Gly Gly Arg Asp Gly Gly Gly Ser
325 330 335
Arg Glu Gln Arg Trp Trp Leu Cys Gly Ser Asp His Glu Ala Phe Arg
340 345 350
Met Phe

(2) INFORMATION FOR SEQ ID NO:1301:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 281 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..281
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500019

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1301:

Met His Ala Asp Asn Ser Pro Thr Pro Thr Ile Val Thr Arg Thr Arg
1 5 10 15
Ser Asn Arg Ser Pro Asn Pro Val Ile Val Leu Arg Gly Ser Ala Ala
20 25 30
Ala Pro Ser Ser Asp Val Val Ser Glu Gly Leu Asp Arg Ser Ala Phe
35 40 45
Gln Met Tyr Tyr Asp Asp Gly Thr Asp Ser Gly Leu Arg Pro Leu Pro
50 55 60
Pro Ser Met Thr Glu Phe Leu Leu Gly Ser Gly Phe Asp Arg Leu Leu
65 70 75 80
Asp Gln Ile Ser Gln Ile Glu Leu Asn Thr Asn Arg Asn Leu Arg Ser
85 90 95
Cys Glu His Pro Pro Ala Ser Lys Ser Ala Ile Glu Ala Leu Pro Leu
100 105 110
Ile Glu Ile Asp Pro Thr His Leu Leu Ser Asp Ser Gln Ser His Cys
115 120 125
Ala Val Cys Lys Glu Asn Phe Val Leu Lys Ser Ser Ala Arg Glu Met
130 135 140
Pro Cys Asn His Ile Tyr His Pro Asp Cys Ile Leu Pro Trp Leu Ala
145 150 155 160
Ile Arg Asn Ser Cys Pro Val Cys Arg His Glu Leu Pro Ala Glu Asp

165 170 175
Leu Thr Asp Gly Thr Gly Ala Ala Leu Thr Ala Val Thr Ala Thr Ala
180 185 190
Glu Glu Glu Glu Asp Ser Ala Ala Gly Leu Thr Ile Trp Arg Leu Pro
195 200 205
Gly Gly Gly Phe Ala Val Gly Arg Ile Pro Gly Gly Trp Arg Gly Gly
210 215 220
Asp Arg Met Met Pro Val Tyr Thr Glu Val Asp Gly Gly Arg Leu
225 230 235 240
Gly Asp Glu Arg Leu Pro Arg Arg Val Ala Trp Gly Ser Arg Arg Gly
245 250 255
Gly Arg Asp Gly Gly Gly Ser Arg Glu Gln Arg Trp Trp Leu Cys Gly
260 265 270
Ser Asp His Glu Ala Phe Arg Met Phe
275 280

(2) INFORMATION FOR SEQ ID NO:1302:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 232 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..232
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500020

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1302:

Met Tyr Tyr Asp Asp Gly Thr Asp Ser Gly Leu Arg Pro Leu Pro Pro
1 5 10 15
Ser Met Thr Glu Phe Leu Leu Gly Ser Gly Phe Asp Arg Leu Leu Asp
20 25 30
Gln Ile Ser Gln Ile Glu Leu Asn Thr Asn Arg Asn Leu Arg Ser Cys
35 40 45
Glu His Pro Pro Ala Ser Lys Ser Ala Ile Glu Ala Leu Pro Leu Ile
50 55 60
Glu Ile Asp Pro Thr His Leu Leu Ser Asp Ser Gln Ser His Cys Ala
65 70 75 80
Val Cys Lys Glu Asn Phe Val Leu Lys Ser Ser Ala Arg Glu Met Pro
85 90 95
Cys Asn His Ile Tyr His Pro Asp Cys Ile Leu Pro Trp Leu Ala Ile
100 105 110
Arg Asn Ser Cys Pro Val Cys Arg His Glu Leu Pro Ala Glu Asp Leu
115 120 125
Thr Asp Gly Thr Gly Ala Ala Leu Thr Ala Val Thr Ala Thr Ala Glu
130 135 140
Glu Glu Glu Asp Ser Ala Ala Gly Leu Thr Ile Trp Arg Leu Pro Gly
145 150 155 160
Gly Gly Phe Ala Val Gly Arg Ile Pro Gly Gly Trp Arg Gly Gly Asp
165 170 175
Arg Met Met Pro Val Val Tyr Thr Glu Val Asp Gly Gly Arg Leu Gly
180 185 190
Asp Glu Arg Leu Pro Arg Arg Val Ala Trp Gly Ser Arg Arg Gly Gly
195 200 205
Arg Asp Gly Gly Gly Ser Arg Glu Gln Arg Trp Trp Leu Cys Gly Ser
210 215 220
Asp His Glu Ala Phe Arg Met Phe
225 230

(2) INFORMATION FOR SEQ ID NO:1303:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1467 base pairs
- (B) TYPE: nucleic acid

- (C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
(A) NAME/KEY: -
(B) LOCATION: 1..1467
(D) OTHER INFORMATION: / Ceres Seq. ID 1500025
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1303:

```
attcttcttc ttctctctct cctctgttct atctctttct aacactcaag cctctcacgg      60
tcacgggctc acggccatgg aagagaactc aagtaaaaaa acgctatcgg aaactatgag      120
cttacaagat acagttctga agtttttcag agtttacata ccaaatacaa ccgcggatga      180
catggtagta cgttgcttaa atctcttaga acagagcatt tccgctctgt ttttgcaaga      240
tcttgtcttt ttccgagttt tgaatgatat gtattgaaca atcttgaaaag ttttagcttt      300
agcagacatt ttttgagttt taggttgtgt gtttatgtga tgtgacaaat ccatacgggtg      360
tatgatattg ttttgaaatt atgttagtgt tgttcaaagt aagatgtgtg tttctctatt      420
gttttgtaca gaatctacct ttggtttcag acaagatctc agggaagcct cttcctcggg      480
aggtaactgt taaaagtgtg tcctcgggga acattttggag gatggaaatg aaagcaaacg      540
gtaacacagt gtttctccga gacgggtgga agaaaatcgt caaggacgag aatgtgactg      600
agccaatttt cttggagttt gagttcgatg gttatggtgt gttccacttt tgcgtgtacg      660
agtatggttc aatgtgtaaa aggatgagat ctccaatgga aaaagaagtg attaaagtgg      720
acagtgaaga agatgtgctt gtggggaatg aagagagcac aaaagggctt gaggagtcgc      780
caagaagagg tggtaacaagt agaagacgtg cgaaactgaa gactaatagt cataagattc      840
atgaacatct agacaacaaa ctaaaccctg cgtttccggt tgatatgact caaaatagaa      900
cggtaaaaga aacgaaatgt gactaaagaa aatttcaaat gactaaatgg tttgtcattc      960
attatgattg gttctgattt tcagcgcata ccgtctttac ttataaagga ctacaacttg     1020
acatttccca acatggttat catgcgtgac aagattggca tattgaagag aagaatcgtg     1080
atttggaaga acagatccgt gtatctaaat ggaatcggta gtatcatccg aaggaatcat     1140
gtgaagccag gtaatgaagt ggtattcgaa cttaagatgg tcaatggtta tcacggtttg     1200
gttcacgaaa tcaaggtcca cattatcaag gcctgatcat attcttacat gttgttctat     1260
cttagagaaat gttaattgaa atgtttaagt tatttatctc gttgtgttga tcatgttagt     1320
tttgcattctg tttttcatta tgcatttcct gacactcgat ggtttgaatt ggtttttttt     1380
ttggcgaaact gtctctctat ctctttgtaa tggcatgact ttgccttttc acaaaaaaaaa     1440
aaaawaaaaa aaaaaamngg awtgtcc
```

(2) INFORMATION FOR SEQ ID NO:1304:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 181 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..181
(D) OTHER INFORMATION: / Ceres Seq. ID 1500026

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1304:

```
Met Leu Val Leu Phe Lys Val Arg Cys Val Phe Leu Tyr Cys Phe Val
1           5           10          15
Gln Asn Leu Pro Leu Val Ser Asp Lys Ile Ser Gly Lys Pro Leu Pro
20          25          30
Arg Lys Val Thr Val Lys Ser Val Ser Ser Gly Asn Ile Trp Arg Met
35          40          45
Glu Met Lys Ala Asn Gly Asn Thr Val Phe Leu Arg Asp Gly Trp Lys
50          55          60
Lys Ile Val Lys Asp Glu Asn Val Thr Glu Pro Ile Phe Leu Glu Phe
65          70          75          80
Glu Phe Asp Gly Tyr Gly Val Phe His Phe Cys Val Tyr Glu Tyr Gly
85          90          95
Ser Met Cys Lys Arg Met Arg Ser Pro Met Glu Lys Glu Val Ile Lys
100         105         110
Val Asp Ser Glu Glu Asp Val Leu Val Gly Asn Glu Glu Ser Thr Lys
115         120         125
```


Gly Leu Glu Glu Ser Pro Arg Arg Gly Gly Thr Ser Arg Arg Arg Ala
130 135 140
Lys Leu Lys Thr Asn Ser His Lys Ile His Glu His Leu Asp Asn Lys
145 150 155 160
Leu Asn Pro Ser Phe Pro Val Asp Met Thr Gln Asn Arg Thr Val Lys
165 170 175
Lys Thr Lys Cys Asp
180

(2) INFORMATION FOR SEQ ID NO:1305:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 134 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..134
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500027

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1305:

Met Glu Met Lys Ala Asn Gly Asn Thr Val Phe Leu Arg Asp Gly Trp
1 5 10 15
Lys Lys Ile Val Lys Asp Glu Asn Val Thr Glu Pro Ile Phe Leu Glu
20 25 30
Phe Glu Phe Asp Gly Tyr Gly Val Phe His Phe Cys Val Tyr Glu Tyr
35 40 45
Gly Ser Met Cys Lys Arg Met Arg Ser Pro Met Glu Lys Glu Val Ile
50 55 60
Lys Val Asp Ser Glu Glu Asp Val Leu Val Gly Asn Glu Glu Ser Thr
65 70 75 80
Lys Gly Leu Glu Glu Ser Pro Arg Arg Gly Gly Thr Ser Arg Arg Arg
85 90 95
Ala Lys Leu Lys Thr Asn Ser His Lys Ile His Glu His Leu Asp Asn
100 105 110
Lys Leu Asn Pro Ser Phe Pro Val Asp Met Thr Gln Asn Arg Thr Val
115 120 125
Lys Lys Thr Lys Cys Asp
130

(2) INFORMATION FOR SEQ ID NO:1306:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 132 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..132
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500028

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1306:

Met Lys Ala Asn Gly Asn Thr Val Phe Leu Arg Asp Gly Trp Lys Lys
1 5 10 15
Ile Val Lys Asp Glu Asn Val Thr Glu Pro Ile Phe Leu Glu Phe Glu
20 25 30
Phe Asp Gly Tyr Gly Val Phe His Phe Cys Val Tyr Glu Tyr Gly Ser
35 40 45
Met Cys Lys Arg Met Arg Ser Pro Met Glu Lys Glu Val Ile Lys Val
50 55 60
Asp Ser Glu Glu Asp Val Leu Val Gly Asn Glu Glu Ser Thr Lys Gly
65 70 75 80
Leu Glu Glu Ser Pro Arg Arg Gly Gly Thr Ser Arg Arg Arg Ala Lys

85 90 95
Leu Lys Thr Asn Ser His Lys Ile His Glu His Leu Asp Asn Lys Leu
100 105 110
Asn Pro Ser Phe Pro Val Asp Met Thr Gln Asn Arg Thr Val Lys Lys
115 120 125
Thr Lys Cys Asp
130

(2) INFORMATION FOR SEQ ID NO:1307:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2031 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..2031
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500036

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1307:

ttttaacgaa	cattttgttg	gtaagaacga	agaagacgtg	gagaagtaga	agaatgatga	60
tgcagaaatt	gagaagatcg	ggggagttca	taagatttgg	atgcaaattct	ctaattagta	120
gccgacccaa	caaggactca	gtgtcacgtt	ctgtgtcagg	ctttgtgaat	cactacaaat	180
caaaaggcaa	gctttttgag	ctaagtgatg	ggaactataa	gacagagctt	catcatccat	240
gtattagtag	aaatgtgggg	atgcttcttc	agcagtataa	gtgttttgga	tcacagcag	300
cttctttaat	tcagagaaac	cctttgtttt	cgctgttgga	ttcgaaagat	gttagctact	360
ttaaggagat	attaggtgaa	aaaaacgtgg	ttgaagataa	agaaaggctt	gagactgcta	420
atacagattg	gatgcataag	tacaaaggat	ctagtaagct	gatgctcttg	cccaagaata	480
gacaagaggt	gtctcagata	cttgagyact	gtgattcgag	gcgttttagca	ggttggtcct	540
caaggaggaa	caactggtct	tgttggttga	agtgtgcctg	tctttgatga	ggtgatcgtc	600
aatgttggtc	tgatgaacaa	aatcttatct	tttgatgagg	ttagtggcgt	cttggtgtgt	660
gaagcaggat	gcataattaga	aaatctggca	actttccttg	acacaaaagg	ttttattatg	720
cctctagact	taggtgcaaa	aggaagctgt	catatcggtg	gaaatgtttc	aactaatgct	780
ggtggtttgc	gtctaattccg	ttatggctca	cttcatggaa	ctgtattggg	tctagaagct	840
gtcacagcaa	atggcaacgt	gcttgacatg	cttggaactt	tacgcaaaga	caatactggg	900
tacgacttaa	aacatttggt	tattggtagt	gaaggatcac	ttggtattgt	aactaaagtt	960
tctattctca	cacaaccaaa	attgtcttct	gtaaaatttag	ccttcattgc	ttgcaaagat	1020
tatctcagct	gccagaaact	tcttggtgaa	gcaaagagaa	atcttgagaa	gatactctcg	1080
gctttcagag	ttcttgataa	caattccatg	gatttggtac	tgaaccacct	agacggtgta	1140
cgtaatccag	tttcctcttc	ggagaacttt	tatattctga	tcgagacaac	agggagtgat	1200
gaaactaatg	acaggggagaa	gcttgaagct	ttcctgttga	agtcactgga	aaaagggtta	1260
gtttctgatg	gtgtaatcgc	tcaagacatt	aaccaggcat	cctcattttg	gcgcatacga	1320
gagggtataa	caagggcggt	acagaaagca	ggagctggtt	acaagtatga	cttatcctta	1380
ccggttgaa	aaatttcaaa	tattgttaac	gatcttcgag	ggagattagg	tgacttagca	1440
aatgttatgg	gatatgggtca	ccttgagagc	ggaaatctac	atttaaacad	ctcagccgcg	1500
gaatataacg	ataagctttt	aggtttgata	gagccttatg	tctatgagtg	gacatcaaag	1560
caccgtggaa	gcatacagtg	ggaacatgga	ttaggtgtaa	tgaaagctaa	tgaaatcttc	1620
tacagcaaat	caccggaaac	tggtgcatta	atggcttcca	ttaaaaagtt	gctggaccca	1680
aagggaattc	tcaaccctta	caaagttctt	cctcactctc	tcttctccaa	ctaagggtgg	1740
tgatgagatg	attcttcaaa	caggaatttg	gaacatgagc	agccaagttt	gagcgatatg	1800
attgatgcaa	aggaacaaaa	atacaagtgc	tgattaaaaa	gtctttaaac	tcaaaagtgt	1860
atatgttcgc	ttcttcttct	ttgttggtgt	tggtgttacc	ttgttttaat	atctttttag	1920
taaaggataa	gaaagaatct	aaacctattg	atcttacgtg	tatttaaagt	taaaatttgc	1980
agtgtatgta	gaccaaact	cgaaaagata	atctataata	atagtatttc	c	

(2) INFORMATION FOR SEQ ID NO:1308:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 373 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(D) OTHER INFORMATION: / Ceres Seq. ID 1500037

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1308:

(2) INFORMATION FOR SEQ ID NO:1309:

(D) TOPOLOGY: linear

(A) NAME/KEY: peptide

(B) LOCATION: 1..338

(D) OTHER INFORMATION: / Ceres Seq. ID 1500038

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1309:

```
Met Pro Leu Asp Leu Gly Ala Lys Gly Ser Cys His Ile Gly Gly Asn
1      5      10      15
Val Ser Thr Asn Ala Gly Gly Leu Arg Leu Ile Arg Tyr Gly Ser Leu
      20      25      30
His Gly Thr Val Leu Gly Leu Glu Ala Val Thr Ala Asn Gly Asn Val
      35      40      45
Leu Asp Met Leu Gly Thr Leu Arg Lys Asp Asn Thr Gly Tyr Asp Leu
      50      55      60
Lys His Leu Phe Ile Gly Ser Glu Gly Ser Leu Gly Ile Val Thr Lys
      65      70      75      80
Val Ser Ile Leu Thr Gln Pro Lys Leu Ser Ser Val Asn Leu Ala Phe
      85      90      95
Ile Ala Cys Lys Asp Tyr Leu Ser Cys Gln Lys Leu Leu Val Glu Ala
      100     105     110
Lys Arg Asn Leu Gly Glu Ile Leu Ser Ala Phe Glu Phe Leu Asp Asn
      115     120     125
Asn Ser Met Asp Leu Val Leu Asn His Leu Asp Gly Val Arg Asn Pro
      130     135     140
Val Ser Ser Ser Glu Asn Phe Tyr Ile Leu Ile Glu Thr Thr Gly Ser
      145     150     155     160
Asp Glu Thr Asn Asp Arg Glu Lys Leu Glu Ala Phe Leu Leu Lys Ser
      165     170     175
Leu Glu Lys Gly Leu Val Ser Asp Gly Val Ile Ala Gln Asp Ile Asn
      180     185     190
Gln Ala Ser Ser Phe Trp Arg Ile Arg Glu Gly Ile Thr Glu Ala Leu
      195     200     205
Gln Lys Ala Gly Ala Val Tyr Lys Tyr Asp Leu Ser Leu Pro Val Glu
      210     215     220
Glu Ile Tyr Asn Ile Val Asn Asp Leu Arg Gly Arg Leu Gly Asp Leu
      225     230     235     240
Ala Asn Val Met Gly Tyr Gly His Leu Gly Asp Gly Asn Leu His Leu
      245     250     255
Asn Ile Ser Ala Ala Glu Tyr Asn Asp Lys Leu Leu Gly Leu Ile Glu
      260     265     270
Pro Tyr Val Tyr Glu Trp Thr Ser Lys His Arg Gly Ser Ile Ser Ala
      275     280     285
Glu His Gly Leu Gly Val Met Lys Ala Asn Glu Ile Phe Tyr Ser Lys
      290     295     300
Ser Pro Glu Thr Val Ala Leu Met Ala Ser Ile Lys Lys Leu Leu Asp
      305     310     315     320
Pro Lys Gly Ile Leu Asn Pro Tyr Lys Val Leu Pro His Ser Leu Phe
      325     330     335
Ser Asn
```

(2) INFORMATION FOR SEQ ID NO:1310:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 288 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..288

(D) OTHER INFORMATION: / Ceres Seq. ID 1500039

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1310:

```
Met Leu Gly Thr Leu Arg Lys Asp Asn Thr Gly Tyr Asp Leu Lys His
1      5      10      15
```

Leu Phe Ile Gly Ser Glu Gly Ser Leu Gly Ile Val Thr Lys Val Ser
20 25 30
Ile Leu Thr Gln Pro Lys Leu Ser Ser Val Asn Leu Ala Phe Ile Ala
35 40 45
Cys Lys Asp Tyr Leu Ser Cys Gln Lys Leu Leu Val Glu Ala Lys Arg
50 55 60
Asn Leu Gly Glu Ile Leu Ser Ala Phe Glu Phe Leu Asp Asn Asn Ser
65 70 75 80
Met Asp Leu Val Leu Asn His Leu Asp Gly Val Arg Asn Pro Val Ser
85 90 95
Ser Ser Glu Asn Phe Tyr Ile Leu Ile Glu Thr Thr Gly Ser Asp Glu
100 105 110
Thr Asn Asp Arg Glu Lys Leu Glu Ala Phe Leu Leu Lys Ser Leu Glu
115 120 125
Lys Gly Leu Val Ser Asp Gly Val Ile Ala Gln Asp Ile Asn Gln Ala
130 135 140
Ser Ser Phe Trp Arg Ile Arg Glu Gly Ile Thr Glu Ala Leu Gln Lys
145 150 155 160
Ala Gly Ala Val Tyr Lys Tyr Asp Leu Ser Leu Pro Val Glu Glu Ile
165 170 175
Tyr Asn Ile Val Asn Asp Leu Arg Gly Arg Leu Gly Asp Leu Ala Asn
180 185 190
Val Met Gly Tyr Gly His Leu Gly Asp Gly Asn Leu His Leu Asn Ile
195 200 205
Ser Ala Ala Glu Tyr Asn Asp Lys Leu Leu Gly Leu Ile Glu Pro Tyr
210 215 220
Val Tyr Glu Trp Thr Ser Lys His Arg Gly Ser Ile Ser Ala Glu His
225 230 235 240
Gly Leu Gly Val Met Lys Ala Asn Glu Ile Phe Tyr Ser Lys Ser Pro
245 250 255
Glu Thr Val Ala Leu Met Ala Ser Ile Lys Lys Leu Leu Asp Pro Lys
260 265 270
Gly Ile Leu Asn Pro Tyr Lys Val Leu Pro His Ser Leu Phe Ser Asn
275 280 285

(2) INFORMATION FOR SEQ ID NO:1311:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1213 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1213
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500040

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1311:

aacaacatct	ttcacacaac	aattcacaca	atttctcgtt	tttttttggt	tatcatcaaa	60
agttttaatc	taaattacgt	atcaaattcc	gagcaagatg	actattcttg	ttgaacattt	120
tgttcctgat	tcaagagtgg	atgaaaagaa	agtgatagag	gagagggata	atgaattggt	180
gttggatgga	ggtttttggt	ttccaaaatc	aaaggaaact	gatgcattcg	atgctcctga	240
tatgaatttc	ytgggccatt	ccttcaggga	ttatgagaat	gatgaaagcg	agagacaaca	300
aggtgttgag	gaattttaca	ggatgcaaca	cattcaccag	acctatgact	ttgtgaagaa	360
gatgaggaaa	gagtatggaa	aacttaacaa	gatggaaatg	agtatatggg	aatgttgtga	420
gttattgaac	aatgttggtg	atgaaagcga	tccggatctt	gatgagcctc	aaattcaaca	480
ccttctccaa	accgctgaag	ccattcgaag	ggactatccc	gacgaagatt	ggctccatct	540
cactgcccta	atccatgatc	ttggcaaggt	tctccttctg	ccagaattcg	gtggtcttcc	600
ccagtgggct	gtcgttggcg	atacatttcc	agttggatgt	accttcgact	cagccaatat	660
tcaccacaag	tatttcaaag	gaaaccatga	tatcaacaac	ccaaagtaca	acacaaaaaa	720
tggagtttac	actgaaggat	gtgggtttaga	caatgttctc	atgtcatggg	gtcatgacga	780

```
ctacatgtat ttggtggcta agaagaatgg caccgacctt cctcacgctg gtctcttcat      840
tattcgatat cattcctttt atccattgca caaggcagga gcctacacac acttgatgaa      900
cgatgaggac agagatgata tcaagtggct ccatgtcttc aataaatatg acctatacag      960
taagagcaaaa gttctggtag atgtcgaaca agtgaagcct tactacattt cactcatcaa    1020
caagtatttt ccggcgaaac taaaatgggtg agataaagct acgagtcaat taattaacta    1080
tcttttatga ggagaacgag atcgaagggtt aacgagtttt ctattgtata caacggaaga    1140
taaattctatc taataaaaaa gttggtgtgt tcatttgtaa ttttttcccc catcagttta    1200
aaagttatgt tgt
```

(2) INFORMATION FOR SEQ ID NO:1312:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 317 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..317
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500041

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1312:

```
Met Thr Ile Leu Val Glu His Phe Val Pro Asp Ser Arg Val Asp Glu
1      5      10      15
Lys Lys Val Ile Glu Glu Arg Asp Asn Glu Leu Val Leu Asp Gly Gly
20     25     30
Phe Val Val Pro Lys Ser Lys Glu Thr Asp Ala Phe Asp Ala Pro Asp
35     40     45
Met Asn Phe Xaa Gly His Ser Phe Arg Asp Tyr Glu Asn Asp Glu Ser
50     55     60
Glu Arg Gln Gln Gly Val Glu Glu Phe Tyr Arg Met Gln His Ile His
65     70     75     80
Gln Thr Tyr Asp Phe Val Lys Lys Met Arg Lys Glu Tyr Gly Lys Leu
85     90     95
Asn Lys Met Glu Met Ser Ile Trp Glu Cys Cys Glu Leu Leu Asn Asn
100    105    110
Val Val Asp Glu Ser Asp Pro Asp Leu Asp Glu Pro Gln Ile Gln His
115    120    125
Leu Leu Gln Thr Ala Glu Ala Ile Arg Arg Asp Tyr Pro Asp Glu Asp
130    135    140
Trp Leu His Leu Thr Ala Leu Ile His Asp Leu Gly Lys Val Leu Leu
145    150    155    160
Leu Pro Glu Phe Gly Gly Leu Pro Gln Trp Ala Val Val Gly Asp Thr
165    170    175
Phe Pro Val Gly Cys Thr Phe Asp Ser Ala Asn Ile His His Lys Tyr
180    185    190
Phe Lys Gly Asn His Asp Ile Asn Asn Pro Lys Tyr Asn Thr Lys Asn
195    200    205
Gly Val Tyr Thr Glu Gly Cys Gly Leu Asp Asn Val Leu Met Ser Trp
210    215    220
Gly His Asp Asp Tyr Met Tyr Leu Val Ala Lys Lys Asn Gly Thr Thr
225    230    235    240
Leu Pro His Ala Gly Leu Phe Ile Ile Arg Tyr His Ser Phe Tyr Pro
245    250    255
Leu His Lys Ala Gly Ala Tyr Thr His Leu Met Asn Asp Glu Asp Arg
260    265    270
Asp Asp Leu Lys Trp Leu His Val Phe Asn Lys Tyr Asp Leu Tyr Ser
275    280    285
Lys Ser Lys Val Leu Val Asp Val Glu Gln Val Lys Pro Tyr Tyr Ile
290    295    300
Ser Leu Ile Asn Lys Tyr Phe Pro Ala Lys Leu Lys Trp
305    310    315
```

(2) INFORMATION FOR SEQ ID NO:1313:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 269 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..269
 (D) OTHER INFORMATION: / Ceres Seq. ID 1500042

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1313:

Met	Asn	Phe	Xaa	Gly	His	Ser	Phe	Arg	Asp	Tyr	Glu	Asn	Asp	Glu	Ser
1				5				10						15	
Glu	Arg	Gln	Gln	Gly	Val	Glu	Glu	Phe	Tyr	Arg	Met	Gln	His	Ile	His
		20						25					30		
Gln	Thr	Tyr	Asp	Phe	Val	Lys	Lys	Met	Arg	Lys	Glu	Tyr	Gly	Lys	Leu
		35					40					45			
Asn	Lys	Met	Glu	Met	Ser	Ile	Trp	Glu	Cys	Cys	Glu	Leu	Leu	Asn	Asn
	50					55					60				
Val	Val	Asp	Glu	Ser	Asp	Pro	Asp	Leu	Asp	Glu	Pro	Gln	Ile	Gln	His
65					70					75					80
Leu	Leu	Gln	Thr	Ala	Glu	Ala	Ile	Arg	Arg	Asp	Tyr	Pro	Asp	Glu	Asp
			85					90					95		
Trp	Leu	His	Leu	Thr	Ala	Leu	Ile	His	Asp	Leu	Gly	Lys	Val	Leu	Leu
		100						105					110		
Leu	Pro	Glu	Phe	Gly	Gly	Leu	Pro	Gln	Trp	Ala	Val	Val	Gly	Asp	Thr
		115						120					125		
Phe	Pro	Val	Gly	Cys	Thr	Phe	Asp	Ser	Ala	Asn	Ile	His	His	Lys	Tyr
	130					135					140				
Phe	Lys	Gly	Asn	His	Asp	Ile	Asn	Asn	Pro	Lys	Tyr	Asn	Thr	Lys	Asn
145					150					155					160
Gly	Val	Tyr	Thr	Glu	Gly	Cys	Gly	Leu	Asp	Asn	Val	Leu	Met	Ser	Trp
			165						170				175		
Gly	His	Asp	Asp	Tyr	Met	Tyr	Leu	Val	Ala	Lys	Lys	Asn	Gly	Thr	Thr
		180						185					190		
Leu	Pro	His	Ala	Gly	Leu	Phe	Ile	Arg	Tyr	His	Ser	Phe	Tyr	Pro	
	195						200				205				
Leu	His	Lys	Ala	Gly	Ala	Tyr	Thr	His	Leu	Met	Asn	Asp	Glu	Asp	Arg
	210					215					220				
Asp	Asp	Leu	Lys	Trp	Leu	His	Val	Phe	Asn	Lys	Tyr	Asp	Leu	Tyr	Ser
225					230					235					240
Lys	Ser	Lys	Val	Leu	Val	Asp	Val	Glu	Gln	Val	Lys	Pro	Tyr	Tyr	Ile
			245						250					255	
Ser	Leu	Ile	Asn	Lys	Tyr	Phe	Pro	Ala	Lys	Leu	Lys	Trp			
		260					265								

(2) INFORMATION FOR SEQ ID NO:1314:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 242 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..242
 (D) OTHER INFORMATION: / Ceres Seq. ID 1500043

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1314:

Met	Gln	His	Ile	Gln	Thr	Tyr	Asp	Phe	Val	Lys	Lys	Met	Arg	Lys
1				5				10					15	
Glu	Tyr	Gly	Lys	Leu	Asn	Lys	Met	Glu	Met	Ser	Ile	Trp	Glu	Cys
		20						25					30	

Glu Leu Leu Asn Asn Val Val Asp Glu Ser Asp Pro Asp Leu Asp Glu
35 40 45
Pro Gln Ile Gln His Leu Leu Gln Thr Ala Glu Ala Ile Arg Arg Asp
50 55 60
Tyr Pro Asp Glu Asp Trp Leu His Leu Thr Ala Leu Ile His Asp Leu
65 70 75 80
Gly Lys Val Leu Leu Pro Glu Phe Gly Gly Leu Pro Gln Trp Ala
85 90 95
Val Val Gly Asp Thr Phe Pro Val Gly Cys Thr Phe Asp Ser Ala Asn
100 105 110
Ile His His Lys Tyr Phe Lys Gly Asn His Asp Ile Asn Asn Pro Lys
115 120 125
Tyr Asn Thr Lys Asn Gly Val Tyr Thr Glu Gly Cys Gly Leu Asp Asn
130 135 140
Val Leu Met Ser Trp Gly His Asp Asp Tyr Met Tyr Leu Val Ala Lys
145 150 155 160
Lys Asn Gly Thr Thr Leu Pro His Ala Gly Leu Phe Ile Ile Arg Tyr
165 170 175
His Ser Phe Tyr Pro Leu His Lys Ala Gly Ala Tyr Thr His Leu Met
180 185 190
Asn Asp Glu Asp Arg Asp Asp Leu Lys Trp Leu His Val Phe Asn Lys
195 200 205
Tyr Asp Leu Tyr Ser Lys Ser Lys Val Leu Val Asp Val Glu Gln Val
210 215 220
Lys Pro Tyr Tyr Ile Ser Leu Ile Asn Lys Tyr Phe Pro Ala Lys Leu
225 230 235 240
Lys Trp

(2) INFORMATION FOR SEQ ID NO:1315:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1579 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1579
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500050

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1315:

agctctgttg	tggaacatcg	gaaatcagaa	ctgaaacaga	aacagaaacc	atggagaaga	60
gagaagacga	acaacaaaag	cgcgacgatt	ctagattcaa	tcaaacactc	aagaacgtcc	120
aagggtttct	taaaggtaga	agtattcctg	gtaagggtatt	gttgactagg	agatcagatc	180
ctcctccata	cccaatctct	ccaacatata	aacggagctt	atctgagaat	gacgccggaa	240
gaaatgagct	attcgaaaagt	cctgttgagg	tgaggagatca	caattcaagc	aagaaacatg	300
ataatacata	tgctggtaag	ctacgatcaa	actctagtgc	tgaaaggagt	gtgaaagaag	360
ttcaaaactt	gaagataggt	gttcgatcaa	gtgactctgc	tagagttatg	aagttcaaca	420
aagtgccttc	agaaacaact	gtcatattag	agaaactgcg	cgagctagca	tggaatggtg	480
taccacacta	tatgcggcct	gatgtctggc	ggcttctctt	gggatatgca	ccacctaat	540
cagatagaag	ggaggctgtt	ctgagaagaa	aacgtcttga	atatctggaa	tctgttggcc	600
aattttatga	ccttccagat	tccgaacgtt	ctgatgatga	gatcaatatg	cttcgccaga	660
ttgctgttga	ctgtccgagg	actgtaccag	atgtcagttt	ctttcagcaa	gaacaggtgc	720
agaaatcact	ggagcgtatt	ctttacacgt	gggccattag	acatccagca	agcggatatg	780
ttcagggaat	aaatgacctg	gtcacgccct	tcctagtgtg	tttcttgtaa	gaatatctag	840
atggcggtgt	agacagttgg	tcaatggatg	atctatctgc	tgaaaaagtc	tcagatgtag	900
aagcggattg	ctactggtgc	ttaacaaagc	tccttgacgg	tatgcaagat	cattacacgt	960
ttgctcaacc	tggaatccag	agacttgtgt	ttaagctgaa	ggaactggtc	aggcgtatcg	1020
atgaacctgt	ttcaagacac	atggaagagc	atgggctaga	gtttcttcaa	tttgctttcc	1080
ggtggtataa	ttgtcttctg	attcgtgaga	tcccattcaa	tctcatcaat	cgactatggg	1140
acacttatct	tgctgaagga	gatgcgttgc	cagacttcct	ggtgtatata	tgctagcttt	1200
ctcttgacgt	ggtctgatga	gctgaagaag	ctagattttc	aagaaatggt	aatgttctctg	1260


```
caacaccttc cgacacataa ctggtcagac caagagctcg aaatgggttt gtcaagagct 1320
tacatgtggc atagtatggt caataattcc ccaaaccatt tggctagctg aaatgacttt 1380
tcctccatgg tgcctgtgc tgtttttccc tttgttatat tatcttcttc ttcttggtgt 1440
ctaaatcagc tttcgttttg ttttggggtta tggtaaagtc taacattctt gtcttggttaa 1500
ttgttattag tttatgtatg gtttcacttg ttgaatctgt caccagtttg tgtgtttgta 1560
atattttag ctttcactg
```

(2) INFORMATION FOR SEQ ID NO:1316:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 275 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..275
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500051

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1316:

```
Leu Cys Cys Gly Thr Ser Glu Ile Arg Thr Glu Thr Glu Thr Glu Thr
1          5          10          15
Met Glu Lys Arg Glu Asp Glu Gln Gln Lys Arg Asp Asp Ser Arg Phe
20          25          30
Asn Gln Thr Leu Lys Asn Val Gln Gly Phe Leu Lys Gly Arg Ser Ile
35          40          45
Pro Gly Lys Val Leu Leu Thr Arg Arg Ser Asp Pro Pro Pro Tyr Pro
50          55          60
Ile Ser Pro Thr Tyr Gln Arg Ser Leu Ser Glu Asn Asp Ala Gly Arg
65          70          75
Asn Glu Leu Phe Glu Ser Pro Val Glu Val Glu Asp His Asn Ser Ser
85          90          95
Lys Lys His Asp Asn Thr Tyr Ala Gly Lys Leu Arg Ser Asn Ser Ser
100          105          110
Ala Glu Arg Ser Val Lys Glu Val Gln Asn Leu Lys Ile Gly Val Arg
115          120          125
Ser Ser Asp Ser Ala Arg Val Met Lys Phe Asn Lys Val Leu Ser Glu
130          135          140
Thr Thr Val Ile Leu Glu Lys Leu Arg Glu Leu Ala Trp Asn Gly Val
145          150          155
Pro His Tyr Met Arg Pro Asp Val Trp Arg Leu Leu Leu Gly Tyr Ala
165          170          175
Pro Pro Asn Ser Asp Arg Arg Glu Ala Val Leu Arg Arg Lys Arg Leu
180          185          190
Glu Tyr Leu Glu Ser Val Gly Gln Phe Tyr Asp Leu Pro Asp Ser Glu
195          200          205
Arg Ser Asp Asp Glu Ile Asn Met Leu Arg Gln Ile Ala Val Asp Cys
210          215          220
Pro Arg Thr Val Pro Asp Val Ser Phe Phe Gln Gln Glu Gln Val Gln
225          230          235
Lys Ser Leu Glu Arg Ile Leu Tyr Thr Trp Ala Ile Arg His Pro Ala
245          250          255
Ser Gly Tyr Val Gln Gly Ile Asn Asp Leu Val Thr Pro Phe Leu Val
260          265          270
Ile Phe Leu
275
```

(2) INFORMATION FOR SEQ ID NO:1317:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 259 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..259

(D) OTHER INFORMATION: / Ceres Seq. ID 1500052

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1317:

Met Glu Lys Arg Glu Asp Glu Gln Gln Lys Arg Asp Asp Ser Arg Phe
1 5 10 15
Asn Gln Thr Leu Lys Asn Val Gln Gly Phe Leu Lys Gly Arg Ser Ile
20 25 30
Pro Gly Lys Val Leu Leu Thr Arg Arg Ser Asp Pro Pro Tyr Pro
35 40 45
Ile Ser Pro Thr Tyr Gln Arg Ser Leu Ser Glu Asn Asp Ala Gly Arg
50 55 60
Asn Glu Leu Phe Glu Ser Pro Val Glu Val Glu Asp His Asn Ser Ser
65 70 75 80
Lys Lys His Asp Asn Thr Tyr Ala Gly Lys Leu Arg Ser Asn Ser Ser
85 90 95
Ala Glu Arg Ser Val Lys Glu Val Gln Asn Leu Lys Ile Gly Val Arg
100 105 110
Ser Ser Asp Ser Ala Arg Val Met Lys Phe Asn Lys Val Leu Ser Glu
115 120 125
Thr Thr Val Ile Leu Glu Lys Leu Arg Glu Leu Ala Trp Asn Gly Val
130 135 140
Pro His Tyr Met Arg Pro Asp Val Trp Arg Leu Leu Leu Gly Tyr Ala
145 150 155 160
Pro Pro Asn Ser Asp Arg Arg Glu Ala Val Leu Arg Arg Lys Arg Leu
165 170 175
Glu Tyr Leu Glu Ser Val Gly Gln Phe Tyr Asp Leu Pro Asp Ser Glu
180 185 190
Arg Ser Asp Asp Glu Ile Asn Met Leu Arg Gln Ile Ala Val Asp Cys
195 200 205
Pro Arg Thr Val Pro Asp Val Ser Phe Phe Gln Gln Glu Gln Val Gln
210 215 220
Lys Ser Leu Glu Arg Ile Leu Tyr Thr Trp Ala Ile Arg His Pro Ala
225 230 235 240
Ser Gly Tyr Val Gln Gly Ile Asn Asp Leu Val Thr Pro Phe Leu Val
245 250 255
Ile Phe Leu

(2) INFORMATION FOR SEQ ID NO:1318:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 140 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..140

(D) OTHER INFORMATION: / Ceres Seq. ID 1500053

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1318:

Met Lys Phe Asn Lys Val Leu Ser Glu Thr Thr Val Ile Leu Glu Lys
1 5 10 15
Leu Arg Glu Leu Ala Trp Asn Gly Val Pro His Tyr Met Arg Pro Asp
20 25 30
Val Trp Arg Leu Leu Leu Gly Tyr Ala Pro Pro Asn Ser Asp Arg Arg
35 40 45
Glu Ala Val Leu Arg Arg Lys Arg Leu Glu Tyr Leu Glu Ser Val Gly
50 55 60
Gln Phe Tyr Asp Leu Pro Asp Ser Glu Arg Ser Asp Asp Glu Ile Asn
65 70 75 80

Met Leu Arg Gln Ile Ala Val Asp Cys Pro Arg Thr Val Pro Asp Val
85 90 95
Ser Phe Phe Gln Gln Glu Gln Val Gln Lys Ser Leu Glu Arg Ile Leu
100 105 110
Tyr Thr Trp Ala Ile Arg His Pro Ala Ser Gly Tyr Val Gln Gly Ile
115 120 125
Asn Asp Leu Val Thr Pro Phe Leu Val Ile Phe Leu
130 135 140

(2) INFORMATION FOR SEQ ID NO:1319:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1239 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1239
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500054

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1319:

```
acaattcaga ttccaatttt ctcaaactct aaaatcaatc tctcaaattct ctcaaccgtg      60
atcaaggtag atttctgagt tcttattgta tttcttcgat ttgtttcggt cgatcgcaat      120
ttaggctctg ttctttgatt ttgatctcgt taatctctga tcggaggcaa attacatagt      180
ttcatcggtta gatctcttct tatttctcga ttagggttcg tatttttcgc agatctgttt      240
attttcttgt tgtttccttg tatttgatcc gatttggtga aagaatttgt gtgttctcga      300
ttatttatgc tttgatctgt gatttttatc tagatttggt gttagtttct tgtttgtgcg      360
atcgaatttg tcgattaatc tcgggttttc tgattaacag atgcagatct tcgttaagac      420
tctcaccgga aagactatca cctcgcaggt ggaaagctct gacaccatcg acaacgttaa      480
ggccaagatc caggataagg aaggtattcc tccggatcag cagaggctta tcttcgccgg      540
aaagcagttg gaggatggcc gcacgttgcc ggattacaat atccagaagg aatccaccct      600
ccacttgggt ctcagggtcc gtggtggtat gcagattttc gttaaaaccc taacgggaaa      660
gacgattact cttgaggtgg agagctctga caccattgac aacgtcaagg ccaagatcca      720
agataaggag ggtattcctc cggaccagca gaggttgatc ttcgccggaa agcaacttga      780
ggacggcaga actttggcgg attacaacat ccagaaggag tctacgcttc atttggtcct      840
tgcgtctgcy tggaggtatg cagatcttcg taaagacttt gaccggaaag accatcactc      900
ttgaagttga gagctccgac accattgata acgtgaaggc taagatccag gacaagggaag      960
gcattcctcc ggaccagcag cgtctcatct tcgctggaaa gcagcttgag gatggacgta     1020
ctttggccga ctacaacatc cagaaggagt ctactcttca cttggtcctc cgtctccgtg     1080
gtggtttcta aaccttgtct ctctctctta tggttactga accaagttca tgtatcggtt     1140
catctagtag tttggtggtt tatgttttgg ggccatgtac agcctctgat aaataattga     1200
tcgactatgt ttccgtttct ttcattcttc ttttctttc
```

(2) INFORMATION FOR SEQ ID NO:1320:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 167 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..167
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500055

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1320:

Met Gln Ile Phe Val Lys Thr Leu Thr Gly Lys Thr Ile Thr Leu Glu
1 5 10 15
Val Glu Ser Ser Asp Thr Ile Asp Asn Val Lys Ala Lys Ile Gln Asp
20 25 30
Lys Glu Gly Ile Pro Pro Asp Gln Gln Arg Leu Ile Phe Ala Gly Lys
35 40 45
Gln Leu Glu Asp Gly Arg Thr Leu Ala Asp Tyr Asn Ile Gln Lys Glu
50 55 60

Ser Thr Leu His Leu Val Leu Arg Leu Arg Gly Gly Met Gln Ile Phe
65 70 75 80
Val Lys Thr Leu Thr Gly Lys Thr Ile Thr Leu Glu Val Glu Ser Ser
85 90 95
Asp Thr Ile Asp Asn Val Lys Ala Lys Ile Gln Asp Lys Glu Gly Ile
100 105 110
Pro Pro Asp Gln Gln Arg Leu Ile Phe Ala Gly Lys Gln Leu Glu Asp
115 120 125
Gly Arg Thr Leu Ala Asp Tyr Asn Ile Gln Lys Glu Ser Thr Leu His
130 135 140
Leu Val Phe Ala Ser Ala Trp Arg Tyr Ala Asp Leu Arg Lys Asp Phe
145 150 155 160
Asp Arg Lys Asp His His Ser
165

(2) INFORMATION FOR SEQ ID NO:1321:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 91 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..91
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500056

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1321:

Met Gln Ile Phe Val Lys Thr Leu Thr Gly Lys Thr Ile Thr Leu Glu
1 5 10 15
Val Glu Ser Ser Asp Thr Ile Asp Asn Val Lys Ala Lys Ile Gln Asp
20 25 30
Lys Glu Gly Ile Pro Pro Asp Gln Gln Arg Leu Ile Phe Ala Gly Lys
35 40 45
Gln Leu Glu Asp Gly Arg Thr Leu Ala Asp Tyr Asn Ile Gln Lys Glu
50 55 60
Ser Thr Leu His Leu Val Phe Ala Ser Ala Trp Arg Tyr Ala Asp Leu
65 70 75 80
Arg Lys Asp Phe Asp Arg Lys Asp His His Ser
85 90

(2) INFORMATION FOR SEQ ID NO:1322:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1338 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1338
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500057

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1322:

ctctcttcgt	gtctgagcac	tcttcttctt	cttcttcaat	ggctttcgcg	tttgagaaac	60
cataaaagga	aacttttcag	agttttctct	tgtctcctgt	tcgtctccgt	gccgtgtatg	120
tcactaaatt	taggtttatc	aatggagatg	aatgcacat	ttcaatcaac	tcgtgtccca	180
ttccaatgcg	cttggtggtt	cccaaattca	atctattgga	ctctcaaaga	accaatcggt	240
ttgaaaatac	ctaattcact	tgcttctttg	aggctctatc	gacacttgga	gttgaaatct	300
gtaggttcat	tgtacaatgt	gtttgagatt	cataggaaag	aagtcaattc	aagtcttttg	360
gaagtgaag	ctatgaacaa	agatactgaa	gctgatagtg	atagtgatag	gaagattaaa	420
gaagaggaaa	ggagaaggaa	gattggatta	gctaatagag	gaaagggtgcc	atggaacaaa	480
gggaggaaac	acagtgaaga	cactcgaaga	cgaatcaagc	agagaacaat	cgaagctttg	540
acaaatccca	aggttcggaa	gaagatgtcc	gatcatcaac	aaccacacag	taatgaaacc	600
aaggagaaga	taagagcttc	agtgaacaaa	gtttgggcag	aacggtcaag	atcgaagcga	660

ttaaaggaga	agttcatgtc	ttcgtgggtca	gaaaacattg	cagaagctgc	aaggaaagga	720
ggaagtggcg	aggcagaact	tgactggggac	agctatgaaa	gaataaaaaca	agatttttca	780
tctgagcagc	ttcagtttagc	tgaagagaaa	gcaagagcta	aggaacaaac	caagatgata	840
gcaaaagaag	ctgcaaaagc	caggaccgag	aagatgagga	gagccgcaga	aaaaaagaaa	900
gaacgtgagg	agaaagaccg	acgagaagga	aagattcgaa	agccaaagca	ggaaagggag	960
aatccaacca	ttgcttcacg	ttctaaacta	aagaagagac	taacaaagat	tcacaagaag	1020
aaaacaagtc	ttggtaaaat	cgcaattgga	acggataggg	ttgtttcagt	tgacgctaaa	1080
ctggagaaac	tggatttggc	tttgataagg	aaagagcgaa	caagaggaga	tatctcactt	1140
gctgatcaga	tccaagctgc	taagaaccac	cgagggaagt	atgttttatc	gagatttggt	1200
ctttttgcca	tgaatcaaat	ggattttgat	taactctttt	ctactcctag	tttatagagc	1260
ttttcttttt	tttttcttgt	gccactaaat	aaataaacia	gattgacttg	aggatataat	1320
aaataaatag	attgacgc					

(2) INFORMATION FOR SEQ ID NO:1323:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 410 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..410

(D) OTHER INFORMATION: / Ceres Seq. ID 1500058

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1323:

Leu	Ser	Ser	Cys	Leu	Arg	Thr	Leu	Leu	Leu	Leu	Gln	Trp	Leu	Ser
1				5				10					15	
Arg	Leu	Arg	Asn	His	Lys	Arg	Lys	Leu	Phe	Arg	Val	Phe	Ser	Cys
			20					25					30	Leu
Leu	Phe	Val	Ser	Val	Pro	Cys	Met	Ser	Leu	Asn	Leu	Gly	Leu	Ser
		35					40					45		Met
Glu	Met	Lys	Cys	Thr	Phe	Gln	Ser	Thr	Arg	Ala	Pro	Phe	Gln	Cys
		50				55					60			Ala
Trp	Trp	Phe	Pro	Asn	Ser	Ile	Tyr	Trp	Thr	Leu	Lys	Glu	Pro	Ile
65				70					75					80
Leu	Lys	Ile	Pro	Asn	Ser	Leu	Ala	Ser	Leu	Arg	Ser	Ile	Arg	His
			85					90					95	Leu
Glu	Leu	Lys	Ser	Val	Gly	Ser	Leu	Tyr	Asn	Val	Phe	Glu	Ile	His
			100					105					110	Arg
Lys	Glu	Val	Asn	Ser	Ser	Leu	Leu	Glu	Val	Lys	Ala	Met	Asn	Lys
		115					120					125		Asp
Thr	Glu	Ala	Asp	Ser	Asp	Ser	Asp	Arg	Lys	Ile	Lys	Glu	Glu	Glu
	130				135						140			Arg
Arg	Arg	Lys	Ile	Gly	Leu	Ala	Asn	Arg	Gly	Lys	Val	Pro	Trp	Asn
145				150					155					160
Gly	Arg	Lys	His	Ser	Glu	Asp	Thr	Arg	Arg	Arg	Ile	Lys	Gln	Arg
			165					170					175	Thr
Ile	Glu	Ala	Leu	Thr	Asn	Pro	Lys	Val	Arg	Lys	Lys	Met	Ser	Asp
		180					185					190		His
Gln	Gln	Pro	His	Ser	Asn	Glu	Thr	Lys	Glu	Lys	Ile	Arg	Ala	Ser
		195					200					205		Val
Lys	Gln	Val	Trp	Ala	Glu	Arg	Ser	Arg	Ser	Lys	Arg	Leu	Lys	Glu
	210					215					220			Lys
Phe	Met	Ser	Ser	Trp	Ser	Glu	Asn	Ile	Ala	Glu	Ala	Ala	Arg	Lys
225				230					235					Gly
Gly	Ser	Gly	Glu	Ala	Glu	Leu	Asp	Trp	Asp	Ser	Tyr	Glu	Arg	Ile
			245					250					255	Lys
Gln	Asp	Phe	Ser	Ser	Glu	Gln	Leu	Gln	Leu	Ala	Glu	Glu	Lys	Ala
		260					265					270		Arg
Ala	Lys	Glu	Gln	Thr	Lys	Met	Ile	Ala	Lys	Glu	Ala	Ala	Lys	Ala
	275					280					285			Arg
Thr	Glu	Lys	Met	Arg	Arg	Ala	Ala	Glu	Lys	Lys	Lys	Glu	Arg	Glu

290	295	300
Lys Asp Arg Arg Glu Gly Lys Ile Arg Lys Pro Lys Gln Glu Arg Glu		
305	310	315
Asn Pro Thr Ile Ala Ser Arg Ser Lys Leu Lys Lys Arg Leu Thr Lys		
	325	330
Ile His Lys Lys Lys Thr Ser Leu Gly Lys Ile Ala Ile Gly Thr Asp		
	340	345
Arg Val Val Ser Val Ala Ala Lys Leu Glu Lys Leu Asp Leu Asp Leu		
	355	360
Ile Arg Lys Glu Arg Thr Arg Gly Asp Ile Ser Leu Ala Asp Gln Ile		
	370	375
Gln Ala Ala Lys Asn Gln Arg Gly Ser Asp Val Leu Ser Arg Phe Gly		
385	390	395
Leu Phe Ala Met Lys Ser Met Asp Phe Asp		
	405	410

(2) INFORMATION FOR SEQ ID NO:1324:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 371 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..371
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500059

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1324:

Met Ser Leu Asn Leu Gly Leu Ser Met Glu Met Lys Cys Thr Phe Gln		
1	5	10
Ser Thr Arg Ala Pro Phe Gln Cys Ala Trp Trp Phe Pro Asn Ser Ile		
	20	25
Tyr Trp Thr Leu Lys Glu Pro Ile Val Leu Lys Ile Pro Asn Ser Leu		
	35	40
Ala Ser Leu Arg Ser Ile Arg His Leu Glu Leu Lys Ser Val Gly Ser		
	50	55
Leu Tyr Asn Val Phe Glu Ile His Arg Lys Glu Val Asn Ser Ser Leu		
65	70	75
Leu Glu Val Lys Ala Met Asn Lys Asp Thr Glu Ala Asp Ser Asp Ser		
	85	90
Asp Arg Lys Ile Lys Glu Glu Glu Arg Arg Arg Lys Ile Gly Leu Ala		
	100	105
Asn Arg Gly Lys Val Pro Trp Asn Lys Gly Arg Lys His Ser Glu Asp		
	115	120
Thr Arg Arg Arg Ile Lys Gln Arg Thr Ile Glu Ala Leu Thr Asn Pro		
	130	135
Lys Val Arg Lys Lys Met Ser Asp His Gln Gln Pro His Ser Asn Glu		
145	150	155
Thr Lys Glu Lys Ile Arg Ala Ser Val Lys Gln Val Trp Ala Glu Arg		
	165	170
Ser Arg Ser Lys Arg Leu Lys Glu Lys Phe Met Ser Ser Trp Ser Glu		
	180	185
Asn Ile Ala Glu Ala Ala Arg Lys Gly Gly Ser Gly Glu Ala Glu Leu		
	195	200
Asp Trp Asp Ser Tyr Glu Arg Ile Lys Gln Asp Phe Ser Ser Glu Gln		
	210	215
Leu Gln Leu Ala Glu Glu Lys Ala Arg Ala Lys Glu Gln Thr Lys Met		
225	230	235
Ile Ala Lys Glu Ala Ala Lys Ala Arg Thr Glu Lys Met Arg Arg Ala		
	245	250
Ala Glu Lys Lys Lys Glu Arg Glu Glu Lys Asp Arg Arg Glu Gly Lys		
	260	265
		270

Ile Arg Lys Pro Lys Gln Glu Arg Glu Asn Pro Thr Ile Ala Ser Arg
275 280 285
Ser Lys Leu Lys Lys Arg Leu Thr Lys Ile His Lys Lys Lys Thr Ser
290 295 300
Leu Gly Lys Ile Ala Ile Gly Thr Asp Arg Val Val Ser Val Ala Ala
305 310 315 320
Lys Leu Glu Lys Leu Asp Leu Asp Leu Ile Arg Lys Glu Arg Thr Arg
325 330 335
Gly Asp Ile Ser Leu Ala Asp Gln Ile Gln Ala Ala Lys Asn Gln Arg
340 345 350
Gly Ser Asp Val Leu Ser Arg Phe Gly Leu Phe Ala Met Lys Ser Met
355 360 365
Asp Phe Asp
370

(2) INFORMATION FOR SEQ ID NO:1325:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 363 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..363
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500060

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1325:

Met Glu Met Lys Cys Thr Phe Gln Ser Thr Arg Ala Pro Phe Gln Cys
1 5 10 15
Ala Trp Trp Phe Pro Asn Ser Ile Tyr Trp Thr Leu Lys Glu Pro Ile
20 25 30
Val Leu Lys Ile Pro Asn Ser Leu Ala Ser Leu Arg Ser Ile Arg His
35 40 45
Leu Glu Leu Lys Ser Val Gly Ser Leu Tyr Asn Val Phe Glu Ile His
50 55 60
Arg Lys Glu Val Asn Ser Ser Leu Leu Glu Val Lys Ala Met Asn Lys
65 70 75 80
Asp Thr Glu Ala Asp Ser Asp Ser Asp Arg Lys Ile Lys Glu Glu Glu
85 90 95
Arg Arg Arg Lys Ile Gly Leu Ala Asn Arg Gly Lys Val Pro Trp Asn
100 105 110
Lys Gly Arg Lys His Ser Glu Asp Thr Arg Arg Arg Ile Lys Gln Arg
115 120 125
Thr Ile Glu Ala Leu Thr Asn Pro Lys Val Arg Lys Lys Met Ser Asp
130 135 140
His Gln Gln Pro His Ser Asn Glu Thr Lys Glu Lys Ile Arg Ala Ser
145 150 155 160
Val Lys Gln Val Trp Ala Glu Arg Ser Arg Ser Lys Arg Leu Lys Glu
165 170 175
Lys Phe Met Ser Ser Trp Ser Glu Asn Ile Ala Glu Ala Ala Arg Lys
180 185 190
Gly Gly Ser Gly Glu Ala Glu Leu Asp Trp Asp Ser Tyr Glu Arg Ile
195 200 205
Lys Gln Asp Phe Ser Ser Glu Gln Leu Gln Leu Ala Glu Glu Lys Ala
210 215 220
Arg Ala Lys Glu Gln Thr Lys Met Ile Ala Lys Glu Ala Ala Lys Ala
225 230 235 240
Arg Thr Glu Lys Met Arg Arg Ala Ala Glu Lys Lys Lys Glu Arg Glu
245 250 255
Glu Lys Asp Arg Arg Glu Gly Lys Ile Arg Lys Pro Lys Gln Glu Arg
260 265 270
Glu Asn Pro Thr Ile Ala Ser Arg Ser Lys Leu Lys Lys Arg Leu Thr

275	280	285
Lys Ile His Lys Lys Lys Thr Ser Leu Gly Lys Ile Ala Ile Gly Thr		
290	295	300
Asp Arg Val Val Ser Val Ala Ala Lys Leu Glu Lys Leu Asp Leu Asp		
305	310	315
Leu Ile Arg Lys Glu Arg Thr Arg Gly Asp Ile Ser Leu Ala Asp Gln		
	325	330
Ile Gln Ala Ala Lys Asn Gln Arg Gly Ser Asp Val Leu Ser Arg Phe		
	340	345
Gly Leu Phe Ala Met Lys Ser Met Asp Phe Asp		
355	360	

(2) INFORMATION FOR SEQ ID NO:1326:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1367 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1367
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500065

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1326:

ccaattctaa	accaaacaac	agattctcat	aatcatctct	tcttttttcc	tctttacgaa	60
aagaagaaag	atcaaacctt	ccaagtaatc	attttctttc	tctctctcac	acacacacat	120
tcactagttt	tagcttcaca	aaatgtgata	taacttcatt	tacctatatg	cagggtttaca	180
caaaaaagaaa	aaagaacgat	ggctcttggt	accttcttgt	ttattgctac	ccttgaggca	240
atgacgtcac	atgtcaatgg	ttacgccgga	ggaggttggt	tcaacgcaca	cgccacattc	300
tacgggtggtg	gtgatgcttc	cggcacaatg	ggaggtgctt	gtggatacgg	aaacctatat	360
agccaaggct	atggaaccaa	cacggcgggc	ctaagcacgg	ctctattcaa	taatgggtcta	420
agttgtggtg	cttgcttcga	gataagatgt	caaaacgatg	gaaaatggtg	tcttcctggc	480
tcaattgtcg	tcacagccac	aaacttttgc	cctcctaaca	acgccttacc	gaacaacgca	540
ggaggttttg	tgtaaccttc	ctcagcagca	ttttgatctc	tctcagcccg	tatttcaacg	600
catcgctcaa	tacagagccg	gcattgtccc	cgctcgcttac	cgaagagtgc	cgtgcgtgag	660
aagaggagga	atacgtttac	gataaacgga	cactcttact	tcaacctagt	tctgattact	720
aacgtcggag	gagccggaga	tgttcactca	gcgatgggta	aagggtcaag	aactggatgg	780
caagcgatgt	caagaaactg	gggacagaa	tggcagagta	actcttacct	taacggacaa	840
tctctgtcat	tcaaagtcac	aacaagcgat	ggccaaacca	ttgtctctaa	caacgtcgct	900
aacgcaggct	ggtcttttgg	ccagaccttc	accggtgcgc	agctacgtta	ggaagagtga	960
ttcgggtgaaa	attcatctca	ttgatcggtg	ggtattgacg	tggtgtagta	gaagcagtta	1020
gagagagggg	catgatagta	atgttgctct	ttctttcaat	tgaggtttac	ctaaaaagaa	1080
gtggtgcttc	gagtgttgta	ttttgcacga	ggccttgatg	atgtcatctt	ttgggaacct	1140
tttcttatct	ttcttcattt	ttattggtaa	ggttttatgt	tatactgatg	cagaggtggt	1200
attgagttga	agtaccaccc	gctagtagta	gtagtctctc	atgtcatttg	tatcccttct	1260
cgaagcgaga	gggagagttt	tagattttta	ttaatctcgt	taaagtcatt	tgtatgttgt	1320
aaatttttca	atttctacaa	gtaagaaata	ttggagattt	gtttgtt		

(2) INFORMATION FOR SEQ ID NO:1327:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 118 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..118
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500066

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1327:

Met	Ala	Leu	Val	Thr	Phe	Leu	Phe	Ile	Ala	Thr	Leu	Gly	Ala	Met	Thr
1				5					10					15	
Ser	His	Val	Asn	Gly	Tyr	Ala	Gly	Gly	Gly	Trp	Val	Asn	Ala	His	Ala

20 25 30
Thr Phe Tyr Gly Gly Gly Asp Ala Ser Gly Thr Met Gly Gly Ala Cys
35 40 45
Gly Tyr Gly Asn Leu Tyr Ser Gln Gly Tyr Gly Thr Asn Thr Ala Ala
50 55 60
Leu Ser Thr Ala Leu Phe Asn Asn Gly Leu Ser Cys Gly Ala Cys Phe
65 70 75 80
Glu Ile Arg Cys Gln Asn Asp Gly Lys Trp Cys Leu Pro Gly Ser Ile
85 90 95
Val Val Thr Ala Thr Asn Phe Cys Pro Pro Asn Asn Ala Leu Pro Asn
100 105 110
Asn Ala Gly Gly Leu Val
115

(2) INFORMATION FOR SEQ ID NO:1328:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 104 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..104
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500067

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1328:

Met Thr Ser His Val Asn Gly Tyr Ala Gly Gly Gly Trp Val Asn Ala
1 5 10 15
His Ala Thr Phe Tyr Gly Gly Gly Asp Ala Ser Gly Thr Met Gly Gly
20 25 30
Ala Cys Gly Tyr Gly Asn Leu Tyr Ser Gln Gly Tyr Gly Thr Asn Thr
35 40 45
Ala Ala Leu Ser Thr Ala Leu Phe Asn Asn Gly Leu Ser Cys Gly Ala
50 55 60
Cys Phe Glu Ile Arg Cys Gln Asn Asp Gly Lys Trp Cys Leu Pro Gly
65 70 75 80
Ser Ile Val Val Thr Ala Thr Asn Phe Cys Pro Pro Asn Asn Ala Leu
85 90 95
Pro Asn Asn Ala Gly Gly Leu Val
100

(2) INFORMATION FOR SEQ ID NO:1329:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 93 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..93
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500068

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1329:

Met Phe Thr Gln Arg Trp Leu Lys Val Gln Glu Leu Asp Gly Lys Arg
1 5 10 15
Cys Gln Glu Thr Gly Asp Arg Thr Gly Arg Val Thr Leu Thr Leu Thr
20 25 30
Asp Asn Leu Cys His Ser Lys Ser Gln Gln Ala Met Ala Lys Pro Leu
35 40 45
Ser Leu Thr Thr Ser Leu Thr Gln Ala Gly Leu Leu Ala Arg Pro Ser
50 55 60
Pro Val Arg Ser Tyr Val Arg Lys Ser Asp Ser Val Lys Ile His Leu
65 70 75 80

Ile Asp Arg Val Val Leu Thr Cys Cys Ser Arg Ser Ser
85 90

(2) INFORMATION FOR SEQ ID NO:1330:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1676 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1676
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500069

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1330:

aagatttatt	ataaactcct	ttttttttta	aattcaagag	atatcaaaca	actacttcat	60
tttttttttt	ttgtagcagc	cgagtacttt	tttttgacgg	tgtccgtggt	cgtgcttggt	120
ctgaaattga	cgaaaaatat	tccgacaaga	caacaacaac	aattagagag	attcagacaa	180
gggatttgaa	attcggagga	tgtttgggat	ccaaagcaga	cgtgatttaa	cgatggagct	240
acaatctcag	attccgattc	tccgtccaag	catccacgca	agacgagcca	acatcgctcg	300
taaattccag	gacttgtacg	gtttcacggg	ggaaggaaat	gtcgacgacg	ttaatgtggt	360
gaacgagggt	agagagaaag	tcaggaatca	aggacgaggt	tgggtgggctc	ttgaagctag	420
caaaggagct	aattgggtatc	ttcagccgga	gatttctctg	atcgggtgacg	gtatcgcttt	480
gaaaacttct	ctcaagctct	ccactttgac	taatgcgatt	acgttgaaga	gattgattcg	540
gaaagggatc	cctcctgtgc	ttagacctaa	ggtttggttt	tctctttctg	gtgctgctaa	600
gaagaaatcc	accgtcccag	agagttatta	tagtgatttg	accaaagccg	tcgaagggat	660
ggtcacgccc	gctacgaggc	agattgatca	tgatctgcca	cgtactttcc	caggccatcc	720
atggttggac	actccggaag	gtcatgctgc	tctacgacgt	gtgcttggtg	ggtattcctt	780
tcgtgattca	gatgttggct	attgtcaggg	tctaaactac	ggtgcagcgt	tactattact	840
tgtcatgaag	acagaagaag	acgcattctg	gatgctagcg	gtccttttgg	aaaacgtatt	900
agtccgtgat	tgttacacaa	ccaactttatc	tggatgtcat	gttgagcagc	gggttttcaa	960
agatttgctt	gcccataaat	gttctcgaat	agctactcat	cttgaagata	tgggctttga	1020
tgtttccctt	gtagccactg	aatggtttct	atgcctcttc	tctaaaagcc	ttccttcaga	1080
gacaactcta	agggtgtggg	atgtactttt	ctatgaagga	gcgaagggtc	tattccatgc	1140
agcttttagca	atattcaaga	tgaaagagaa	cgagctgctt	atgacccacc	aggtcggcga	1200
tgttatcaac	dtattacaga	aaacttcaca	ccagcttttt	gacccggatg	aattattaac	1260
ggtggcattt	gagaaaaatc	gatcaatgac	taccaacacg	atatcaaagc	agaggaagaa	1320
gcaggaacca	gcagtgatgg	cagaacttga	ccagagactt	cggagactta	actctcttaa	1380
agaaaagtggg	aagagcacat	aaataaaaaa	gaactgttgg	gagaagatga	gccaaaaagt	1440
gcaaacgagg	gagtccaaca	atggtttatt	tatccctctt	gatgtttttt	tttttttttc	1500
ctttttttct	aagtatatat	aaataggatt	ttttaagtgt	attttgagag	caaaacatta	1560
accaagatcc	atttctgaga	tgggaaatgt	caagtttctt	cacattccaa	gaggtgtcac	1620
ttgccttttg	cattttttac	ccctcttcat	atatcaattg	tgatcttcat	gttttt	

(2) INFORMATION FOR SEQ ID NO:1331:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..400
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500070

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1331:

Met	Phe	Gly	Ile	Gln	Ser	Arg	Arg	Asp	Leu	Thr	Met	Glu	Leu	Gln	Ser
1				5				10						15	
Gln	Ile	Pro	Ile	Leu	Arg	Pro	Ser	Ile	His	Ala	Arg	Arg	Ala	Asn	Ile
				20				25					30		
Val	Val	Lys	Phe	Gln	Asp	Leu	Tyr	Gly	Phe	Thr	Val	Glu	Gly	Asn	Val
				35				40				45			
Asp	Asp	Val	Asn	Val	Leu	Asn	Glu	Val	Arg	Glu	Lys	Val	Arg	Asn	Gln

50	55	60
Gly Arg Val Trp Trp Ala Leu Glu Ala Ser Lys Gly Ala Asn Trp Tyr		
65	70	75
Leu Gln Pro Glu Ile Leu Leu Ile Gly Asp Gly Ile Ala Leu Lys Thr		
	85	90
Ser Leu Lys Leu Ser Thr Leu Thr Asn Ala Ile Thr Leu Lys Arg Leu		
	100	105
Ile Arg Lys Gly Ile Pro Pro Val Leu Arg Pro Lys Val Trp Phe Ser		
	115	120
Leu Ser Gly Ala Ala Lys Lys Lys Ser Thr Val Pro Glu Ser Tyr Tyr		
	130	135
Ser Asp Leu Thr Lys Ala Val Glu Gly Met Val Thr Pro Ala Thr Arg		
145	150	155
Gln Ile Asp His Asp Leu Pro Arg Thr Phe Pro Gly His Pro Trp Leu		
	165	170
Asp Thr Pro Glu Gly His Ala Ala Leu Arg Arg Val Leu Val Gly Tyr		
	180	185
Ser Phe Arg Asp Ser Asp Val Gly Tyr Cys Gln Gly Leu Asn Tyr Val		
	195	200
Ala Ala Leu Leu Leu Leu Val Met Lys Thr Glu Glu Asp Ala Phe Trp		
	210	215
Met Leu Ala Val Leu Leu Glu Asn Val Leu Val Arg Asp Cys Tyr Thr		
225	230	235
Thr Asn Leu Ser Gly Cys His Val Glu Gln Arg Val Phe Lys Asp Leu		
	245	250
Leu Ala Gln Lys Cys Ser Arg Ile Ala Thr His Leu Glu Asp Met Gly		
	260	265
Phe Asp Val Ser Leu Val Ala Thr Glu Trp Phe Leu Cys Leu Phe Ser		
	275	280
Lys Ser Leu Pro Ser Glu Thr Thr Leu Arg Val Trp Asp Val Leu Phe		
	290	295
Tyr Glu Gly Ala Lys Val Leu Phe His Ala Ala Leu Ala Ile Phe Lys		
305	310	315
Met Lys Glu Asn Glu Leu Leu Met Thr His Gln Val Gly Asp Val Ile		
	325	330
Asn Xaa Leu Gln Lys Thr Ser His Gln Leu Phe Asp Pro Asp Glu Leu		
	340	345
Leu Thr Val Ala Phe Glu Lys Ile Gly Ser Met Thr Thr Asn Thr Ile		
	355	360
Ser Lys Gln Arg Lys Lys Gln Glu Pro Ala Val Met Ala Glu Leu Asp		
	370	375
Gln Arg Leu Arg Arg Leu Asn Ser Leu Lys Glu Ser Gly Lys Ser Thr		
385	390	395
		400

(2) INFORMATION FOR SEQ ID NO:1332:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 389 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..389

(D) OTHER INFORMATION: / Ceres Seq. ID 1500071

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1332:

Met	Glu	Leu	Gln	Ser	Gln	Ile	Pro	Ile	Leu	Arg	Pro	Ser	Ile	His	Ala
1			5					10					15		
Arg	Arg	Ala	Asn	Ile	Val	Val	Lys	Phe	Gln	Asp	Leu	Tyr	Gly	Phe	Thr
		20					25						30		

Val Glu Gly Asn Val Asp Asp Val Asn Val Leu Asn Glu Val Arg Glu
35 40 45
Lys Val Arg Asn Gln Gly Arg Val Trp Trp Ala Leu Glu Ala Ser Lys
50 55 60
Gly Ala Asn Trp Tyr Leu Gln Pro Glu Ile Leu Leu Ile Gly Asp Gly
65 70 75 80
Ile Ala Leu Lys Thr Ser Leu Lys Leu Ser Thr Leu Thr Asn Ala Ile
85 90 95
Thr Leu Lys Arg Leu Ile Arg Lys Gly Ile Pro Pro Val Leu Arg Pro
100 105 110
Lys Val Trp Phe Ser Leu Ser Gly Ala Ala Lys Lys Lys Ser Thr Val
115 120 125
Pro Glu Ser Tyr Tyr Ser Asp Leu Thr Lys Ala Val Glu Gly Met Val
130 135 140
Thr Pro Ala Thr Arg Gln Ile Asp His Asp Leu Pro Arg Thr Phe Pro
145 150 155 160
Gly His Pro Trp Leu Asp Thr Pro Glu Gly His Ala Ala Leu Arg Arg
165 170 175
Val Leu Val Gly Tyr Ser Phe Arg Asp Ser Asp Val Gly Tyr Cys Gln
180 185 190
Gly Leu Asn Tyr Val Ala Ala Leu Leu Leu Val Met Lys Thr Glu
195 200 205
Glu Asp Ala Phe Trp Met Leu Ala Val Leu Leu Glu Asn Val Leu Val
210 215 220
Arg Asp Cys Tyr Thr Thr Asn Leu Ser Gly Cys His Val Glu Gln Arg
225 230 235 240
Val Phe Lys Asp Leu Leu Ala Gln Lys Cys Ser Arg Ile Ala Thr His
245 250 255
Leu Glu Asp Met Gly Phe Asp Val Ser Leu Val Ala Thr Glu Trp Phe
260 265 270
Leu Cys Leu Phe Ser Lys Ser Leu Pro Ser Glu Thr Thr Leu Arg Val
275 280 285
Trp Asp Val Leu Phe Tyr Glu Gly Ala Lys Val Leu Phe His Ala Ala
290 295 300
Leu Ala Ile Phe Lys Met Lys Glu Asn Glu Leu Leu Met Thr His Gln
305 310 315 320
Val Gly Asp Val Ile Asn Xaa Leu Gln Lys Thr Ser His Gln Leu Phe
325 330 335
Asp Pro Asp Glu Leu Leu Thr Val Ala Phe Glu Lys Ile Gly Ser Met
340 345 350
Thr Thr Asn Thr Ile Ser Lys Gln Arg Lys Lys Gln Glu Pro Ala Val
355 360 365
Met Ala Glu Leu Asp Gln Arg Leu Arg Arg Leu Asn Ser Leu Lys Glu
370 375 380
Ser Gly Lys Ser Thr
385

(2) INFORMATION FOR SEQ ID NO:1333:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 247 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..247
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500072

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1333:

Met Val Thr Pro Ala Thr Arg Gln Ile Asp His Asp Leu Pro Arg Thr
1 5 10 15
Phe Pro Gly His Pro Trp Leu Asp Thr Pro Glu Gly His Ala Ala Leu

	20		25		30										
Arg	Arg	Val	Leu	Val	Gly	Tyr	Ser	Phe	Arg	Asp	Ser	Asp	Val	Gly	Tyr
	35		40		45										
Cys	Gln	Gly	Leu	Asn	Tyr	Val	Ala	Ala	Leu	Leu	Leu	Leu	Val	Met	Lys
	50		55		60										
Thr	Glu	Glu	Asp	Ala	Phe	Trp	Met	Leu	Ala	Val	Leu	Leu	Glu	Asn	Val
65			70		75									80	
Leu	Val	Arg	Asp	Cys	Tyr	Thr	Thr	Asn	Leu	Ser	Gly	Cys	His	Val	Glu
			85		90									95	
Gln	Arg	Val	Phe	Lys	Asp	Leu	Leu	Ala	Gln	Lys	Cys	Ser	Arg	Ile	Ala
			100		105									110	
Thr	His	Leu	Glu	Asp	Met	Gly	Phe	Asp	Val	Ser	Leu	Val	Ala	Thr	Glu
			115		120									125	
Trp	Phe	Leu	Cys	Leu	Phe	Ser	Lys	Ser	Leu	Pro	Ser	Glu	Thr	Thr	Leu
			130		135									140	
Arg	Val	Trp	Asp	Val	Leu	Phe	Tyr	Glu	Gly	Ala	Lys	Val	Leu	Phe	His
145					150					155					160
Ala	Ala	Leu	Ala	Ile	Phe	Lys	Met	Lys	Glu	Asn	Glu	Leu	Leu	Met	Thr
					165					170					175
His	Gln	Val	Gly	Asp	Val	Ile	Asn	Xaa	Leu	Gln	Lys	Thr	Ser	His	Gln
			180							185				190	
Leu	Phe	Asp	Pro	Asp	Glu	Leu	Leu	Thr	Val	Ala	Phe	Glu	Lys	Ile	Gly
			195							200				205	
Ser	Met	Thr	Thr	Asn	Thr	Ile	Ser	Lys	Gln	Arg	Lys	Lys	Gln	Glu	Pro
			210							215				220	
Ala	Val	Met	Ala	Glu	Leu	Asp	Gln	Arg	Leu	Arg	Arg	Leu	Asn	Ser	Leu
225					230					235					240
Lys	Glu	Ser	Gly	Lys	Ser	Thr									
					245										

(2) INFORMATION FOR SEQ ID NO:1334:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1674 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1674
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500073

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1334:

agatgtaatt	tgtataattt	tagtaactct	tcagtttttt	tttgttttta	aaatatattt	60
tctctctctc	tgtcttcctg	caatctatcg	cgggccgatt	caataatttc	gctttactct	120
gccaaaaaag	tttgttcttt	tgttttctgg	gattatccaa	agagaagaaa	cagaggaaat	180
cagtctcttt	tttagtttca	gaccctaaat	cctaggtttt	gaagttttgt	ttcttttagta	240
attttgtcag	gttttggtgc	tggtggtggg	atttttcgga	gcttggtttc	ttgaaccagc	300
tccattttct	aaaaattcct	tccttaaatc	cccattgttg	taagtcttaa	agaaaaaaga	360
agatgacttg	ttgtttctct	tgtttgaatc	ctcgaaccaa	ggacataaga	gtcgacattg	420
ataacgctcg	atgcaactct	cgttaccaaa	ccgattcatc	agttcatgga	agtatacaaa	480
caggaacaga	gtcgatttcg	ggtatcttag	taaatggtaa	agtgaatagt	ccgataacctg	540
gtggtggagc	tcggagcttc	acgttcaagg	agttagctgc	agctacaaga	aacttcggg	600
aagttaattt	gctcggagaa	ggaggttttg	gcagagttta	taagggacgt	ttagattcag	660
gacaagtagt	ggctattaag	caattgaatc	cagatgggct	tcaagggaac	cgagagttta	720
tagtagaagt	tcctatgctt	agcttattgc	atcatcccaa	tctcgttaca	ttgatcggtt	780
actgtacttc	tggtgatcaa	agacttcttg	tctatgaata	catgccaatg	ggaagcttag	840
aagatcacct	ttttgatctt	gagtctaata	aagaaccatt	aagctggaat	actcgaatga	900
aaatcgcggt	tggtgcagct	cgaggaatat	agtatcttca	ctgcacagct	aaccgcgag	960
tgatttacgg	tgatttgaaa	tccgcaaaca	tattgttaga	taaagagttc	agtcacaaac	1020
tctcggattt	cggattggcg	aaactcggtc	cagttggtga	tcgaactcat	gtatcgactc	1080
gtgtcatggg	aacttacggg	tactgtgctc	ctgaatacgc	aatgagcggg	aaattaactg	1140
ttaaatcgga	tatctactgc	ttcgggtgtag	tggtgcttga	gctgattact	gggagaaaaag	1200

```
ctattgattt aggtcaaaag caaggcgagc agaatcttgt tacttgggtca cgtccataacc 1260
tcaaggatca gaagaagttt ggacatttag tggatccgtc tctacgagga aaatacccaa 1320
gacgggtgtt aaactatgcg attgcgatta ttgcaatgtg tcttaatgaa gaagctcatt 1380
atcgaccgtt cataggtgac atagttgtgg cactagagta cttagccgca cagagcagat 1440
ctcatgaagc tcgaaacgtc tcatcaccgt caccagagat ttcaagaacg ccgcgacgag 1500
acttgtaaaa actcaaaaac agcttttaag aatttcagtt tgggtgttgtg taaaaatggt 1560
ttttttgttt ctttctcaga aaacaatata tgtttggtaa atgtttcggt attagtctct 1620
tttacttgat gtatatggca attatggaaa caattaaagt tcttttatat gtgt
```

(2) INFORMATION FOR SEQ ID NO:1335:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 381 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..381

(D) OTHER INFORMATION: / Ceres Seq. ID 1500074

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1335:

```
Met Thr Cys Cys Phe Ser Cys Leu Asn Pro Arg Thr Lys Asp Ile Arg
1          5          10          15
Val Asp Ile Asp Asn Ala Arg Cys Asn Ser Arg Tyr Gln Thr Asp Ser
20          25          30
Ser Val His Gly Ser Asp Thr Thr Gly Thr Glu Ser Ile Ser Gly Ile
35          40          45
Leu Val Asn Gly Lys Val Asn Ser Pro Ile Pro Gly Gly Gly Ala Arg
50          55          60
Ser Phe Thr Phe Lys Glu Leu Ala Ala Ala Thr Arg Asn Phe Arg Glu
65          70          75          80
Val Asn Leu Leu Gly Glu Gly Gly Phe Gly Arg Val Tyr Lys Gly Arg
85          90          95
Leu Asp Ser Gly Gln Val Val Ala Ile Lys Gln Leu Asn Pro Asp Gly
100          105          110
Leu Gln Gly Asn Arg Glu Phe Ile Val Glu Val Leu Met Leu Ser Leu
115          120          125
Leu His His Pro Asn Leu Val Thr Leu Ile Gly Tyr Cys Thr Ser Gly
130          135          140
Asp Gln Arg Leu Leu Val Tyr Glu Tyr Met Pro Met Gly Ser Leu Glu
145          150          155          160
Asp His Leu Phe Asp Leu Glu Ser Asn Gln Glu Pro Leu Ser Trp Asn
165          170          175
Thr Arg Met Lys Ile Ala Val Gly Ala Ala Arg Gly Ile Glu Tyr Leu
180          185          190
His Cys Thr Ala Asn Pro Pro Val Ile Tyr Arg Asp Leu Lys Ser Ala
195          200          205
Asn Ile Leu Leu Asp Lys Glu Phe Ser Pro Lys Leu Ser Asp Phe Gly
210          215          220
Leu Ala Lys Leu Gly Pro Val Gly Asp Arg Thr His Val Ser Thr Arg
225          230          235          240
Val Met Gly Thr Tyr Gly Tyr Cys Ala Pro Glu Tyr Ala Met Ser Gly
245          250          255
Lys Leu Thr Val Lys Ser Asp Ile Tyr Cys Phe Gly Val Val Leu Leu
260          265          270
Glu Leu Ile Thr Gly Arg Lys Ala Ile Asp Leu Gly Gln Lys Gln Gly
275          280          285
Glu Gln Asn Leu Val Thr Trp Ser Arg Pro Tyr Leu Lys Asp Gln Lys
290          295          300
Lys Phe Gly His Leu Val Asp Pro Ser Leu Arg Gly Lys Tyr Pro Arg
305          310          315          320
Arg Cys Leu Asn Tyr Ala Ile Ala Ile Ile Ala Met Cys Leu Asn Glu
```

325 330 335
Glu Ala His Tyr Arg Pro Phe Ile Gly Asp Ile Val Val Ala Leu Glu
340 345 350
Tyr Leu Ala Ala Gln Ser Arg Ser His Glu Ala Arg Asn Val Ser Ser
355 360 365
Pro Ser Pro Glu Ile Ser Arg Thr Pro Arg Arg Asp Leu
370 375 380

(2) INFORMATION FOR SEQ ID NO:1336:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 257 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..257

(D) OTHER INFORMATION: / Ceres Seq. ID 1500075

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1336:

Met Leu Ser Leu Leu His His Pro Asn Leu Val Thr Leu Ile Gly Tyr
1 5 10 15
Cys Thr Ser Gly Asp Gln Arg Leu Leu Val Tyr Glu Tyr Met Pro Met
20 25 30
Gly Ser Leu Glu Asp His Leu Phe Asp Leu Glu Ser Asn Gln Glu Pro
35 40 45
Leu Ser Trp Asn Thr Arg Met Lys Ile Ala Val Gly Ala Ala Arg Gly
50 55 60
Ile Glu Tyr Leu His Cys Thr Ala Asn Pro Pro Val Ile Tyr Arg Asp
65 70 75 80
Leu Lys Ser Ala Asn Ile Leu Leu Asp Lys Glu Phe Ser Pro Lys Leu
85 90 95
Ser Asp Phe Gly Leu Ala Lys Leu Gly Pro Val Gly Asp Arg Thr His
100 105 110
Val Ser Thr Arg Val Met Gly Thr Tyr Gly Tyr Cys Ala Pro Glu Tyr
115 120 125
Ala Met Ser Gly Lys Leu Thr Val Lys Ser Asp Ile Tyr Cys Phe Gly
130 135 140
Val Val Leu Leu Glu Leu Ile Thr Gly Arg Lys Ala Ile Asp Leu Gly
145 150 155 160
Gln Lys Gln Gly Glu Gln Asn Leu Val Thr Trp Ser Arg Pro Tyr Leu
165 170 175
Lys Asp Gln Lys Lys Phe Gly His Leu Val Asp Pro Ser Leu Arg Gly
180 185 190
Lys Tyr Pro Arg Arg Cys Leu Asn Tyr Ala Ile Ala Ile Ala Met
195 200 205
Cys Leu Asn Glu Glu Ala His Tyr Arg Pro Phe Ile Gly Asp Ile Val
210 215 220
Val Ala Leu Glu Tyr Leu Ala Ala Gln Ser Arg Ser His Glu Ala Arg
225 230 235 240
Asn Val Ser Ser Pro Ser Pro Glu Ile Ser Arg Thr Pro Arg Arg Asp
245 250 255
Leu

(2) INFORMATION FOR SEQ ID NO:1337:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 228 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide
(B) LOCATION: 1..228
(D) OTHER INFORMATION: / Ceres Seq. ID 1500076

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1337:

Met	Pro	Met	Gly	Ser	Leu	Glu	Asp	His	Leu	Phe	Asp	Leu	Glu	Ser	Asn
1				5					10					15	
Gln	Glu	Pro	Leu	Ser	Trp	Asn	Thr	Arg	Met	Lys	Ile	Ala	Val	Gly	Ala
			20					25					30		
Ala	Arg	Gly	Ile	Glu	Tyr	Leu	His	Cys	Thr	Ala	Asn	Pro	Pro	Val	Ile
		35					40				45				
Tyr	Arg	Asp	Leu	Lys	Ser	Ala	Asn	Ile	Leu	Leu	Asp	Lys	Glu	Phe	Ser
	50					55				60					
Pro	Lys	Leu	Ser	Asp	Phe	Gly	Leu	Ala	Lys	Leu	Gly	Pro	Val	Gly	Asp
65					70				75					80	
Arg	Thr	His	Val	Ser	Thr	Arg	Val	Met	Gly	Thr	Tyr	Gly	Tyr	Cys	Ala
			85					90						95	
Pro	Glu	Tyr	Ala	Met	Ser	Gly	Lys	Leu	Thr	Val	Lys	Ser	Asp	Ile	Tyr
			100					105					110		
Cys	Phe	Gly	Val	Val	Leu	Leu	Glu	Leu	Ile	Thr	Gly	Arg	Lys	Ala	Ile
		115					120					125			
Asp	Leu	Gly	Gln	Lys	Gln	Gly	Glu	Gln	Asn	Leu	Val	Thr	Trp	Ser	Arg
	130					135					140				
Pro	Tyr	Leu	Lys	Asp	Gln	Lys	Lys	Phe	Gly	His	Leu	Val	Asp	Pro	Ser
145					150					155					160
Leu	Arg	Gly	Lys	Tyr	Pro	Arg	Arg	Cys	Leu	Asn	Tyr	Ala	Ile	Ala	Ile
			165					170						175	
Ile	Ala	Met	Cys	Leu	Asn	Glu	Glu	Ala	His	Tyr	Arg	Pro	Phe	Ile	Gly
			180					185					190		
Asp	Ile	Val	Val	Ala	Leu	Glu	Tyr	Leu	Ala	Ala	Gln	Ser	Arg	Ser	His
	195						200				205				
Glu	Ala	Arg	Asn	Val	Ser	Ser	Pro	Ser	Pro	Glu	Ile	Ser	Arg	Thr	Pro
	210					215					220				
Arg	Arg	Asp	Leu												
225															

(2) INFORMATION FOR SEQ ID NO:1338:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1690 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -
(B) LOCATION: 1..1690
(D) OTHER INFORMATION: / Ceres Seq. ID 1500077

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1338:

atcaataaac	acaaaaacaa	aagaagaaga	gaataaacaa	aagaagaaaa	aaaactaata	60
aaacaaaatc	aataaaaaga	gaataaaaaa	tggtgggttc	tcacaaagca	agcggagtgc	120
ttcttgctg	actagtgggt	atggccacca	caatagcaaa	cgggacaccg	gttgctcgata	180
aagcaaaaaa	tgcagctaca	gcagttgaag	atacagcaaa	aaatgcagct	acagcagttg	240
gcggtgcagc	tgcattcagtt	gggtgctaaa	tatcaggtgc	caaaccaggc	gcagcagttg	300
atgttaaagc	atcaggagcc	aaaggagacg	gcaaaactga	tgatagtgcg	gcatttgccg	360
ctgcatggaa	agaagcttgt	gcagcagggg	gcacaattac	agtgcacaaa	ggtgagtata	420
tggtagagag	cctagagtgc	aaaggtccat	gcaaaggtcc	agtcactttg	gaattgaatg	480
gcaatttcaa	ggctccggct	acggtcaaga	ccactaagcc	acatgccgga	tggattgatt	540
tcgaaaatat	agctgatttc	actttgaatg	gaaacaaagc	tatttttgac	ggtcaagggt	600
ccctcgcttg	gaaggccaat	gattgtgcca	aaactggcaa	atgcaactct	ctccctatca	660
acatccgatt	cactggtcta	acaaactcaa	agattaatag	tattacatca	acaaacagca	720
aactttttcca	catgaacatc	cttaactgca	agaacattac	tctttcggat	attggtattg	780
atgcacctcc	ggagagtctc	aacaccgatg	gtatccacat	cggaaggtcc	aatggagtca	840
acttaattgg	ggcaaagatc	aaaaccggag	atgactgcgt	ttccattgga	gatgggtaccg	900


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aaaatctcat tgttgagaac gtagaatgtg gaccaggaca cggaatttcc attggaagtc 960
ttggaagata ccctaagtga caaccagtaa aaggagtcac cgtgaggaaa tgcctcatca 1020
agaacactga caatggtgtt cgcacaaaga catggccagg atctccccc ggcatcgctt 1080
ccaacattct tttcgaagat atcacaaatg acaatgttag ccttcccgtt ctcacgcacc 1140
aagagtactg tccttatggc cactgcaaag ctgggggtacc atcgcaagtg aagttgtcag 1200
acgtgactat caagggcatt aagggtacat cagcaacaaa ggtggctgtg aagctaattg 1260
gcagcaaagg agtgccttgc accaatattg ctctctctga catcaacttg gtccacaacg 1320
gcaaagaggg accagctgtc tcggcatgtt ctaacatcaa gcctattctc agcggaaaagt 1380
tggttccagc ggcttgcaat gaagttgcta aaccgggtcc ataaattaaa gtcgcttgct 1440
caccataaat ccatccaatc tggcgaagac gctttgatta ggggtcgatg aaaaaatttt 1500
gcaatatttt tttgacatat aaattatat gatattttat agataagacg gagtccattc 1560
aggattggag tttataacct gaagagtgc tcgtgaattg ggtagtaatt gttgtgtgga 1620
ttcgcattta tgcgagaatg ttttaataat tattcgaaaa gtaataatat cattgaaatt 1680
ttgaagtttt
```

(2) INFORMATION FOR SEQ ID NO:1339:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 444 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..444

(D) OTHER INFORMATION: / Ceres Seq. ID 1500078

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1339:

```
Met Val Gly Ser His Lys Ala Ser Gly Val Leu Leu Val Leu Leu Val
1          5          10          15
Val Met Ala Thr Thr Ile Ala Asn Gly Thr Pro Val Val Asp Lys Ala
20          25          30
Lys Asn Ala Ala Thr Ala Val Glu Asp Thr Ala Lys Asn Ala Ala Thr
35          40          45
Ala Val Gly Gly Ala Ala Ala Ser Val Gly Ala Lys Val Ser Gly Ala
50          55          60
Lys Pro Gly Ala Ala Val Asp Val Lys Ala Ser Gly Ala Lys Gly Asp
65          70          75          80
Gly Lys Thr Asp Asp Ser Ala Ala Phe Ala Ala Ala Trp Lys Glu Ala
85          90          95
Cys Ala Ala Gly Ser Thr Ile Thr Val Pro Lys Gly Glu Tyr Met Val
100          105          110
Glu Ser Leu Glu Phe Lys Gly Pro Cys Lys Gly Pro Val Thr Leu Glu
115          120          125
Leu Asn Gly Asn Phe Lys Ala Pro Ala Thr Val Lys Thr Thr Lys Pro
130          135          140
His Ala Gly Trp Ile Asp Phe Glu Asn Ile Ala Asp Phe Thr Leu Asn
145          150          155          160
Gly Asn Lys Ala Ile Phe Asp Gly Gln Gly Ser Leu Ala Trp Lys Ala
165          170          175
Asn Asp Cys Ala Lys Thr Gly Lys Cys Asn Ser Leu Pro Ile Asn Ile
180          185          190
Arg Phe Thr Gly Leu Thr Asn Ser Lys Ile Asn Ser Ile Thr Ser Thr
195          200          205
Asn Ser Lys Leu Phe His Met Asn Ile Leu Asn Cys Lys Asn Ile Thr
210          215          220
Leu Ser Asp Ile Gly Ile Asp Ala Pro Pro Glu Ser Leu Asn Thr Asp
225          230          235          240
Gly Ile His Ile Gly Arg Ser Asn Gly Val Asn Leu Ile Gly Ala Lys
245          250          255
Ile Lys Thr Gly Asp Asp Cys Val Ser Ile Gly Asp Gly Thr Glu Asn
260          265          270
Leu Ile Val Glu Asn Val Glu Cys Gly Pro Gly His Gly Ile Ser Ile
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275	280	285
Gly Ser Leu Gly Arg Tyr Pro Asn Glu Gln Pro Val Lys Gly Val Thr		
290	295	300
Val Arg Lys Cys Leu Ile Lys Asn Thr Asp Asn Gly Val Arg Ile Lys		
305	310	315
Thr Trp Pro Gly Ser Pro Pro Gly Ile Ala Ser Asn Ile Leu Phe Glu		
	325	330
Asp Ile Thr Met Asp Asn Val Ser Leu Pro Val Leu Ile Asp Gln Glu		
	340	345
Tyr Cys Pro Tyr Gly His Cys Lys Ala Gly Val Pro Ser Gln Val Lys		
	355	360
Leu Ser Asp Val Thr Ile Lys Gly Ile Lys Gly Thr Ser Ala Thr Lys		
	370	375
Val Ala Val Lys Leu Met Cys Ser Lys Gly Val Pro Cys Thr Asn Ile		
385	390	395
Ala Leu Ser Asp Ile Asn Leu Val His Asn Gly Lys Glu Gly Pro Ala		
	405	410
Val Ser Ala Cys Ser Asn Ile Lys Pro Ile Leu Ser Gly Lys Leu Val		
	420	425
Pro Ala Ala Cys Thr Glu Val Ala Lys Pro Gly Pro		
	435	440

(2) INFORMATION FOR SEQ ID NO:1340:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 427 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..427

(D) OTHER INFORMATION: / Ceres Seq. ID 1500079

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1340:

Met Ala Thr Thr Ile Ala Asn Gly Thr Pro Val Val Asp Lys Ala Lys		
1	5	10
Asn Ala Ala Thr Ala Val Glu Asp Thr Ala Lys Asn Ala Ala Thr Ala		
	20	25
Val Gly Gly Ala Ala Ala Ser Val Gly Ala Lys Val Ser Gly Ala Lys		
	35	40
Pro Gly Ala Ala Val Asp Val Lys Ala Ser Gly Ala Lys Gly Asp Gly		
	50	55
Lys Thr Asp Asp Ser Ala Ala Phe Ala Ala Ala Trp Lys Glu Ala Cys		
65	70	75
Ala Ala Gly Ser Thr Ile Thr Val Pro Lys Gly Glu Tyr Met Val Glu		
	85	90
Ser Leu Glu Phe Lys Gly Pro Cys Lys Gly Pro Val Thr Leu Glu Leu		
	100	105
Asn Gly Asn Phe Lys Ala Pro Ala Thr Val Lys Thr Thr Lys Pro His		
	115	120
Ala Gly Trp Ile Asp Phe Glu Asn Ile Ala Asp Phe Thr Leu Asn Gly		
	130	135
Asn Lys Ala Ile Phe Asp Gly Gln Gly Ser Leu Ala Trp Lys Ala Asn		
145	150	155
Asp Cys Ala Lys Thr Gly Lys Cys Asn Ser Leu Pro Ile Asn Ile Arg		
	165	170
Phe Thr Gly Leu Thr Asn Ser Lys Ile Asn Ser Ile Thr Ser Thr Asn		
	180	185
Ser Lys Leu Phe His Met Asn Ile Leu Asn Cys Lys Asn Ile Thr Leu		
	195	200
Ser Asp Ile Gly Ile Asp Ala Pro Pro Glu Ser Leu Asn Thr Asp Gly		
	210	215
		220

Ile His Ile Gly Arg Ser Asn Gly Val Asn Leu Ile Gly Ala Lys Ile
225 230 235 240
Lys Thr Gly Asp Asp Cys Val Ser Ile Gly Asp Gly Thr Glu Asn Leu
245 250 255
Ile Val Glu Asn Val Glu Cys Gly Pro Gly His Gly Ile Ser Ile Gly
260 265 270
Ser Leu Gly Arg Tyr Pro Asn Glu Gln Pro Val Lys Gly Val Thr Val
275 280 285
Arg Lys Cys Leu Ile Lys Asn Thr Asp Asn Gly Val Arg Ile Lys Thr
290 295 300
Trp Pro Gly Ser Pro Pro Gly Ile Ala Ser Asn Ile Leu Phe Glu Asp
305 310 315 320
Ile Thr Met Asp Asn Val Ser Leu Pro Val Leu Ile Asp Gln Glu Tyr
325 330 335
Cys Pro Tyr Gly His Cys Lys Ala Gly Val Pro Ser Gln Val Lys Leu
340 345 350
Ser Asp Val Thr Ile Lys Gly Ile Lys Gly Thr Ser Ala Thr Lys Val
355 360 365
Ala Val Lys Leu Met Cys Ser Lys Gly Val Pro Cys Thr Asn Ile Ala
370 375 380
Leu Ser Asp Ile Asn Leu Val His Asn Gly Lys Glu Gly Pro Ala Val
385 390 395 400
Ser Ala Cys Ser Asn Ile Lys Pro Ile Leu Ser Gly Lys Leu Val Pro
405 410 415
Ala Ala Cys Thr Glu Val Ala Lys Pro Gly Pro
420 425

(2) INFORMATION FOR SEQ ID NO:1341:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 334 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..334
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500080

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1341:

Met Val Glu Ser Leu Glu Phe Lys Gly Pro Cys Lys Gly Pro Val Thr
1 5 10 15
Leu Glu Leu Asn Gly Asn Phe Lys Ala Pro Ala Thr Val Lys Thr Thr
20 25 30
Lys Pro His Ala Gly Trp Ile Asp Phe Glu Asn Ile Ala Asp Phe Thr
35 40 45
Leu Asn Gly Asn Lys Ala Ile Phe Asp Gly Gln Gly Ser Leu Ala Trp
50 55 60
Lys Ala Asn Asp Cys Ala Lys Thr Gly Lys Cys Asn Ser Leu Pro Ile
65 70 75 80
Asn Ile Arg Phe Thr Gly Leu Thr Asn Ser Lys Ile Asn Ser Ile Thr
85 90 95
Ser Thr Asn Ser Lys Leu Phe His Met Asn Ile Leu Asn Cys Lys Asn
100 105 110
Ile Thr Leu Ser Asp Ile Gly Ile Asp Ala Pro Pro Glu Ser Leu Asn
115 120 125
Thr Asp Gly Ile His Ile Gly Arg Ser Asn Gly Val Asn Leu Ile Gly
130 135 140
Ala Lys Ile Lys Thr Gly Asp Asp Cys Val Ser Ile Gly Asp Gly Thr
145 150 155 160
Glu Asn Leu Ile Val Glu Asn Val Glu Cys Gly Pro Gly His Gly Ile
165 170 175
Ser Ile Gly Ser Leu Gly Arg Tyr Pro Asn Glu Gln Pro Val Lys Gly

	180		185		190
Val Thr	Val Arg Lys Cys Leu Ile	Lys Asn Thr Asp Asn Gly	Val Arg		
	195	200	205		
Ile Lys	Thr Trp Pro Gly Ser Pro	Pro Gly Ile Ala Ser Asn	Ile Leu		
	210	215	220		
Phe Glu	Asp Ile Thr Met Asp Asn	Val Ser Leu Pro Val Leu	Ile Asp		
225		230	235		240
Gln Glu	Tyr Cys Pro Tyr Gly His	Cys Lys Ala Gly Val Pro	Ser Gln		
	245	250	255		
Val Lys	Leu Ser Asp Val Thr Ile	Lys Gly Ile Lys Gly Thr	Ser Ala		
	260	265	270		
Thr Lys	Val Ala Val Lys Leu Met	Cys Ser Lys Gly Val Pro	Cys Thr		
	275	280	285		
Asn Ile	Ala Leu Ser Asp Ile Asn	Leu Val His Asn Gly Lys	Glu Gly		
	290	295	300		
Pro Ala	Val Ser Ala Cys Ser Asn	Ile Lys Pro Ile Leu Ser	Gly Lys		
305		310	315		320
Leu Val	Pro Ala Ala Cys Thr Glu	Val Ala Lys Pro Gly Pro			
	325	330			

(2) INFORMATION FOR SEQ ID NO:1342:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1396 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1396
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500081

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1342:

aatgtattaa	gacttgacaa	cttgtctttc	tcacacacaaa	cccctctcct	ctgtttcata	60
acatcttctc	tttttttttt	tcctaagccc	ctaattgacaa	accataatgc	cttaaatctct	120
gatgctaaag	gcagcatcgg	agttgcggtt	agagttccaa	accaatctct	gtttttctccc	180
ggaggtggcc	gatacatcag	cattccccgg	aagaaactcg	tgcagaagct	agaggccgac	240
ccgagtcaaa	cccgtatcca	cacttggatc	gaagccatga	gggcttcttc	cccaaccctg	300
acccgaccgg	ggaacatatc	tccccctcac	gagtcctgat	aggaggatga	atactcttct	360
tggatggctc	aacacccgct	agcttttaac	atgtttgaag	agatagctga	agcttcaaaa	420
gggaacaaaa	tcgtgatgtt	tctcgactat	gacggtacat	tatcccccat	tgttgaaaac	480
cctgatcgag	cttcatgttc	tgaagagatg	agagaggcag	tgaaggcgct	ggctagatat	540
ttcccgaccg	cgattgtcac	tgggaagatg	cgtgataagg	ttcgtagatt	tgtgaaactt	600
cccggacttt	actatgcagg	tagccatgga	atggacatca	aaggaccttc	caaaagaaac	660
aaacataata	agaacaataa	aggagttctt	ttccaagcgg	cgaatgagtt	tttgccctatg	720
attgacaagg	tctctaagtg	tctagtagag	aaaatgagag	acatagaagg	agcaaacgtc	780
gagaacaaca	agtttttgtg	ctccgtacat	taccgttgtg	ttgatcaaaa	ggactgggga	840
ttggtagcgg	aacacgtgac	atcgatattg	agtgagtatc	cgaaactgag	tttgacacaa	900
ggaagaaaag	tcttagagat	tcgaccaacc	atcaaatggg	ataaaggcaa	agctctcgag	960
ttcttgctcg	aatccttagg	attcgctaac	tctaacgatg	ttttgcccct	ctatatagga	1020
gatgatcgta	cggacgagga	tgctttcaag	gttttgagaa	acaaaggaca	aggctttggt	1080
atacttggtg	ccaaaattcc	aaaggaaacg	agtgtctacat	attctctaca	agaaccttcc	1140
gaggtaggag	agttttttgca	gcgactcgtg	gaatggaaac	aaatgtcact	aagaggaaga	1200
tagccaattt	cctgacataa	atttattttt	aattaataaa	tgaattagtt	ttcactatgc	1260
aacaaaaatt	gttgatatata	tgatcaatgt	ttttttaatt	attttactct	tcattgaacaa	1320
atgtaagttt	ataggaactt	tcttaaccaa	gaaaaaaaag	aagtttgcta	tataatattt	1380
tcattcattct	cttttt					

(2) INFORMATION FOR SEQ ID NO:1343:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..400

(D) OTHER INFORMATION: / Ceres Seq. ID 1500082

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1343:

Asn	Val	Leu	Arg	Leu	Asp	Asn	Leu	Ser	Phe	Ser	His	Gln	Thr	Pro	Leu	
1				5					10					15		
Leu	Cys	Phe	Ile	Thr	Ser	Ser	Leu	Phe	Phe	Pro	Lys	Pro	Leu	Met		
			20					25				30				
Thr	Asn	His	Asn	Ala	Leu	Ile	Ser	Asp	Ala	Lys	Gly	Ser	Ile	Gly	Val	
		35					40					45				
Ala	Val	Arg	Val	Pro	Asn	Gln	Ser	Leu	Phe	Ser	Pro	Gly	Gly	Gly	Arg	
	50					55					60					
Tyr	Ile	Ser	Ile	Pro	Arg	Lys	Lys	Leu	Val	Gln	Lys	Leu	Glu	Ala	Asp	
65					70					75					80	
Pro	Ser	Gln	Thr	Arg	Ile	His	Thr	Trp	Ile	Glu	Ala	Met	Arg	Ala	Ser	
			85						90					95		
Ser	Pro	Thr	Arg	Thr	Arg	Pro	Gly	Asn	Ile	Ser	Pro	Leu	Thr	Glu	Ser	
			100					105					110			
Asp	Glu	Glu	Asp	Glu	Tyr	Ser	Ser	Trp	Met	Ala	Gln	His	Pro	Ser	Ala	
		115					120				125					
Leu	Thr	Met	Phe	Glu	Glu	Ile	Ala	Glu	Ala	Ser	Lys	Gly	Lys	Gln	Ile	
	130						135				140					
Val	Met	Phe	Leu	Asp	Tyr	Asp	Gly	Thr	Leu	Ser	Pro	Ile	Val	Glu	Asn	
145					150					155					160	
Pro	Asp	Arg	Ala	Tyr	Met	Ser	Glu	Glu	Met	Arg	Glu	Ala	Val	Lys	Gly	
			165					170						175		
Val	Ala	Arg	Tyr	Phe	Pro	Thr	Ala	Ile	Val	Thr	Gly	Arg	Cys	Arg	Asp	
		180						185					190			
Lys	Val	Arg	Arg	Phe	Val	Lys	Leu	Pro	Gly	Leu	Tyr	Tyr	Ala	Gly	Ser	
		195					200					205				
His	Gly	Met	Asp	Ile	Lys	Gly	Pro	Ser	Lys	Arg	Asn	Lys	His	Asn	Lys	
	210					215				220						
Asn	Asn	Lys	Gly	Val	Leu	Phe	Gln	Ala	Ala	Asn	Glu	Phe	Leu	Pro	Met	
225					230					235					240	
Ile	Asp	Lys	Val	Ser	Lys	Cys	Leu	Val	Glu	Lys	Met	Arg	Asp	Ile	Glu	
			245						250					255		
Gly	Ala	Asn	Val	Glu	Asn	Asn	Lys	Phe	Cys	Val	Ser	Val	His	Tyr	Arg	
		260						265					270			
Cys	Val	Asp	Gln	Lys	Asp	Trp	Gly	Leu	Val	Ala	Glu	His	Val	Thr	Ser	
		275					280					285				
Ile	Leu	Ser	Glu	Tyr	Pro	Lys	Leu	Ser	Leu	Thr	Gln	Gly	Arg	Lys	Val	
	290					295					300					
Leu	Glu	Ile	Arg	Pro	Thr	Ile	Lys	Trp	Asp	Lys	Gly	Lys	Ala	Leu	Glu	
305					310					315					320	
Phe	Leu	Leu	Glu	Ser	Leu	Gly	Phe	Ala	Asn	Ser	Asn	Asp	Val	Leu	Pro	
			325					330						335		
Ile	Tyr	Ile	Gly	Asp	Asp	Arg	Thr	Asp	Glu	Asp	Ala	Phe	Lys	Val	Leu	
		340						345					350			
Arg	Asn	Lys	Gly	Gln	Gly	Phe	Gly	Ile	Leu	Val	Ser	Lys	Ile	Pro	Lys	
		355					360					365				
Glu	Thr	Ser	Ala	Thr	Tyr	Ser	Leu	Gln	Glu	Pro	Ser	Glu	Val	Gly	Glu	
	370					375					380					
Phe	Leu	Gln	Arg	Leu	Val	Glu	Trp	Lys	Gln	Met	Ser	Leu	Arg	Gly	Arg	
385					390					395					400	

(2) INFORMATION FOR SEQ ID NO:1344:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 369 amino acids

- (B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..369
(D) OTHER INFORMATION: / Ceres Seq. ID 1500083
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1344:

Met	Thr	Asn	His	Asn	Ala	Leu	Ile	Ser	Asp	Ala	Lys	Gly	Ser	Ile	Gly
1			5					10					15		
Val	Ala	Val	Arg	Val	Pro	Asn	Gln	Ser	Leu	Phe	Ser	Pro	Gly	Gly	Gly
		20					25					30			
Arg	Tyr	Ile	Ser	Ile	Pro	Arg	Lys	Lys	Leu	Val	Gln	Lys	Leu	Glu	Ala
		35				40					45				
Asp	Pro	Ser	Gln	Thr	Arg	Ile	His	Thr	Trp	Ile	Glu	Ala	Met	Arg	Ala
	50				55				60						
Ser	Ser	Pro	Thr	Arg	Thr	Arg	Pro	Gly	Asn	Ile	Ser	Pro	Leu	Thr	Glu
65				70					75				80		
Ser	Asp	Glu	Glu	Asp	Glu	Tyr	Ser	Ser	Trp	Met	Ala	Gln	His	Pro	Ser
			85					90					95		
Ala	Leu	Thr	Met	Phe	Glu	Glu	Ile	Ala	Glu	Ala	Ser	Lys	Gly	Lys	Gln
		100						105					110		
Ile	Val	Met	Phe	Leu	Asp	Tyr	Asp	Gly	Thr	Leu	Ser	Pro	Ile	Val	Glu
		115					120					125			
Asn	Pro	Asp	Arg	Ala	Tyr	Met	Ser	Glu	Glu	Met	Arg	Glu	Ala	Val	Lys
	130					135					140				
Gly	Val	Ala	Arg	Tyr	Phe	Pro	Thr	Ala	Ile	Val	Thr	Gly	Arg	Cys	Arg
145				150					155					160	
Asp	Lys	Val	Arg	Arg	Phe	Val	Lys	Leu	Pro	Gly	Leu	Tyr	Tyr	Ala	Gly
			165					170						175	
Ser	His	Gly	Met	Asp	Ile	Lys	Gly	Pro	Ser	Lys	Arg	Asn	Lys	His	Asn
		180						185				190			
Lys	Asn	Asn	Lys	Gly	Val	Leu	Phe	Gln	Ala	Ala	Asn	Glu	Phe	Leu	Pro
	195					200						205			
Met	Ile	Asp	Lys	Val	Ser	Lys	Cys	Leu	Val	Glu	Lys	Met	Arg	Asp	Ile
	210					215					220				
Glu	Gly	Ala	Asn	Val	Glu	Asn	Asn	Lys	Phe	Cys	Val	Ser	Val	His	Tyr
225				230					235					240	
Arg	Cys	Val	Asp	Gln	Lys	Asp	Trp	Gly	Leu	Val	Ala	Glu	His	Val	Thr
			245					250						255	
Ser	Ile	Leu	Ser	Glu	Tyr	Pro	Lys	Leu	Ser	Leu	Thr	Gln	Gly	Arg	Lys
		260					265					270			
Val	Leu	Glu	Ile	Arg	Pro	Thr	Ile	Lys	Trp	Asp	Lys	Gly	Lys	Ala	Leu
		275					280					285			
Glu	Phe	Leu	Leu	Glu	Ser	Leu	Gly	Phe	Ala	Asn	Ser	Asn	Asp	Val	Leu
	290					295					300				
Pro	Ile	Tyr	Ile	Gly	Asp	Asp	Arg	Thr	Asp	Glu	Asp	Ala	Phe	Lys	Val
305				310						315				320	
Leu	Arg	Asn	Lys	Gly	Gln	Gly	Phe	Gly	Ile	Leu	Val	Ser	Lys	Ile	Pro
			325					330						335	
Lys	Glu	Thr	Ser	Ala	Thr	Tyr	Ser	Leu	Gln	Glu	Pro	Ser	Glu	Val	Gly
		340					345					350			
Glu	Phe	Leu	Gln	Arg	Leu	Val	Glu	Trp	Lys	Gln	Met	Ser	Leu	Arg	Gly
		355				360						365			

Arg

- (2) INFORMATION FOR SEQ ID NO:1345:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 308 amino acids
(B) TYPE: amino acid

- (C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..308
(D) OTHER INFORMATION: / Ceres Seq. ID 1500084
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1345:

```
Met Arg Ala Ser Ser Pro Thr Arg Thr Arg Pro Gly Asn Ile Ser Pro
1      5      10      15
Leu Thr Glu Ser Asp Glu Glu Asp Glu Tyr Ser Ser Trp Met Ala Gln
      20      25      30
His Pro Ser Ala Leu Thr Met Phe Glu Glu Ile Ala Glu Ala Ser Lys
      35      40      45
Gly Lys Glu Ile Val Met Phe Leu Asp Tyr Asp Gly Thr Leu Ser Pro
      50      55      60
Ile Val Glu Asn Pro Asp Arg Ala Tyr Met Ser Glu Glu Met Arg Glu
      65      70      75      80
Ala Val Lys Gly Val Ala Arg Tyr Phe Pro Thr Ala Ile Val Thr Gly
      85      90      95
Arg Cys Arg Asp Lys Val Arg Arg Phe Val Lys Leu Pro Gly Leu Tyr
      100      105      110
Tyr Ala Gly Ser His Gly Met Asp Ile Lys Gly Pro Ser Lys Arg Asn
      115      120      125
Lys His Asn Lys Asn Asn Lys Gly Val Leu Phe Gln Ala Ala Asn Glu
      130      135      140
Phe Leu Pro Met Ile Asp Lys Val Ser Lys Cys Leu Val Glu Lys Met
      145      150      155      160
Arg Asp Ile Glu Gly Ala Asn Val Glu Asn Asn Lys Phe Cys Val Ser
      165      170      175
Val His Tyr Arg Cys Val Asp Gln Lys Asp Trp Gly Leu Val Ala Glu
      180      185      190
His Val Thr Ser Ile Leu Ser Glu Tyr Pro Lys Leu Ser Leu Thr Gln
      195      200      205
Gly Arg Lys Val Leu Glu Ile Arg Pro Thr Ile Lys Trp Asp Lys Gly
      210      215      220
Lys Ala Leu Glu Phe Leu Leu Glu Ser Leu Gly Phe Ala Asn Ser Asn
      225      230      235      240
Asp Val Leu Pro Ile Tyr Ile Gly Asp Asp Arg Thr Asp Glu Asp Ala
      245      250      255
Phe Lys Val Leu Arg Asn Lys Gly Gln Gly Phe Gly Ile Leu Val Ser
      260      265      270
Lys Ile Pro Lys Glu Thr Ser Ala Thr Tyr Ser Leu Gln Glu Pro Ser
      275      280      285
Glu Val Gly Glu Phe Leu Gln Arg Leu Val Glu Trp Lys Gln Met Ser
      290      295      300
Leu Arg Gly Arg
305
```

(2) INFORMATION FOR SEQ ID NO:1346:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1510 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
(A) NAME/KEY: -
(B) LOCATION: 1..1510
(D) OTHER INFORMATION: / Ceres Seq. ID 1500085
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1346:

ttttaatttt ttcattcttct tgggttttggg tgggtcactc ttcagggtcag gtgtgtataaa

Glu Glu Ile Asn Ser Ser Ala Pro Arg Asp Asp Asp Pro Glu Asn Arg
195 200 205
Ser Lys Phe Tyr Glu Ser Ala Ser Ala Arg Lys Arg Thr Val Thr Ala
210 215 220
Glu Glu Arg Glu Arg Ala Ile Asn Ala Ala Lys Thr Phe Glu Pro Thr
225 230 235 240
Asn Pro Phe Phe Arg Val Val Leu Arg Pro Ser Tyr Leu Tyr Arg Gly
245 250 255
Cys Ile Met Tyr Leu Pro Ser Gly Phe Ala Glu Lys Tyr Leu Ser Gly
260 265 270
Ile Ser Gly Phe Ile Lys Val Gln Leu Ala Glu Lys Gln Trp Pro Val
275 280 285
Arg Cys Leu Tyr Lys Ala Gly Arg Ala Lys Phe Ser Gln Gly Trp Tyr
290 295 300
Glu Phe Thr Leu Glu Asn Asn Leu Gly Glu Gly Asp Val Cys Val Phe
305 310 315 320
Glu Leu Leu Arg Thr Arg Asp Phe Val Leu Lys Val Thr Ala Phe Arg
325 330 335
Val Asn Glu Tyr Val
340

(2) INFORMATION FOR SEQ ID NO:1348:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 232 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..232

(D) OTHER INFORMATION: / Ceres Seq. ID 1500087

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1348:

Met Asp Ser Ala His Asn His Phe Lys Arg Ala Arg Leu Phe Glu Asp
1 5 10 15
Leu Glu Asp Glu Asp Ala Glu Val Ile Phe Pro Ser Ser Val Tyr Pro
20 25 30
Ser Pro Leu Pro Glu Ser Thr Val Pro Ala Asn Lys Gly Tyr Ala Ser
35 40 45
Ser Ala Ile Gln Thr Leu Phe Thr Gly Pro Val Lys Ala Glu Glu Pro
50 55 60
Thr Pro Thr Pro Lys Ile Pro Lys Lys Arg Gly Arg Lys Lys Lys Asn
65 70 75 80
Ala Asp Pro Glu Glu Ile Asn Ser Ser Ala Pro Arg Asp Asp Asp Pro
85 90 95
Glu Asn Arg Ser Lys Phe Tyr Glu Ser Ala Ser Ala Arg Lys Arg Thr
100 105 110
Val Thr Ala Glu Glu Arg Glu Arg Ala Ile Asn Ala Ala Lys Thr Phe
115 120 125
Glu Pro Thr Asn Pro Phe Phe Arg Val Val Leu Arg Pro Ser Tyr Leu
130 135 140
Tyr Arg Gly Cys Ile Met Tyr Leu Pro Ser Gly Phe Ala Glu Lys Tyr
145 150 155 160
Leu Ser Gly Ile Ser Gly Phe Ile Lys Val Gln Leu Ala Glu Lys Gln
165 170 175
Trp Pro Val Arg Cys Leu Tyr Lys Ala Gly Arg Ala Lys Phe Ser Gln
180 185 190
Gly Trp Tyr Glu Phe Thr Leu Glu Asn Asn Leu Gly Glu Gly Asp Val
195 200 205
Cys Val Phe Glu Leu Leu Arg Thr Arg Asp Phe Val Leu Lys Val Thr
210 215 220
Ala Phe Arg Val Asn Glu Tyr Val

225

230

(2) INFORMATION FOR SEQ ID NO:1349:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1597 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1597
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500088

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1349:

```
aaaataaaga accttgacaa cttctctaca acactcactt tttctctcta atggtggaag      60
caagaagcctt gaagaaacca atccaattgg gtaataaaga agatcaaaac cctagaaaat      120
tctactctcg attcatcttt aaagctctta tcctcaccgt gctctgcgcc gtcgtacctg      180
tcttcctttc tcagacacca gagcttgcta accaaacaag actcctcgag cttctccacc      240
ttgttttcgt cggatcgca gtctcttacg gtctcttcag ccgcaggaac tacgacggag      300
gaggaggtgg aggaacaagc aatagtgatc acaacaaagc tgatcatagt aataataatt      360
cgcattcata tgtgcctaag attcttgaag tatcctctgt ttttaacgtg ggtcacgaga      420
gtgaatctga accgtccgat gattcctccg gtgatcaacg taagtttcag acatggaaga      480
acaagtacca catgaaaatc cccgaggttg agactcgttt cgttgatcga gttagttcag      540
aaaacagaga gaagcctctg cttttgccgg ttcggagcct gaattattct cgtgtttctg      600
attcttcggg cgataattcc ggtcgatggg agaaagttag atctaagaga gaacttctga      660
agactcttgg cgatgataat agtgatgtgc ttccttctcc gattccatgg aggtcaagat      720
catcttcata atcatcatca tcatcaaagg aggttgaatc tctaccgtcc gttaagaatc      780
tgactacagt tgaatcacag ccgttgatca agaactctgac accatcttct tctttctctt      840
ctccaagaaa gtggaatcct atacctaatc tcgcatctga gttccatcca tctccgccac      900
cgctcctctc gccgcgcgca ccactaccgg cgttttataa ctctcgtcg agaaaagatc      960
atcccgaat ttacagggtt gagaggagag aatcatcagt tcacaagacg aaatttgtag      1020
gaggtgagtt tcatcctccg ccgcctcctc ctccaccacc tccggtggag tattataagt      1080
cacctccgac aaaattcaga ctaagtaacg aacggagaaa gtcctcggag caaaagatgw      1140
aaagaaacgc tcctaaaaag gtttggtggt ccgatccaat cgtggaatcg aaggaacaag      1200
acacagagaa gaatgatcaa agaagtaact tgggaagcaa ggcagtggaa gaatccgaga      1260
atggagaaca gagaagagga gaaaatgaaa tccacgacga ggttgagaag aagatagtag      1320
aggaagaagg agttagttag atcaacaatg gaagtgcagt ggacaagaag gcagatgagt      1380
tcattgcaaa gttcagagaa cagattaggt tacaagaatc cgagtctatc aagagatcta      1440
ctaataagat ctctgcaaat tcttcgaggt agaactcatt atttattaat aataggtata      1500
cattttaagt atgttttggt aatcatcata aggttgtaat attaagggga acaaatattt      1560
ttgttacatt tattcagcca caaaaacagg attggag
```

(2) INFORMATION FOR SEQ ID NO:1350:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 473 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..473
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500089

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1350:

```
Met Val Glu Ala Arg Ser Leu Lys Lys Pro Ile Gln Leu Gly Asn Lys
1          5          10          15
Glu Asp Gln Asn Pro Arg Lys Phe Tyr Ser Arg Phe Ile Phe Lys Ala
20          25          30
Leu Ile Leu Thr Val Leu Cys Ala Val Val Pro Val Phe Leu Ser Gln
35          40          45
Thr Pro Glu Leu Ala Asn Gln Thr Arg Leu Leu Glu Leu Leu His Leu
50          55          60
Val Phe Val Gly Ile Ala Val Ser Tyr Gly Leu Phe Ser Arg Arg Asn
```

65					70					75					80
Tyr	Asp	Gly	Gly	Gly	Gly	Gly	Gly	Thr	Ser	Asn	Ser	Asp	His	Asn	Lys
				85					90					95	
Ala	Asp	His	Ser	Asn	Asn	Asn	Ser	His	Ser	Tyr	Val	Pro	Lys	Ile	Leu
			100					105					110		
Glu	Val	Ser	Ser	Val	Phe	Asn	Val	Gly	His	Glu	Ser	Glu	Ser	Glu	Pro
		115					120					125			
Ser	Asp	Asp	Ser	Ser	Gly	Asp	Gln	Arg	Lys	Phe	Gln	Thr	Trp	Lys	Asn
	130					135					140				
Lys	Tyr	His	Met	Lys	Ile	Pro	Glu	Val	Glu	Thr	Arg	Phe	Val	Asp	Arg
145					150					155					160
Val	Ser	Ser	Glu	Asn	Arg	Glu	Lys	Pro	Leu	Leu	Leu	Pro	Val	Arg	Ser
				165					170					175	
Leu	Asn	Tyr	Ser	Arg	Val	Ser	Asp	Ser	Ser	Gly	Asp	Asn	Ser	Gly	Arg
			180					185					190		
Trp	Glu	Lys	Val	Arg	Ser	Lys	Arg	Glu	Leu	Leu	Lys	Thr	Leu	Gly	Asp
		195					200					205			
Asp	Asn	Ser	Asp	Val	Leu	Pro	Ser	Pro	Ile	Pro	Trp	Arg	Ser	Arg	Ser
	210					215					220				
Ser	Ser	Ser	Ser	Ser	Ser	Ser	Ser	Lys	Glu	Val	Glu	Ser	Leu	Pro	Ser
225					230					235					240
Val	Lys	Asn	Leu	Thr	Thr	Val	Glu	Ser	Gln	Pro	Leu	Ile	Lys	Asn	Leu
				245					250					255	
Thr	Pro	Ser	Ser	Ser	Phe	Ser	Ser	Pro	Arg	Lys	Ser	Asn	Pro	Ile	Pro
			260				265						270		
Asn	Leu	Ala	Ser	Glu	Phe	His	Pro	Ser	Pro	Pro	Pro	Pro	Pro	Pro	Pro
	275						280					285			
Pro	Pro	Pro	Leu	Pro	Ala	Phe	Tyr	Asn	Ser	Ser	Ser	Arg	Lys	Asp	His
	290					295					300				
Pro	Gly	Ile	Tyr	Arg	Val	Glu	Arg	Arg	Glu	Ser	Ser	Val	His	Lys	Thr
305					310				315						320
Lys	Phe	Ala	Gly	Gly	Glu	Phe	His	Pro	Pro	Pro	Pro	Pro	Pro	Pro	Pro
			325						330					335	
Pro	Pro	Val	Glu	Tyr	Tyr	Lys	Ser	Pro	Pro	Thr	Lys	Phe	Arg	Leu	Ser
		340						345					350		
Asn	Glu	Arg	Arg	Lys	Ser	Ser	Glu	Gln	Lys	Met	Xaa	Arg	Asn	Ala	Pro
		355					360					365			
Lys	Lys	Val	Trp	Trp	Ser	Asp	Pro	Ile	Val	Glu	Ser	Lys	Glu	Gln	Asp
	370					375					380				
Thr	Glu	Lys	Asn	Asp	Gln	Arg	Ser	Asn	Leu	Gly	Ser	Lys	Ala	Val	Glu
385					390					395					400
Glu	Ser	Glu	Asn	Gly	Glu	Gln	Arg	Arg	Gly	Glu	Asn	Glu	Ile	His	Asp
			405						410					415	
Glu	Val	Glu	Lys	Lys	Ile	Val	Glu	Glu	Glu	Gly	Val	Ser	Glu	Ile	Asn
			420					425					430		
Asn	Gly	Ser	Asp	Val	Asp	Lys	Lys	Ala	Asp	Glu	Phe	Ile	Ala	Lys	Phe
	435						440					445			
Arg	Glu	Gln	Ile	Arg	Leu	Gln	Arg	Ile	Glu	Ser	Ile	Lys	Arg	Ser	Thr
	450					455					460				
Asn	Lys	Ile	Ser	Ala	Asn	Ser	Ser	Arg							
465					470										

(2) INFORMATION FOR SEQ ID NO:1351:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 326 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..326

(D) OTHER INFORMATION: / Ceres Seq. ID 1500090

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1351:

Met	Lys	Ile	Pro	Glu	Val	Glu	Thr	Arg	Phe	Val	Asp	Arg	Val	Ser	Ser
1				5					10					15	
Glu	Asn	Arg	Glu	Lys	Pro	Leu	Leu	Leu	Pro	Val	Arg	Ser	Leu	Asn	Tyr
			20					25					30		
Ser	Arg	Val	Ser	Asp	Ser	Ser	Gly	Asp	Asn	Ser	Gly	Arg	Trp	Glu	Lys
	35						40					45			
Val	Arg	Ser	Lys	Arg	Glu	Leu	Leu	Lys	Thr	Leu	Gly	Asp	Asp	Asn	Ser
	50					55					60				
Asp	Val	Leu	Pro	Ser	Pro	Ile	Pro	Trp	Arg	Ser	Arg	Ser	Ser	Ser	Ser
65					70					75				80	
Ser	Ser	Ser	Ser	Ser	Lys	Glu	Val	Glu	Ser	Leu	Pro	Ser	Val	Lys	Asn
				85					90					95	
Leu	Thr	Thr	Val	Glu	Ser	Gln	Pro	Leu	Ile	Lys	Asn	Leu	Thr	Pro	Ser
			100					105					110		
Ser	Ser	Phe	Ser	Ser	Pro	Arg	Lys	Ser	Asn	Pro	Ile	Pro	Asn	Leu	Ala
		115					120						125		
Ser	Glu	Phe	His	Pro	Ser	Pro	Pro	Pro	Pro	Pro	Pro	Pro	Pro	Pro	Pro
	130					135						140			
Leu	Pro	Ala	Phe	Tyr	Asn	Ser	Ser	Ser	Arg	Lys	Asp	His	Pro	Gly	Ile
145					150					155					160
Tyr	Arg	Val	Glu	Arg	Glu	Ser	Ser	Val	His	Lys	Thr	Lys	Phe	Ala	
			165					170					175		
Gly	Gly	Glu	Phe	His	Pro	Pro	Pro	Pro	Pro	Pro	Pro	Pro	Pro	Pro	Val
			180					185					190		
Glu	Tyr	Tyr	Lys	Ser	Pro	Pro	Thr	Lys	Phe	Arg	Leu	Ser	Asn	Glu	Arg
	195						200					205			
Arg	Lys	Ser	Ser	Glu	Gln	Lys	Met	Xaa	Arg	Asn	Ala	Pro	Lys	Lys	Val
	210					215					220				
Trp	Trp	Ser	Asp	Pro	Ile	Val	Glu	Ser	Lys	Glu	Gln	Asp	Thr	Glu	Lys
225					230					235				240	
Asn	Asp	Gln	Arg	Ser	Asn	Leu	Gly	Ser	Lys	Ala	Val	Glu	Glu	Ser	Glu
				245					250					255	
Asn	Gly	Glu	Gln	Arg	Arg	Gly	Glu	Asn	Glu	Ile	His	Asp	Glu	Val	Glu
			260					265					270		
Lys	Lys	Ile	Val	Glu	Glu	Glu	Gly	Val	Ser	Glu	Ile	Asn	Asn	Gly	Ser
		275					280					285			
Asp	Val	Asp	Lys	Lys	Ala	Asp	Glu	Phe	Ile	Ala	Lys	Phe	Arg	Glu	Gln
	290					295					300				
Ile	Arg	Leu	Gln	Arg	Ile	Glu	Ser	Ile	Lys	Arg	Ser	Thr	Asn	Lys	Ile
305					310					315					320
Ser	Ala	Asn	Ser	Ser	Arg										
				325											

(2) INFORMATION FOR SEQ ID NO:1352:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 798 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..798

(D) OTHER INFORMATION: / Ceres Seq. ID 1500091

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1352:

ttgtcaaaag	ctgattcttc	gccttatggc	atcgattttg	caccttcgaa	cggccaaccc	60
acgggaagat	tcactaatgg	tcgaaccatt	tcgatattg	tgggtgaagc	cttaggagca	120
aaatcaccac	caccaccata	tcttgaacca	aacactgagg	ctaacacaat	tctcaatgga	180
atcaactatg	cttctggtgc	tgctggaatc	ttggacgaca	ctggacttct	ggttcacg	240
ggcgagtcc	gctgagagaa	caagttagta	attttgagaa	gagtagagaa	tatatggtaa	300

```
gcgtgattgg tgaatatggg acaaaagaga tgttgaagaa tgcaatgttc acaatcacaa 360
ttggatcaaa tgatatattg aattatattc aaccatcaat acctttcttc tctcaagaca 420
agctcccccac tgaatgtcct acaagattcc atggctcctc attttaacca cacatcttaa 480
gcgattgcat cagctaggag gtaggaagtt cgtgggtgggt ggagtagggc cactcggttg 540
catacccttt gctcgagcgt tgaattttwat accagccgga aaatgctccg aacaagtcaa 600
ccaagtagtc cgagggtata acatgaagct tatacactct ctttaagacat tgaacaatga 660
gttaagatcc gaagattaca aactacatt tgtctacgcc aactcttacg acctattctt 720
gaaactagtt ttgaactatc aactatttgg cttgaagaac gcagacaagc cgtgttgtgg 780
cggctacttt ccaccgtt
```

(2) INFORMATION FOR SEQ ID NO:1353:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 84 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..84
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500092

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1353:

```
Leu Ser Lys Ala Asp Ser Ser Pro Tyr Gly Ile Asp Phe Ala Pro Ser
1          5          10          15
Asn Gly Gln Pro Thr Gly Arg Phe Thr Asn Gly Arg Thr Ile Ser Asp
20          25          30
Ile Val Gly Glu Ala Leu Gly Ala Lys Ser Pro Pro Pro Pro Tyr Leu
35          40          45
Glu Pro Asn Thr Glu Ala Asn Thr Ile Leu Asn Gly Ile Asn Tyr Ala
50          55          60
Ser Gly Ala Ala Gly Ile Leu Asp Asp Thr Gly Leu Leu Val His Arg
65          70          75          80
Gly Glu Phe Arg
```

(2) INFORMATION FOR SEQ ID NO:1354:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 121 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..121
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500093

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1354:

```
Met Ser Tyr Lys Ile Pro Trp Ser Ser Ile Leu Thr Thr His Leu Lys
1          5          10          15
Arg Leu His Gln Leu Gly Gly Arg Lys Phe Val Val Val Gly Val Gly
20          25          30
Pro Leu Gly Cys Ile Pro Phe Ala Arg Ala Leu Asn Xaa Ile Pro Ala
35          40          45
Gly Lys Cys Ser Glu Gln Val Asn Gln Val Val Arg Gly Tyr Asn Met
50          55          60
Lys Leu Ile His Ser Leu Lys Thr Leu Asn Asn Glu Leu Arg Ser Glu
65          70          75          80
Asp Tyr Asn Thr Thr Phe Val Tyr Ala Asn Ser Tyr Asp Leu Phe Leu
85          90          95
Lys Leu Val Leu Asn Tyr Gln Leu Phe Gly Leu Lys Asn Ala Asp Lys
100          105          110
Pro Cys Cys Gly Gly Tyr Phe Pro Pro
115          120
```

(2) INFORMATION FOR SEQ ID NO:1355:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1474 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1474
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500097

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1355:

```
agttggagct cgaaaccctt cttcatcttc ttcttctcct ccacctaacc aatgggagca      60
attgatctct ctttctcaca gagtcttctc ttctcttcgt cgcgttccaa tctttcctcc      120
tccacacacc gttccgtctc ttttttgccg ccgggaagca agtcacggtg tctgccgccg      180
ttgcgttcaa tgagtcacga cgacgacacg gcctcaaagg aggtgaagct atgggggtgga      240
aggttcgaag agagtgtcac tgagaaagtg gagaagttca ctgagtcaat ttcatttgat      300
aaggttctct acaagcagga cattatgggt agcaaagctc atgcttcaat gcttgctcac      360
caggggctaa taactgatag cgataaagat agcattttga gaggtcttga tgatattgag      420
agacaaattg aagcaaataa gtttgaatgg aggactgacg gagaagatgt gcatatgaac      480
attgaagcag ctcttactga tcttattggt gaacctgcaa agaaacttca tactgcaagg      540
agcagaaatg accaagttgc tactgacttc aggccttggg gtcgtgatgc tatcgataca      600
attattgtca aaatcagaaa tcttcagaga gcacttggtg aactggcttt gaagaatgag      660
gctttgattg ttcttggtta tactcatctt caaagagctc agcctgtttt actcccacac      720
gttctcttaa cttttgtaga gcagctcgaa cgtgatgctg gtcgttatgt ggactgtcga      780
gcaaggctaa atttctcccc cctgggagct tgtgctttgg ctggaactgg tctgcctatt      840
gatagggtta tgactgcaaa tgctcttgga tttaccgaac caatgagaaa cagtatcgat      900
gcagtctcag accgagactt cgtgctggag ttcttatata caaatgccaa caccggtatt      960
catttatcac ggcttgagga agagtgggta ctgtgggctt ccgaggagtt tgggttcatg     1020
actccaagtg attctgtgtc aaccggaagt agtataatgc cacagaagaa aaatccagac     1080
ccaatggaac ttgtcagagg aaaaaccgca agagtcatag gcgatctggt cactgtctta     1140
acactgtgca aaggacttcc ccttgcttac aacagagatt ttcaagaaga caaagagccg     1200
atgttcgata gtaccaagac aataatggga atgatcgatg tatctgcaga atttgctcag     1260
aatgttacat tcaacgaaga cagaatcaag aaaagctctc ccgcaggaca tcttgatgcg     1320
actactctcg ctgattatct tgtgaagaag gggatgcctt ttaggtcatc tcatgacata     1380
gttgaaaaac tagttggagt ttgcgtctca aaaggctgtg aacttcagaa cttaagtctt     1440
gaagagatga aaaagctgag ccctgtgttt gaag
```

(2) INFORMATION FOR SEQ ID NO:1356:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 474 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..474
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500098

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1356:

```
Met Gly Ala Ile Asp Leu Ser Phe Ser Gln Ser Leu Leu Phe Ser Ser
1           5           10           15
Ser Arg Ser Asn Leu Ser Ser Ser Thr His Arg Ser Val Ser Phe Leu
20          25          30
Pro Pro Gly Ser Lys Ser Arg Cys Leu Pro Pro Leu Arg Ser Met Ser
35          40          45
His Asp Asp Asp Thr Ala Ser Lys Glu Val Lys Leu Trp Gly Gly Arg
50          55          60
Phe Glu Glu Ser Val Thr Glu Lys Val Glu Lys Phe Thr Glu Ser Ile
65          70          75          80
Ser Phe Asp Lys Val Leu Tyr Lys Gln Asp Ile Met Gly Ser Lys Ala
85          90          95
```

His Ala Ser Met Leu Ala His Gln Gly Leu Ile Thr Asp Ser Asp Lys
100 105 110
Asp Ser Ile Leu Arg Gly Leu Asp Asp Ile Glu Arg Gln Ile Glu Ala
115 120 125
Asn Lys Phe Glu Trp Arg Thr Asp Arg Glu Asp Val His Met Asn Ile
130 135 140
Glu Ala Ala Leu Thr Asp Leu Ile Gly Glu Pro Ala Lys Lys Leu His
145 150 155 160
Thr Ala Arg Ser Arg Asn Asp Gln Val Ala Thr Asp Phe Arg Leu Trp
165 170 175
Cys Arg Asp Ala Ile Asp Thr Ile Ile Val Lys Ile Arg Asn Leu Gln
180 185 190
Arg Ala Leu Val Glu Leu Ala Leu Lys Asn Glu Ala Leu Ile Val Pro
195 200 205
Gly Tyr Thr His Leu Gln Arg Ala Gln Pro Val Leu Leu Pro His Val
210 215 220
Leu Leu Thr Phe Val Glu Gln Leu Glu Arg Asp Ala Gly Arg Tyr Val
225 230 235 240
Asp Cys Arg Ala Arg Leu Asn Phe Ser Pro Leu Gly Ala Cys Ala Leu
245 250 255
Ala Gly Thr Gly Leu Pro Ile Asp Arg Phe Met Thr Ala Asn Ala Leu
260 265 270
Gly Phe Thr Glu Pro Met Arg Asn Ser Ile Asp Ala Val Ser Asp Arg
275 280 285
Asp Phe Val Leu Glu Phe Leu Tyr Thr Asn Ala Asn Thr Gly Ile His
290 295 300
Leu Ser Arg Leu Gly Glu Trp Val Leu Trp Ala Ser Glu Glu Phe
305 310 315 320
Gly Phe Met Thr Pro Ser Asp Ser Val Ser Thr Gly Ser Ser Ile Met
325 330 335
Pro Gln Lys Lys Asn Pro Asp Pro Met Glu Leu Val Arg Gly Lys Ser
340 345 350
Ala Arg Val Ile Gly Asp Leu Val Thr Val Leu Thr Leu Cys Lys Gly
355 360 365
Leu Pro Leu Ala Tyr Asn Arg Asp Phe Gln Glu Asp Lys Glu Pro Met
370 375 380
Phe Asp Ser Thr Lys Thr Ile Met Gly Met Ile Asp Val Ser Ala Glu
385 390 395 400
Phe Ala Gln Asn Val Thr Phe Asn Glu Asp Arg Ile Lys Lys Ser Leu
405 410 415
Pro Ala Gly His Leu Asp Ala Thr Thr Leu Ala Asp Tyr Leu Val Lys
420 425 430
Lys Gly Met Pro Phe Arg Ser Ser His Asp Ile Val Gly Lys Leu Val
435 440 445
Gly Val Cys Val Ser Lys Gly Cys Glu Leu Gln Asn Leu Ser Leu Glu
450 455 460
Glu Met Lys Lys Leu Ser Pro Val Phe Glu
465 470

(2) INFORMATION FOR SEQ ID NO:1357:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 428 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..428
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500099

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1357:

Met Ser His Asp Asp Asp Thr Ala Ser Lys Glu Val Lys Leu Trp Gly

1				5					10					15		
Gly	Arg	Phe	Glu	Glu	Ser	Val	Thr	Glu	Lys	Val	Glu	Lys	Phe	Thr	Glu	
			20					25					30			
Ser	Ile	Ser	Phe	Asp	Lys	Val	Leu	Tyr	Lys	Gln	Asp	Ile	Met	Gly	Ser	
		35					40					45				
Lys	Ala	His	Ala	Ser	Met	Leu	Ala	His	Gln	Gly	Leu	Ile	Thr	Asp	Ser	
	50					55					60					
Asp	Lys	Asp	Ser	Ile	Leu	Arg	Gly	Leu	Asp	Asp	Ile	Glu	Arg	Gln	Ile	
65					70					75					80	
Glu	Ala	Asn	Lys	Phe	Glu	Trp	Arg	Thr	Asp	Arg	Glu	Asp	Val	His	Met	
				85					90					95		
Asn	Ile	Glu	Ala	Ala	Leu	Thr	Asp	Leu	Ile	Gly	Glu	Pro	Ala	Lys	Lys	
			100					105					110			
Leu	His	Thr	Ala	Arg	Ser	Arg	Asn	Asp	Gln	Val	Ala	Thr	Asp	Phe	Arg	
	115						120						125			
Leu	Trp	Cys	Arg	Asp	Ala	Ile	Asp	Thr	Ile	Ile	Val	Lys	Ile	Arg	Asn	
	130					135					140					
Leu	Gln	Arg	Ala	Leu	Val	Glu	Leu	Ala	Leu	Lys	Asn	Glu	Ala	Leu	Ile	
145					150					155					160	
Val	Pro	Gly	Tyr	Thr	His	Leu	Gln	Arg	Ala	Gln	Pro	Val	Leu	Leu	Pro	
				165					170					175		
His	Val	Leu	Leu	Thr	Phe	Val	Glu	Gln	Leu	Glu	Arg	Asp	Ala	Gly	Arg	
			180					185					190			
Tyr	Val	Asp	Cys	Arg	Ala	Arg	Leu	Asn	Phe	Ser	Pro	Leu	Gly	Ala	Cys	
	195						200					205				
Ala	Leu	Ala	Gly	Thr	Gly	Leu	Pro	Ile	Asp	Arg	Phe	Met	Thr	Ala	Asn	
	210					215					220					
Ala	Leu	Gly	Phe	Thr	Glu	Pro	Met	Arg	Asn	Ser	Ile	Asp	Ala	Val	Ser	
225					230					235					240	
Asp	Arg	Asp	Phe	Val	Leu	Glu	Phe	Leu	Tyr	Thr	Asn	Ala	Asn	Thr	Gly	
				245					250					255		
Ile	His	Leu	Ser	Arg	Leu	Gly	Glu	Glu	Trp	Val	Leu	Trp	Ala	Ser	Glu	
		260						265					270			
Glu	Phe	Gly	Phe	Met	Thr	Pro	Ser	Asp	Ser	Val	Ser	Thr	Gly	Ser	Ser	
	275						280					285				
Ile	Met	Pro	Gln	Lys	Lys	Asn	Pro	Asp	Pro	Met	Glu	Leu	Val	Arg	Gly	
	290					295					300					
Lys	Ser	Ala	Arg	Val	Ile	Gly	Asp	Leu	Val	Thr	Val	Leu	Thr	Leu	Cys	
305					310					315					320	
Lys	Gly	Leu	Pro	Leu	Ala	Tyr	Asn	Arg	Asp	Phe	Gln	Glu	Asp	Lys	Glu	
				325					330					335		
Pro	Met	Phe	Asp	Ser	Thr	Lys	Thr	Ile	Met	Gly	Met	Ile	Asp	Val	Ser	
			340					345				350				
Ala	Glu	Phe	Ala	Gln	Asn	Val	Thr	Phe	Asn	Glu	Asp	Arg	Ile	Lys	Lys	
	355						360					365				
Ser	Leu	Pro	Ala	Gly	His	Leu	Asp	Ala	Thr	Thr	Leu	Ala	Asp	Tyr	Leu	
	370					375					380					
Val	Lys	Lys	Gly	Met	Pro	Phe	Arg	Ser	Ser	His	Asp	Ile	Val	Gly	Lys	
385					390					395					400	
Leu	Val	Gly	Val	Cys	Val	Ser	Lys	Gly	Cys	Glu	Leu	Gln	Asn	Leu	Ser	
				405					410					415		
Leu	Glu	Glu	Met	Lys	Lys	Leu	Ser	Pro	Val	Phe	Glu					
			420					425								

(2) INFORMATION FOR SEQ ID NO:1358:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 383 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..383

(D) OTHER INFORMATION: / Ceres Seq. ID 1500100

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1358:

Met	Gly	Ser	Lys	Ala	His	Ala	Ser	Met	Leu	Ala	His	Gln	Gly	Leu	Ile
1			5					10						15	
Thr	Asp	Ser	Asp	Lys	Asp	Ser	Ile	Leu	Arg	Gly	Leu	Asp	Asp	Ile	Glu
			20					25					30		
Arg	Gln	Ile	Glu	Ala	Asn	Lys	Phe	Glu	Trp	Arg	Thr	Asp	Arg	Glu	Asp
		35					40					45			
Val	His	Met	Asn	Ile	Glu	Ala	Ala	Leu	Thr	Asp	Leu	Ile	Gly	Glu	Pro
	50					55				60					
Ala	Lys	Lys	Leu	His	Thr	Ala	Arg	Ser	Arg	Asn	Asp	Gln	Val	Ala	Thr
65					70					75					80
Asp	Phe	Arg	Leu	Trp	Cys	Arg	Asp	Ala	Ile	Asp	Thr	Ile	Ile	Val	Lys
			85						90					95	
Ile	Arg	Asn	Leu	Gln	Arg	Ala	Leu	Val	Glu	Leu	Ala	Leu	Lys	Asn	Glu
			100					105					110		
Ala	Leu	Ile	Val	Pro	Gly	Tyr	Thr	His	Leu	Gln	Arg	Ala	Gln	Pro	Val
	115					120						125			
Leu	Leu	Pro	His	Val	Leu	Leu	Thr	Phe	Val	Glu	Gln	Leu	Glu	Arg	Asp
	130					135					140				
Ala	Gly	Arg	Tyr	Val	Asp	Cys	Arg	Ala	Arg	Leu	Asn	Phe	Ser	Pro	Leu
145					150					155					160
Gly	Ala	Cys	Ala	Leu	Ala	Gly	Thr	Gly	Leu	Pro	Ile	Asp	Arg	Phe	Met
			165						170					175	
Thr	Ala	Asn	Ala	Leu	Gly	Phe	Thr	Glu	Pro	Met	Arg	Asn	Ser	Ile	Asp
		180						185						190	
Ala	Val	Ser	Asp	Arg	Asp	Phe	Val	Leu	Glu	Phe	Leu	Tyr	Thr	Asn	Ala
		195					200					205			
Asn	Thr	Gly	Ile	His	Leu	Ser	Arg	Leu	Gly	Glu	Glu	Trp	Val	Leu	Trp
	210					215						220			
Ala	Ser	Glu	Glu	Phe	Gly	Phe	Met	Thr	Pro	Ser	Asp	Ser	Val	Ser	Thr
225					230					235					240
Gly	Ser	Ser	Ile	Met	Pro	Gln	Lys	Lys	Asn	Pro	Asp	Pro	Met	Glu	Leu
			245						250					255	
Val	Arg	Gly	Lys	Ser	Ala	Arg	Val	Ile	Gly	Asp	Leu	Val	Thr	Val	Leu
		260						265					270		
Thr	Leu	Cys	Lys	Gly	Leu	Pro	Leu	Ala	Tyr	Asn	Arg	Asp	Phe	Gln	Glu
	275						280					285			
Asp	Lys	Glu	Pro	Met	Phe	Asp	Ser	Thr	Lys	Thr	Ile	Met	Gly	Met	Ile
	290					295					300				
Asp	Val	Ser	Ala	Glu	Phe	Ala	Gln	Asn	Val	Thr	Phe	Asn	Glu	Asp	Arg
305					310					315					320
Ile	Lys	Lys	Ser	Leu	Pro	Ala	Gly	His	Leu	Asp	Ala	Thr	Thr	Leu	Ala
			325						330					335	
Asp	Tyr	Leu	Val	Lys	Lys	Gly	Met	Pro	Phe	Arg	Ser	Ser	His	Asp	Ile
		340					345						350		
Val	Gly	Lys	Leu	Val	Gly	Val	Cys	Val	Ser	Lys	Gly	Cys	Glu	Leu	Gln
	355					360						365			
Asn	Leu	Ser	Leu	Glu	Glu	Met	Lys	Lys	Leu	Ser	Pro	Val	Phe	Glu	
	370					375					380				

(2) INFORMATION FOR SEQ ID NO:1359:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 904 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..904

(D) OTHER INFORMATION: / Ceres Seq. ID 1500101

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1359:

actcttactc	tgttctcgct	acagaatctc	ctgggaaaaa	aaaaagaaac	ttgatccacc	60
cgaattcccc	aaatcttcac	aatttctgga	aactctctcg	atcgtgaagc	agaaaagtga	120
ggttccaaat	gggttctggt	tcgggtcaaa	cccgaattac	aacgatgaac	ctctcgctct	180
caacagcaga	gaagaacctt	aatttctgct	cggcgcttct	caattctaag	aacgcaattt	240
cagatacttt	aggggtctct	tccaaatgca	gtacattcct	caggggtcaa	tttcaaagaa	300
tacatttttc	ttggctacaa	cacactcgac	ctttgagaaa	acgaacagta	tttggtcacg	360
tgagctgcgt	catgccgtta	acggaagaga	atgtggagag	agtgttagac	gaagtacgac	420
catctctaata	ggccgacgga	ggaaacgtgg	cgttgcacga	aatcgacgga	cttgtggtgg	480
ttttaagct	acaaggagct	tgtggttcgt	gtcctagctc	atcaatgacg	ttgaagatgg	540
gaatcgagag	tcgtcttcga	gacaagattc	cagagatcat	gtccgttgag	cagtttcttg	600
aatccgagac	aggaggttta	gagctgaacg	atgagaacat	tgagaagggt	ctctctgagt	660
taaggccgta	cctatccggt	actggagggtg	gggggcttga	gttagttgag	attgatgggt	720
acgtgggtcaa	ggttcgactc	actggaccag	ctgctggagt	catgactgtt	cgtgtcgcgt	780
tgactcaaaa	actgagggaa	acaattcctt	ctataggtgc	agtccagctt	ctagagtgc	840
attaaccttt	ttattttgta	acttatatac	aaggcctatt	tttgattcaa	tatattttat	900
ttcc						

(2) INFORMATION FOR SEQ ID NO:1360:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 236 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..236

(D) OTHER INFORMATION: / Ceres Seq. ID 1500102

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1360:

Met	Gly	Ser	Val	Ser	Gly	Gln	Thr	Arg	Ile	Thr	Thr	Met	Asn	Leu	Ser
1				5					10					15	
Leu	Ser	Thr	Ala	Glu	Lys	Asn	Pro	Asn	Phe	Cys	Ser	Ala	Leu	Leu	Asn
			20					25					30		
Ser	Lys	Asn	Ala	Ile	Ser	Asp	Thr	Leu	Gly	Val	Ser	Ser	Lys	Cys	Ser
		35					40					45			
Thr	Phe	Leu	Arg	Gly	Gln	Phe	Gln	Arg	Ile	His	Phe	Ser	Trp	Leu	Gln
		50				55					60				
His	Thr	Arg	Pro	Leu	Arg	Lys	Arg	Thr	Val	Phe	Gly	His	Val	Ser	Cys
65					70					75				80	
Val	Met	Pro	Leu	Thr	Glu	Glu	Asn	Val	Glu	Arg	Val	Leu	Asp	Glu	Val
			85						90					95	
Arg	Pro	Ser	Leu	Met	Ala	Asp	Gly	Gly	Asn	Val	Ala	Leu	His	Glu	Ile
			100					105					110		
Asp	Gly	Leu	Val	Val	Val	Leu	Lys	Leu	Gln	Gly	Ala	Cys	Gly	Ser	Cys
		115					120					125			
Pro	Ser	Ser	Ser	Met	Thr	Leu	Lys	Met	Gly	Ile	Glu	Ser	Arg	Leu	Arg
		130				135					140				
Asp	Lys	Ile	Pro	Glu	Ile	Met	Ser	Val	Glu	Gln	Phe	Leu	Glu	Ser	Glu
145					150					155					160
Thr	Gly	Gly	Leu	Glu	Leu	Asn	Asp	Glu	Asn	Ile	Glu	Lys	Val	Leu	Ser
			165						170					175	
Glu	Leu	Arg	Pro	Tyr	Leu	Ser	Gly	Thr	Gly	Gly	Gly	Gly	Leu	Glu	Leu
			180					185						190	
Val	Glu	Ile	Asp	Gly	Tyr	Val	Val	Lys	Val	Arg	Leu	Thr	Gly	Pro	Ala
		195					200					205			
Ala	Gly	Val	Met	Thr	Val	Arg	Val	Ala	Leu	Thr	Gln	Lys	Leu	Arg	Glu
		210				215						220			
Thr	Ile	Pro	Ser	Ile	Gly	Ala	Val	Gln	Leu	Leu	Glu				
225						230					235				

(2) INFORMATION FOR SEQ ID NO:1361:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 224 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..224

(D) OTHER INFORMATION: / Ceres Seq. ID 1500103

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1361:

Met	Asn	Leu	Ser	Leu	Ser	Thr	Ala	Glu	Lys	Asn	Pro	Asn	Phe	Cys	Ser
1				5					10					15	
Ala	Leu	Leu	Asn	Ser	Lys	Asn	Ala	Ile	Ser	Asp	Thr	Leu	Gly	Val	Ser
			20					25					30		
Ser	Lys	Cys	Ser	Thr	Phe	Leu	Arg	Gly	Gln	Phe	Gln	Arg	Ile	His	Phe
		35					40					45			
Ser	Trp	Leu	Gln	His	Thr	Arg	Pro	Leu	Arg	Lys	Arg	Thr	Val	Phe	Gly
	50					55					60				
His	Val	Ser	Cys	Val	Met	Pro	Leu	Thr	Glu	Glu	Asn	Val	Glu	Arg	Val
65					70					75					80
Leu	Asp	Glu	Val	Arg	Pro	Ser	Leu	Met	Ala	Asp	Gly	Gly	Asn	Val	Ala
			85						90					95	
Leu	His	Glu	Ile	Asp	Gly	Leu	Val	Val	Val	Leu	Lys	Leu	Gln	Gly	Ala
			100					105					110		
Cys	Gly	Ser	Cys	Pro	Ser	Ser	Ser	Met	Thr	Leu	Lys	Met	Gly	Ile	Glu
		115					120					125			
Ser	Arg	Leu	Arg	Asp	Lys	Ile	Pro	Glu	Ile	Met	Ser	Val	Glu	Gln	Phe
	130					135						140			
Leu	Glu	Ser	Glu	Thr	Gly	Gly	Leu	Glu	Leu	Asn	Asp	Glu	Asn	Ile	Glu
			150							155					160
Lys	Val	Leu	Ser	Glu	Leu	Arg	Pro	Tyr	Leu	Ser	Gly	Thr	Gly	Gly	Gly
			165						170					175	
Gly	Leu	Glu	Leu	Val	Glu	Ile	Asp	Gly	Tyr	Val	Val	Lys	Val	Arg	Leu
		180						185					190		
Thr	Gly	Pro	Ala	Ala	Gly	Val	Met	Thr	Val	Arg	Val	Ala	Leu	Thr	Gln
		195					200					205			
Lys	Leu	Arg	Glu	Thr	Ile	Pro	Ser	Ile	Gly	Ala	Val	Gln	Leu	Leu	Glu
	210						215					220			

(2) INFORMATION FOR SEQ ID NO:1362:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 155 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..155

(D) OTHER INFORMATION: / Ceres Seq. ID 1500104

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1362:

Met	Pro	Leu	Thr	Glu	Glu	Asn	Val	Glu	Arg	Val	Leu	Asp	Glu	Val	Arg
1				5					10					15	
Pro	Ser	Leu	Met	Ala	Asp	Gly	Gly	Asn	Val	Ala	Leu	His	Glu	Ile	Asp
			20					25					30		
Gly	Leu	Val	Val	Val	Leu	Lys	Leu	Gln	Gly	Ala	Cys	Gly	Ser	Cys	Pro
		35					40					45			
Ser	Ser	Ser	Met	Thr	Leu	Lys	Met	Gly	Ile	Glu	Ser	Arg	Leu	Arg	Asp

```

      50              55              60
Lys Ile Pro Glu Ile Met Ser Val Glu Gln Phe Leu Glu Ser Glu Thr
65
Gly Gly Leu Glu Leu Asn Asp Glu Asn Ile Glu Lys Val Leu Ser Glu
      70              80
      85              90              95
Leu Arg Pro Tyr Leu Ser Gly Thr Gly Gly Gly Gly Leu Glu Leu Val
      100              105              110
Glu Ile Asp Gly Tyr Val Val Lys Val Arg Leu Thr Gly Pro Ala Ala
      115              120              125
Gly Val Met Thr Val Arg Val Ala Leu Thr Gln Lys Leu Arg Glu Thr
      130              135              140
Ile Pro Ser Ile Gly Ala Val Gln Leu Leu Glu
145              150              155
```

(2) INFORMATION FOR SEQ ID NO:1363:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1640 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1640
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500105

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1363:

```

acatgggtctt gttctttctc tctccttctt ttctcatctt gcggcttccc tttctctctc      60
tattcgccaca atgattcatta ccaaccaaac tgattgaaac tcatttggtc tctctctctc      120
aaatccactc tctctctttc tttctctctc tctctctgt gtctctatcg ccatggctga      180
tgataaggag atgcctgctg ctgtagttga tggacatgat caagtcactg gtcattattat      240
ttccaccaca atcgggtggca aaaatgggtga accaaaacag acaattagtt acatggcgga      300
sgagttggtg gtacaggctc gttcgggacg gttttccaag caaaatgttt ggagactgga      360
gaaaccgtgg cgataaagaa ggttttgcaa gatagaagat acaagaaccg agaacttcag      420
ttgatgcgtg tgatggatca tccgaatgtg gtttggttga agcattgctt cttttcgact      480
acaagtaaag acgagctttt cttgaacttg gttatggagt atgtccctga gagcttgtat      540
cgagttctga aacattatag tagtgcaaac caaagaatgc ctcttgctta tgttaaactt      600
tacatgtatc agatcttccg gggacttgct tacattcaca atgttgctgg agtttgctac      660
agagatctaa agcctcaaaa tcttctggtt gatcctctta ctcattcaagt caaaatctgt      720
gactttggca gtgcgaaaca gtcgttaaaa ggtgaagcca acatttctta catctgctca      780
cgattctacc gtgcacccga gctcatattt ggtgccactg agtacacaac ttctattgat      840
atctggtctg ctggttggtg tcttgctgag cttcttcttg gtcagccatt atttcccgga      900
gaaaatgctg tggatcagct cgttgaaatt ataaaagttc ttggtacacc aactcgagaa      960
gaaatccggt gtatgaatcc acattacaca gatttcaggt ttccacagat aaaggcacat      1020
ccctggcaca agatcttcca caaaaggatg cccccagaag cgattgattt tgcattcaagg      1080
ctgcttcaat actctccaag tctaagatgc acagcgctcg aagcttggtc acatccgttc      1140
tttgatgaac tcagagaagc whmccaaacg ctcgtttmcc aaatggacgg cctttcccgc      1200
ctctcttcaa cttcaaacaa gaagtagctg gatcatcacc tgaactggtc aacaagttga      1260
ttccagacca tatcaagaga caattgggtc taagcttctt gaatcaatct ggaacttaaa      1320
agggatcctg caaaagacaa ctactttttt atatataatg taccattaca cgagccacaa      1380
ggtcgtagtt gaaggcaaac gtggaggaca caattcaaag tttttcctcc tcaaactcgt      1440
tcagacaaaag ccagctgcta gcaaaaccaa ctacccaaat ctgcgaaaac aaaaactctc      1500
cagtgttgta tctgcttatt tctcttctct tttcaagttt ggtgaaaaac acagtctcct      1560
ctttgcttca tttcttcttt ctttccccct tatgtaaatg agtttagtca gaagtttttt      1620
tatatagtaa agtttgggcg
```

(2) INFORMATION FOR SEQ ID NO:1364:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 267 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..267

(D) OTHER INFORMATION: / Ceres Seq. ID 1500106

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1364:

Met	Arg	Val	Met	Asp	His	Pro	Asn	Val	Val	Cys	Leu	Lys	His	Cys	Phe
1			5						10					15	
Phe	Ser	Thr	Thr	Ser	Lys	Asp	Glu	Leu	Phe	Leu	Asn	Leu	Val	Met	Glu
		20					25						30		
Tyr	Val	Pro	Glu	Ser	Leu	Tyr	Arg	Val	Leu	Lys	His	Tyr	Ser	Ser	Ala
		35				40					45				
Asn	Gln	Arg	Met	Pro	Leu	Val	Tyr	Val	Lys	Leu	Tyr	Met	Tyr	Gln	Ile
	50				55						60				
Phe	Arg	Gly	Leu	Ala	Tyr	Ile	His	Asn	Val	Ala	Gly	Val	Cys	His	Arg
65					70					75				80	
Asp	Leu	Lys	Pro	Gln	Asn	Leu	Leu	Val	Asp	Pro	Leu	Thr	His	Gln	Val
			85					90					95		
Lys	Ile	Cys	Asp	Phe	Gly	Ser	Ala	Lys	Gln	Leu	Val	Lys	Gly	Glu	Ala
		100						105					110		
Asn	Ile	Ser	Tyr	Ile	Cys	Ser	Arg	Phe	Tyr	Arg	Ala	Pro	Glu	Leu	Ile
	115					120					125				
Phe	Gly	Ala	Thr	Glu	Tyr	Thr	Thr	Ser	Ile	Asp	Ile	Trp	Ser	Ala	Gly
	130					135					140				
Cys	Val	Leu	Ala	Glu	Leu	Leu	Gly	Gln	Pro	Leu	Phe	Pro	Gly	Glu	
145				150					155					160	
Asn	Ala	Val	Asp	Gln	Leu	Val	Glu	Ile	Ile	Lys	Val	Leu	Gly	Thr	Pro
			165					170						175	
Thr	Arg	Glu	Glu	Ile	Arg	Cys	Met	Asn	Pro	His	Tyr	Thr	Asp	Phe	Arg
		180					185						190		
Phe	Pro	Gln	Ile	Lys	Ala	His	Pro	Trp	His	Lys	Ile	Phe	His	Lys	Arg
	195					200						205			
Met	Pro	Pro	Glu	Ala	Ile	Asp	Phe	Ala	Ser	Arg	Leu	Leu	Gln	Tyr	Ser
	210				215						220				
Pro	Ser	Leu	Arg	Cys	Thr	Ala	Leu	Glu	Ala	Cys	Ala	His	Pro	Phe	Phe
225				230						235				240	
Asp	Glu	Leu	Arg	Glu	Xaa	Xaa	Gln	Thr	Leu	Val	Xaa	Gln	Met	Asp	Gly
			245					250						255	
Leu	Ser	Arg	Leu	Ser	Ser	Thr	Ser	Asn	Lys	Lys					
		260					265								

(2) INFORMATION FOR SEQ ID NO:1365:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 264 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..264

(D) OTHER INFORMATION: / Ceres Seq. ID 1500107

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1365:

Met	Asp	His	Pro	Asn	Val	Val	Cys	Leu	Lys	His	Cys	Phe	Phe	Ser	Thr
1			5						10					15	
Thr	Ser	Lys	Asp	Glu	Leu	Phe	Leu	Asn	Leu	Val	Met	Glu	Tyr	Val	Pro
		20					25						30		
Glu	Ser	Leu	Tyr	Arg	Val	Leu	Lys	His	Tyr	Ser	Ser	Ala	Asn	Gln	Arg
		35				40						45			
Met	Pro	Leu	Val	Tyr	Val	Lys	Leu	Tyr	Met	Tyr	Gln	Ile	Phe	Arg	Gly
	50					55					60				
Leu	Ala	Tyr	Ile	His	Asn	Val	Ala	Gly	Val	Cys	His	Arg	Asp	Leu	Lys
65				70						75				80	
Pro	Gln	Asn	Leu	Leu	Val	Asp	Pro	Leu	Thr	His	Gln	Val	Lys	Ile	Cys

Asp	Phe	Gly	Ser	Ala	Lys	Gln	Leu	Val	Lys	Gly	Glu	Ala	Asn	Ile	Ser
			100					105					110		
Tyr	Ile	Cys	Ser	Arg	Phe	Tyr	Arg	Ala	Pro	Glu	Leu	Ile	Phe	Gly	Ala
		115					120					125			
Thr	Glu	Tyr	Thr	Thr	Ser	Ile	Asp	Ile	Trp	Ser	Ala	Gly	Cys	Val	Leu
	130					135					140				
Ala	Glu	Leu	Leu	Leu	Gly	Gln	Pro	Leu	Phe	Pro	Gly	Glu	Asn	Ala	Val
145					150					155					160
Asp	Gln	Leu	Val	Glu	Ile	Ile	Lys	Val	Leu	Gly	Thr	Pro	Thr	Arg	Glu
			165					170						175	
Glu	Ile	Arg	Cys	Met	Asn	Pro	His	Tyr	Thr	Asp	Phe	Arg	Phe	Pro	Gln
			180					185					190		
Ile	Lys	Ala	His	Pro	Trp	His	Lys	Ile	Phe	His	Lys	Arg	Met	Pro	Pro
	195					200						205			
Glu	Ala	Ile	Asp	Phe	Ala	Ser	Arg	Leu	Leu	Gln	Tyr	Ser	Pro	Ser	Leu
	210					215					220				
Arg	Cys	Thr	Ala	Leu	Glu	Ala	Cys	Ala	His	Pro	Phe	Phe	Asp	Glu	Leu
225					230					235					240
Arg	Glu	Xaa	Xaa	Gln	Thr	Leu	Val	Xaa	Gln	Met	Asp	Gly	Leu	Ser	Arg
			245					250						255	
Leu	Ser	Ser	Thr	Ser	Asn	Lys	Lys								
			260												

(2) INFORMATION FOR SEQ ID NO:1366:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 237 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..237

(D) OTHER INFORMATION: / Ceres Seq. ID 1500108

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1366:

Met	Glu	Tyr	Val	Pro	Glu	Ser	Leu	Tyr	Arg	Val	Leu	Lys	His	Tyr	Ser
1			5					10						15	
Ser	Ala	Asn	Gln	Arg	Met	Pro	Leu	Val	Tyr	Val	Lys	Leu	Tyr	Met	Tyr
		20						25				30			
Gln	Ile	Phe	Arg	Gly	Leu	Ala	Tyr	Ile	His	Asn	Val	Ala	Gly	Val	Cys
	35					40						45			
His	Arg	Asp	Leu	Lys	Pro	Gln	Asn	Leu	Leu	Val	Asp	Pro	Leu	Thr	His
	50					55					60				
Gln	Val	Lys	Ile	Cys	Asp	Phe	Gly	Ser	Ala	Lys	Gln	Leu	Val	Lys	Gly
65					70					75				80	
Glu	Ala	Asn	Ile	Ser	Tyr	Ile	Cys	Ser	Arg	Phe	Tyr	Arg	Ala	Pro	Glu
			85					90						95	
Leu	Ile	Phe	Gly	Ala	Thr	Glu	Tyr	Thr	Ser	Ile	Asp	Ile	Trp	Ser	
	100							105				110			
Ala	Gly	Cys	Val	Leu	Ala	Glu	Leu	Leu	Gly	Gln	Pro	Leu	Phe	Pro	
	115							120				125			
Gly	Glu	Asn	Ala	Val	Asp	Gln	Leu	Val	Glu	Ile	Ile	Lys	Val	Leu	Gly
	130					135						140			
Thr	Pro	Thr	Arg	Glu	Glu	Ile	Arg	Cys	Met	Asn	Pro	His	Tyr	Thr	Asp
145					150					155					160
Phe	Arg	Phe	Pro	Gln	Ile	Lys	Ala	His	Pro	Trp	His	Lys	Ile	Phe	His
			165					170						175	
Lys	Arg	Met	Pro	Pro	Glu	Ala	Ile	Asp	Phe	Ala	Ser	Arg	Leu	Leu	Gln
			180					185					190		
Tyr	Ser	Pro	Ser	Leu	Arg	Cys	Thr	Ala	Leu	Glu	Ala	Cys	Ala	His	Pro
	195						200					205			

Phe Phe Asp Glu Leu Arg Glu Xaa Xaa Gln Thr Leu Val Xaa Gln Met
210 215 220
Asp Gly Leu Ser Arg Leu Ser Ser Thr Ser Asn Lys Lys
225 230 235

(2) INFORMATION FOR SEQ ID NO:1367:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1841 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1841
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500109

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1367:

cattaggatt	ttgaatttcc	aaatacattt	tcagaaaaaa	aagaattaaa	agatcccatt	60
gttgttatcc	tcacagtaaa	tgcttttgct	tgagagagag	tctgttagag	gttttttggt	120
tgtttctgtt	tccttctgtc	accagaaaaa	ctaaaaagca	aacaaattca	agaagagaga	180
gagagagata	gcctcaaaac	caagtcctaa	ccattgttga	tagaagagaa	agcttttctt	240
ttcttggtgc	ttatggtgaa	agaatgaaag	agagagagga	ggagaagtaa	gaagcagaga	300
aagtgtttag	agcttttgcat	gttcctttct	ctccaagttt	atatcttcat	cggtttcaca	360
agttcactta	aaaagttgaa	aagagtcctt	cttcttcaac	tattgtaaat	gcgaaatgga	420
tcgaagagat	gcaatgggat	tatccgggtc	aggttcttac	tatatccata	gaggattacc	480
cgggtcgggt	cctccaacgt	ttcatggatc	accacagcaa	cagcaaggtc	ttcgtcactt	540
acctaataca	aactctccat	tcgggtcagg	ctccactggg	ttcggatctc	cttctttaca	600
cgggtgatcct	tctctggcaa	cagcagccgg	aggagccgga	gctcttcctc	atcatatcgg	660
cgtaaatatg	attgctcctc	ctccacctcc	cagtgaacct	ccgatgaaac	gaaagagagg	720
acggcctaga	aaatacgggc	aagacggctc	tgtttctttg	gctctgtcgt	cttctctgtg	780
ttcgaccatt	actccaaca	actctaacaa	acgcggccgt	ggtcgacctc	cgggctccgg	840
caagaaacag	agaatggctt	ccgttggtga	actgatgcct	tcattctctg	gaatgagctt	900
cacgccacat	gttatcgcg	tttcaatagg	agaagatatt	gcatacaagg	ttatagcttt	960
ctctcaacaa	ggtcgcgag	ccatttgctg	tttatctgca	agtgggtgcg	tctctactgc	1020
aacacttatt	caaccatcag	catctcccgg	agccattaaa	tacgagggcc	ggtttgaaat	1080
cctagcggtta	tcaacatctt	atatagtggc	aactgatgga	agcttccgta	accgaactgg	1140
aaactttatcg	gtttcgcttg	ctagcccgga	tgggcggtgtg	attggcggtg	ccattgggtg	1200
gcctttaata	gctgcaagtc	ctgttcagg	tattgtagg	agctttatat	gggcagctcc	1260
aaagatcaag	agcaagaac	gagaagaaga	agcttctgaa	gttggttcaag	aaactgatga	1320
tcaccacgtt	ctggacaata	ataacaacac	gatttcgcct	gtccctcagc	agcagccaaa	1380
ccaaaacctg	atttggtcaa	caggttcaag	gcaaatggat	atgcgtcatg	ctcatgctga	1440
tattgattta	atgcgcgggt	gatgatagcg	agaaagaact	ctgtgtatat	aaagcatgga	1500
atctaggaag	aagaagaagg	aatataagct	aacctctgaa	caaaagtatg	tggaaatggt	1560
agggaaaaag	attaactcta	ttagtgtacc	tctcatatct	ctaagcttgt	ttgggtttac	1620
tgtttctgtg	actctgaaga	tttgacaggt	tcctttcttt	ctctgtttta	gattgttcag	1680
tccttatgta	atttgcttgc	aattctgatt	ctacagctta	gattcagtac	attgtgtaga	1740
agtttacatg	ggaacctgaa	aattgggcat	ttcatgggcc	ttcatatgat	ccaatttatt	1800
ttcatcaa	attgtattag	acataattaa	ttttgttttt	t		

(2) INFORMATION FOR SEQ ID NO:1368:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 348 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..348
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500110

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1368:

Met	Asp	Arg	Arg	Asp	Ala	Met	Gly	Leu	Ser	Gly	Ser	Gly	Ser	Tyr	Tyr
1								5						10	15

Ile His Arg Gly Leu Pro Gly Ser Gly Pro Pro Thr Phe His Gly Ser
20 25 30
Pro Gln Gln Gln Gly Leu Arg His Leu Pro Asn Gln Asn Ser Pro
35 40 45
Phe Gly Ser Gly Ser Thr Gly Phe Gly Ser Pro Ser Leu His Gly Asp
50 55 60
Pro Ser Leu Ala Thr Ala Ala Gly Gly Ala Gly Ala Leu Pro His His
65 70 75 80
Ile Gly Val Asn Met Ile Ala Pro Pro Pro Pro Ser Glu Thr Pro
85 90 95
Met Lys Arg Lys Arg Gly Arg Pro Arg Lys Tyr Gly Gln Asp Gly Ser
100 105 110
Val Ser Leu Ala Leu Ser Ser Ser Ser Val Ser Thr Ile Thr Pro Asn
115 120 125
Asn Ser Asn Lys Arg Gly Arg Gly Arg Pro Pro Gly Ser Gly Lys Lys
130 135 140
Gln Arg Met Ala Ser Val Gly Glu Leu Met Pro Ser Ser Ser Gly Met
145 150 155 160
Ser Phe Thr Pro His Val Ile Ala Val Ser Ile Gly Glu Asp Ile Ala
165 170 175
Ser Lys Val Ile Ala Phe Ser Gln Gln Gly Pro Arg Ala Ile Cys Val
180 185 190
Leu Ser Ala Ser Gly Ala Val Ser Thr Ala Thr Leu Ile Gln Pro Ser
195 200 205
Ala Ser Pro Gly Ala Ile Lys Tyr Glu Gly Arg Phe Glu Ile Leu Ala
210 215 220
Leu Ser Thr Ser Tyr Ile Val Ala Thr Asp Gly Ser Phe Arg Asn Arg
225 230 235 240
Thr Gly Asn Leu Ser Val Ser Leu Ala Ser Pro Asp Gly Arg Val Ile
245 250 255
Gly Gly Ala Ile Gly Gly Pro Leu Ile Ala Ala Ser Pro Val Gln Val
260 265 270
Ile Val Gly Ser Phe Ile Trp Ala Ala Pro Lys Ile Lys Ser Lys Lys
275 280 285
Arg Glu Glu Glu Ala Ser Glu Val Val Gln Glu Thr Asp Asp His His
290 295 300
Val Leu Asp Asn Asn Asn Asn Thr Ile Ser Pro Val Pro Gln Gln Gln
305 310 315 320
Pro Asn Gln Asn Leu Ile Trp Ser Thr Gly Ser Arg Gln Met Asp Met
325 330 335
Arg His Ala His Ala Asp Ile Asp Leu Met Arg Gly
340 345

(2) INFORMATION FOR SEQ ID NO:1369:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 342 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..342
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500111

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1369:

Met Gly Leu Ser Gly Ser Gly Ser Tyr Ile His Arg Gly Leu Pro
1 5 10 15
Gly Ser Gly Pro Pro Thr Phe His Gly Ser Pro Gln Gln Gln Gln Gly
20 25 30
Leu Arg His Leu Pro Asn Gln Asn Ser Pro Phe Gly Ser Gly Ser Thr
35 40 45
Gly Phe Gly Ser Pro Ser Leu His Gly Asp Pro Ser Leu Ala Thr Ala


```

      50      55      60
Ala Gly Gly Ala Gly Ala Leu Pro His His Ile Gly Val Asn Met Ile
65      70      75      80
Ala Pro Pro Pro Pro Pro Ser Glu Thr Pro Met Lys Arg Lys Arg Gly
      85      90      95
Arg Pro Arg Lys Tyr Gly Gln Asp Gly Ser Val Ser Leu Ala Leu Ser
      100      105      110
Ser Ser Ser Val Ser Thr Ile Thr Pro Asn Asn Ser Asn Lys Arg Gly
      115      120      125
Arg Gly Arg Pro Pro Gly Ser Gly Lys Lys Gln Arg Met Ala Ser Val
      130      135      140
Gly Glu Leu Met Pro Ser Ser Ser Gly Met Ser Phe Thr Pro His Val
145      150      155      160
Ile Ala Val Ser Ile Gly Glu Asp Ile Ala Ser Lys Val Ile Ala Phe
      165      170      175
Ser Gln Gln Gly Pro Arg Ala Ile Cys Val Leu Ser Ala Ser Gly Ala
      180      185      190
Val Ser Thr Ala Thr Leu Ile Gln Pro Ser Ala Ser Pro Gly Ala Ile
      195      200      205
Lys Tyr Glu Gly Arg Phe Glu Ile Leu Ala Leu Ser Thr Ser Tyr Ile
      210      215      220
Val Ala Thr Asp Gly Ser Phe Arg Asn Arg Thr Gly Asn Leu Ser Val
225      230      235      240
Ser Leu Ala Ser Pro Asp Gly Arg Val Ile Gly Gly Ala Ile Gly Gly
      245      250      255
Pro Leu Ile Ala Ala Ser Pro Val Gln Val Ile Val Gly Ser Phe Ile
      260      265      270
Trp Ala Ala Pro Lys Ile Lys Ser Lys Lys Arg Glu Glu Glu Ala Ser
      275      280      285
Glu Val Val Gln Glu Thr Asp Asp His His Val Leu Asp Asn Asn Asn
290      295      300
Asn Thr Ile Ser Pro Val Pro Gln Gln Gln Pro Asn Gln Asn Leu Ile
305      310      315      320
Trp Ser Thr Gly Ser Arg Gln Met Asp Met Arg His Ala His Ala Asp
      325      330      335
Ile Asp Leu Met Arg Gly
      340
```

(2) INFORMATION FOR SEQ ID NO:1370:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 264 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..264

(D) OTHER INFORMATION: / Ceres Seq. ID 1500112

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1370:

```

Met Ile Ala Pro Pro Pro Pro Ser Glu Thr Pro Met Lys Arg Lys
1      5      10      15
Arg Gly Arg Pro Arg Lys Tyr Gly Gln Asp Gly Ser Val Ser Leu Ala
      20      25      30
Leu Ser Ser Ser Val Ser Thr Ile Thr Pro Asn Asn Ser Asn Lys
      35      40      45
Arg Gly Arg Gly Arg Pro Pro Gly Ser Gly Lys Lys Gln Arg Met Ala
50      55      60
Ser Val Gly Glu Leu Met Pro Ser Ser Ser Gly Met Ser Phe Thr Pro
65      70      75      80
His Val Ile Ala Val Ser Ile Gly Glu Asp Ile Ala Ser Lys Val Ile
      85      90      95
```

Ala Phe Ser Gln Gln Gly Pro Arg Ala Ile Cys Val Leu Ser Ala Ser
100 105 110
Gly Ala Val Ser Thr Ala Thr Leu Ile Gln Pro Ser Ala Ser Pro Gly
115 120 125
Ala Ile Lys Tyr Glu Gly Arg Phe Glu Ile Leu Ala Leu Ser Thr Ser
130 135 140
Tyr Ile Val Ala Thr Asp Gly Ser Phe Arg Asn Arg Thr Gly Asn Leu
145 150 155 160
Ser Val Ser Leu Ala Ser Pro Asp Gly Arg Val Ile Gly Gly Ala Ile
165 170 175
Gly Gly Pro Leu Ile Ala Ala Ser Pro Val Gln Val Ile Val Gly Ser
180 185 190
Phe Ile Trp Ala Ala Pro Lys Ile Lys Ser Lys Lys Arg Glu Glu Glu
195 200 205
Ala Ser Glu Val Val Gln Glu Thr Asp Asp His His Val Leu Asp Asn
210 215 220
Asn Asn Asn Thr Ile Ser Pro Val Pro Gln Gln Gln Pro Asn Gln Asn
225 230 235 240
Leu Ile Trp Ser Thr Gly Ser Arg Gln Met Asp Met Arg His Ala His
245 250 255
Ala Asp Ile Asp Leu Met Arg Gly
260

(2) INFORMATION FOR SEQ ID NO:1371:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1270 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1270
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500115

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1371:

atctacaact	ttcattcttc	cactacattt	ctctccttga	gtatcttctt	atcctatctt	60
ccaaattcca	aaacaattca	caaaatggct	acatgctggc	ctgagccgat	tgtttccgtg	120
caatccttgt	cccaaaccgg	tgtaccaact	gtaccaaac	gctatgtgaa	gccggctcat	180
cagagaccgg	tctttaacac	cacccaatcc	gatgctggga	tagaaatccc	tgttctagac	240
atgaacgacg	tttgggggaa	accagagggg	ctaaggctcg	tgaggagcgc	gtgtgaggag	300
tggggtttct	tccaaatggt	gaaccatggt	gtgacccact	cgttgatgga	gagagtgaga	360
ggagcgtggc	gagagttctt	cgagctaccg	ctagaggaga	aacggaagta	tgcaaactca	420
ccggacacgt	acgagggata	tggaagccgc	cttgggggtg	tgagagatgc	taaattagat	480
tggagtgatt	atttcttctt	caattacttg	ccttcttcca	taagaaaccc	ttccaagtgc	540
ccatactcag	cctcctaaga	tcagagaatt	gatcgaaaag	tacggagaag	aagtgagaaa	600
actgtgcgaa	aggctaacag	agacgttgtc	agagagttta	ggtttaaaac	caaacaagct	660
catgcaggct	ttaggaggag	gcgacaaagt	cggagcttct	ctgaggacaa	acttctaccc	720
aaaatgccct	cagccgcagc	tcacttttag	tctctcttct	cattctgacc	ctggaggcat	780
caccattctt	ctcccggacg	agaaggtcgc	tggccttcag	gtccgctcgtg	gtgatggctg	840
ggtcaccatt	aaatcagtc	ctaattgctt	gatcgtaaac	attggagatc	aacttcagat	900
acttagcaat	ggaatttaca	aaagcgtgga	acatcaagtg	atcgtaatt	ccggtatgga	960
acgagtctct	ttggcattct	tctataaccc	gagaagtgtg	atcccggttg	gaccaatcga	1020
agaactagta	actgcaaacc	gacctgctct	ttataaacca	atcaggttcg	acgagtaccg	1080
ttctctgata	aggcaaaagg	gtccttggtg	aaaaaaccaa	gtcgactcac	tgttattaac	1140
tagataataa	ttgataaaca	ttccaagtat	tatctgttat	tcctatgtcc	ttgatatagt	1200
cgttactaaa	taatatgtaa	accgtatctt	cactttttct	tattatattg	ctgctctctc	1260
ttgaggtttg						

(2) INFORMATION FOR SEQ ID NO:1372:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 185 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:

- (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..185
(D) OTHER INFORMATION: / Ceres Seq. ID 1500116

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1372:

Ile	Tyr	Asn	Phe	His	Ser	Ser	Thr	Thr	Phe	Leu	Ser	Leu	Ser	Ile	Phe
1				5					10					15	
Leu	Ser	Tyr	Phe	Pro	Asn	Ser	Lys	Thr	Ile	His	Lys	Met	Ala	Thr	Cys
			20					25					30		
Trp	Pro	Glu	Pro	Ile	Val	Ser	Val	Gln	Ser	Leu	Ser	Gln	Thr	Gly	Val
		35					40					45			
Pro	Thr	Val	Pro	Asn	Arg	Tyr	Val	Lys	Pro	Ala	His	Gln	Arg	Pro	Val
	50					55					60				
Phe	Asn	Thr	Thr	Gln	Ser	Asp	Ala	Gly	Ile	Glu	Ile	Pro	Val	Leu	Asp
65					70				75					80	
Met	Asn	Asp	Val	Trp	Gly	Lys	Pro	Glu	Gly	Leu	Arg	Leu	Val	Arg	Ser
			85					90						95	
Ala	Cys	Glu	Glu	Trp	Gly	Phe	Phe	Gln	Met	Val	Asn	His	Gly	Val	Thr
			100					105					110		
His	Ser	Leu	Met	Glu	Arg	Val	Arg	Gly	Ala	Trp	Arg	Glu	Phe	Phe	Glu
		115					120					125			
Leu	Pro	Leu	Glu	Glu	Lys	Arg	Lys	Tyr	Ala	Asn	Ser	Pro	Asp	Thr	Tyr
	130					135					140				
Glu	Gly	Tyr	Gly	Ser	Arg	Leu	Gly	Val	Val	Arg	Asp	Ala	Lys	Leu	Asp
145					150					155				160	
Trp	Ser	Asp	Tyr	Phe	Phe	Leu	Asn	Tyr	Leu	Pro	Ser	Ser	Ile	Arg	Asn
			165					170						175	
Pro	Ser	Lys	Trp	Pro	Tyr	Ser	Ala	Ser							
		180						185							

(2) INFORMATION FOR SEQ ID NO:1373:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 157 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..157
(D) OTHER INFORMATION: / Ceres Seq. ID 1500117

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1373:

Met	Ala	Thr	Cys	Trp	Pro	Glu	Pro	Ile	Val	Ser	Val	Gln	Ser	Leu	Ser
1				5					10					15	
Gln	Thr	Gly	Val	Pro	Thr	Val	Pro	Asn	Arg	Tyr	Val	Lys	Pro	Ala	His
			20					25					30		
Gln	Arg	Pro	Val	Phe	Asn	Thr	Thr	Gln	Ser	Asp	Ala	Gly	Ile	Glu	Ile
		35					40					45			
Pro	Val	Leu	Asp	Met	Asn	Asp	Val	Trp	Gly	Lys	Pro	Glu	Gly	Leu	Arg
	50					55					60				
Leu	Val	Arg	Ser	Ala	Cys	Glu	Glu	Trp	Gly	Phe	Phe	Gln	Met	Val	Asn
65					70				75					80	
His	Gly	Val	Thr	His	Ser	Leu	Met	Glu	Arg	Val	Arg	Gly	Ala	Trp	Arg
			85					90					95		
Glu	Phe	Phe	Glu	Leu	Pro	Leu	Glu	Glu	Lys	Arg	Lys	Tyr	Ala	Asn	Ser
		100						105					110		
Pro	Asp	Thr	Tyr	Glu	Gly	Tyr	Gly	Ser	Arg	Leu	Gly	Val	Val	Arg	Asp
		115					120					125			
Ala	Lys	Leu	Asp	Trp	Ser	Asp	Tyr	Phe	Phe	Leu	Asn	Tyr	Leu	Pro	Ser
	130					135						140			

Ser Ile Arg Asn Pro Ser Lys Trp Pro Tyr Ser Ala Ser
145 150 155

(2) INFORMATION FOR SEQ ID NO:1374:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 161 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..161

(D) OTHER INFORMATION: / Ceres Seq. ID 1500118

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1374:

Met Gln Ala Leu Gly Gly Gly Asp Lys Val Gly Ala Ser Leu Arg Thr
1 5 10 15
Asn Phe Tyr Pro Lys Cys Pro Gln Pro Gln Leu Thr Leu Gly Leu Ser
20 25 30
Ser His Ser Asp Pro Gly Gly Ile Thr Ile Leu Leu Pro Asp Glu Lys
35 40 45
Val Ala Gly Leu Gln Val Arg Arg Gly Asp Gly Trp Val Thr Ile Lys
50 55 60
Ser Val Pro Asn Ala Leu Ile Val Asn Ile Gly Asp Gln Leu Gln Ile
65 70 75 80
Leu Ser Asn Gly Ile Tyr Lys Ser Val Glu His Gln Val Ile Val Asn
85 90 95
Ser Gly Met Glu Arg Val Ser Leu Ala Phe Phe Tyr Asn Pro Arg Ser
100 105 110
Asp Ile Pro Val Gly Pro Ile Glu Leu Val Thr Ala Asn Arg Pro
115 120 125
Ala Leu Tyr Lys Pro Ile Arg Phe Asp Glu Tyr Arg Ser Leu Ile Arg
130 135 140
Gln Lys Gly Pro Cys Gly Lys Asn Gln Val Asp Ser Leu Leu Leu Thr
145 150 155 160
Arg

(2) INFORMATION FOR SEQ ID NO:1375:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1756 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1756

(D) OTHER INFORMATION: / Ceres Seq. ID 1500131

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1375:

gctctgattc attcacaat aacaatcctc tcttcgtttt tgtttttctt ttggatccaa	60
agctctctta aatctgtaaa tcaacaatgg ccgccaccac tgagaatctc cctcaactca	120
aatccgccgt cgatggcctt actgagatga gtgagagtga gaagagcgga ttcatcagcc	180
tggtttcacg ttacctgagc ggtgaggcac aacacattga gtggagtaag atccagactc	240
ctaccgatga aatcggtgtt ccctacgaga aaatgacccc tgtctcccaa gatgttgccg	300
agaccaagaa tctgttggac aaacttgttg tgttgaagct taatggaggt cttggaacaa	360
caatgggatg cactggcccc aagtcctgta tcgaagtctg tgatggtttg acattttctt	420
atctgattgt tatccagatt gagaatctca acaacaagta tggctgcaag gttccgttag	480
ttctcatgaa ctcgtttaat acacatgatg acagacataa gattgtggaa aagtacacca	540
actcaaattg tgacattcac acttttaacc agagcaaata tccccgtgtt gtggcagatg	600
agtttgtgcc atggcccagc aagggaagaa cgcacaagga gggctggtat cctcccggtc	660
atgggtgatg attcccagcc ctcatgaaca gtggaaagct cgatactttc ttatcacagg	720
gtaaggaata tgtgtttgtt gccaatcag acaacttggg tgccatcgtt gacttaacaa	780

tcctgaagca	tttgcaccag	aacaagaacg	aatactgcat	ggaggttaca	cccaaaacct	840
tagctgatgt	aaagggggga	actctcattt	cttatgaagg	caaagtccag	cttctggaga	900
ttgctcagtt	tcctgatgaa	catgtcaatg	agttcaaadc	aattgagaag	ttcaagatat	960
tcaacacaaa	caacctatgg	gttaacttga	aggccatcaa	aaagcttggt	gaagctgatg	1020
cacttaaaat	ggagatcatt	ccaaacccaa	aggaagttga	tggagtcaaa	gttcttcaac	1080
tggaaactgc	agccggtgct	gcgataaggt	tctttgacaa	cgctatcggt	gttaatgtac	1140
ctcgcctcacg	gttcttgcca	gtgaaggcaa	gttcagactt	gctgctcgct	cagctctgatc	1200
tctacacctt	agttgatggc	tttgtcactc	gaaacaaagc	tagaactaac	ccctcgaaac	1260
cgtcaattga	attgggaccc	gagttcaaga	agggtggctac	tttcttgagc	cggtttaagt	1320
ccattcctag	tatagtcgag	ctcgacagcc	ttaaggtgtc	tggatgatgtc	tggtttgggt	1380
cttccattgt	tctcaagggc	aaggtgactg	tggcggcaaa	atccggtgtg	aagcttgaaa	1440
ttccggacag	ggccgtgggc	gagaacaaga	acatcaatgg	tccagaagac	ctctgaataa	1500
aacaaattca	agtcttcttc	cctctctcat	ggaagacaca	tcttgatact	cctttaattg	1560
gtgtgaaaag	atcacaagtg	gcacagcaaa	gcaagtttat	gaagaaagaa	taaataatgt	1620
ttctttttct	ttttgcagct	tagcaaagtc	ttttcctctt	tggactttat	tttaattttg	1680
ctctttgaat	tttcccaaaa	catcacattt	atatgttcga	ttatatttgg	gttctatcca	1740
caatcatttt	tctttt					

(2) INFORMATION FOR SEQ ID NO:1376:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 469 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..469

(D) OTHER INFORMATION: / Ceres Seq. ID 1500132

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1376:

Met	Ala	Ala	Thr	Thr	Glu	Asn	Leu	Pro	Gln	Leu	Lys	Ser	Ala	Val	Asp
1			5						10					15	
Gly	Leu	Thr	Glu	Met	Ser	Glu	Ser	Glu	Lys	Ser	Gly	Phe	Ile	Ser	Leu
			20					25					30		
Val	Ser	Arg	Tyr	Leu	Ser	Gly	Glu	Ala	Gln	His	Ile	Glu	Trp	Ser	Lys
		35					40				45				
Ile	Gln	Thr	Pro	Thr	Asp	Glu	Ile	Val	Val	Pro	Tyr	Glu	Lys	Met	Thr
	50				55						60				
Pro	Val	Ser	Gln	Asp	Val	Ala	Glu	Thr	Lys	Asn	Leu	Leu	Asp	Lys	Leu
65				70					75					80	
Val	Val	Leu	Lys	Leu	Asn	Gly	Gly	Leu	Gly	Thr	Thr	Met	Gly	Cys	Thr
			85					90					95		
Gly	Pro	Lys	Ser	Val	Ile	Glu	Val	Arg	Asp	Gly	Leu	Thr	Phe	Leu	Asp
		100					105					110			
Leu	Ile	Val	Ile	Gln	Ile	Glu	Asn	Asn	Lys	Tyr	Gly	Cys	Lys		
	115					120				125					
Val	Pro	Leu	Val	Leu	Met	Asn	Ser	Phe	Asn	Thr	His	Asp	Asp	Arg	His
	130					135				140					
Lys	Ile	Val	Glu	Lys	Tyr	Thr	Asn	Ser	Asn	Val	Asp	Ile	His	Thr	Phe
145				150					155					160	
Asn	Gln	Ser	Lys	Tyr	Pro	Arg	Val	Val	Ala	Asp	Glu	Phe	Val	Pro	Trp
		165						170					175		
Pro	Ser	Lys	Gly	Lys	Thr	Asp	Lys	Glu	Gly	Trp	Tyr	Pro	Pro	Gly	His
		180					185					190			
Gly	Asp	Val	Phe	Pro	Ala	Leu	Met	Asn	Ser	Gly	Lys	Leu	Asp	Thr	Phe
	195					200					205				
Leu	Ser	Gln	Gly	Lys	Glu	Tyr	Val	Phe	Val	Ala	Asn	Ser	Asp	Asn	Leu
	210					215					220				
Gly	Ala	Ile	Val	Asp	Leu	Thr	Ile	Leu	Lys	His	Leu	Ile	Gln	Asn	Lys
225				230					235					240	
Asn	Glu	Tyr	Cys	Met	Glu	Val	Thr	Pro	Lys	Thr	Leu	Ala	Asp	Val	Lys
		245						250					255		

Gly Gly Thr Leu Ile Ser Tyr Glu Gly Lys Val Gln Leu Leu Glu Ile
260 265 270
Ala Gln Phe Pro Asp Glu His Val Asn Glu Phe Lys Ser Ile Glu Lys
275 280 285
Phe Lys Ile Phe Asn Thr Asn Asn Leu Trp Val Asn Leu Lys Ala Ile
290 295 300
Lys Lys Leu Val Glu Ala Asp Ala Leu Lys Met Glu Ile Ile Pro Asn
305 310 315 320
Pro Lys Glu Val Asp Gly Val Lys Val Leu Gln Leu Glu Thr Ala Ala
325 330 335
Gly Ala Ala Ile Arg Phe Phe Asp Asn Ala Ile Gly Val Asn Val Pro
340 345 350
Arg Ser Arg Phe Leu Pro Val Lys Ala Ser Ser Asp Leu Leu Leu Val
355 360 365
Gln Ser Asp Leu Tyr Thr Leu Val Asp Gly Phe Val Thr Arg Asn Lys
370 375 380
Ala Arg Thr Asn Pro Ser Asn Pro Ser Ile Glu Leu Gly Pro Glu Phe
385 390 395 400
Lys Lys Val Ala Thr Phe Leu Ser Arg Phe Lys Ser Ile Pro Ser Ile
405 410 415
Val Glu Leu Asp Ser Leu Lys Val Ser Gly Asp Val Trp Phe Gly Ser
420 425 430
Ser Ile Val Leu Lys Gly Lys Val Thr Val Ala Ala Lys Ser Gly Val
435 440 445
Lys Leu Glu Ile Pro Asp Arg Ala Val Val Glu Asn Lys Asn Ile Asn
450 455 460
Gly Pro Glu Asp Leu
465

(2) INFORMATION FOR SEQ ID NO:1377:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 449 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..449

(D) OTHER INFORMATION: / Ceres Seq. ID 1500133

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1377:

Met Ser Glu Ser Glu Lys Ser Gly Phe Ile Ser Leu Val Ser Arg Tyr
1 5 10 15
Leu Ser Gly Glu Ala Gln His Ile Glu Trp Ser Lys Ile Gln Thr Pro
20 25 30
Thr Asp Glu Ile Val Val Pro Tyr Glu Lys Met Thr Pro Val Ser Gln
35 40 45
Asp Val Ala Glu Thr Lys Asn Leu Leu Asp Lys Leu Val Val Leu Lys
50 55 60
Leu Asn Gly Gly Leu Gly Thr Thr Met Gly Cys Thr Gly Pro Lys Ser
65 70 75 80
Val Ile Glu Val Arg Asp Gly Leu Thr Phe Leu Asp Leu Ile Val Ile
85 90 95
Gln Ile Glu Asn Leu Asn Asn Lys Tyr Gly Cys Lys Val Pro Leu Val
100 105 110
Leu Met Asn Ser Phe Asn Thr His Asp Asp Arg His Lys Ile Val Glu
115 120 125
Lys Tyr Thr Asn Ser Asn Val Asp Ile His Thr Phe Asn Gln Ser Lys
130 135 140
Tyr Pro Arg Val Val Ala Asp Glu Phe Val Pro Trp Pro Ser Lys Gly
145 150 155 160
Lys Thr Asp Lys Glu Gly Trp Tyr Pro Pro Gly His Gly Asp Val Phe

				165					170					175	
Pro	Ala	Leu	Met	Asn	Ser	Gly	Lys	Leu	Asp	Thr	Phe	Leu	Ser	Gln	Gly
			180					185					190		
Lys	Glu	Tyr	Val	Phe	Val	Ala	Asn	Ser	Asp	Asn	Leu	Gly	Ala	Ile	Val
		195					200					205			
Asp	Leu	Thr	Ile	Leu	Lys	His	Leu	Ile	Gln	Asn	Lys	Asn	Glu	Tyr	Cys
	210					215					220				
Met	Glu	Val	Thr	Pro	Lys	Thr	Leu	Ala	Asp	Val	Lys	Gly	Gly	Thr	Leu
225					230					235				240	
Ile	Ser	Tyr	Glu	Gly	Lys	Val	Gln	Leu	Leu	Glu	Ile	Ala	Gln	Phe	Pro
				245					250					255	
Asp	Glu	His	Val	Asn	Glu	Phe	Lys	Ser	Ile	Glu	Lys	Phe	Lys	Ile	Phe
			260					265					270		
Asn	Thr	Asn	Asn	Leu	Trp	Val	Asn	Leu	Lys	Ala	Ile	Lys	Lys	Leu	Val
		275					280					285			
Glu	Ala	Asp	Ala	Leu	Lys	Met	Glu	Ile	Ile	Pro	Asn	Pro	Lys	Glu	Val
	290					295				300					
Asp	Gly	Val	Lys	Val	Leu	Gln	Leu	Glu	Thr	Ala	Ala	Gly	Ala	Ala	Ile
305					310					315					320
Arg	Phe	Phe	Asp	Asn	Ala	Ile	Gly	Val	Asn	Val	Pro	Arg	Ser	Arg	Phe
				325					330					335	
Leu	Pro	Val	Lys	Ala	Ser	Ser	Asp	Leu	Leu	Leu	Val	Gln	Ser	Asp	Leu
		340						345					350		
Tyr	Thr	Leu	Val	Asp	Gly	Phe	Val	Thr	Arg	Asn	Lys	Ala	Arg	Thr	Asn
		355					360					365			
Pro	Ser	Asn	Pro	Ser	Ile	Glu	Leu	Gly	Pro	Glu	Phe	Lys	Lys	Val	Ala
	370					375					380				
Thr	Phe	Leu	Ser	Arg	Phe	Lys	Ser	Ile	Pro	Ser	Ile	Val	Glu	Leu	Asp
385					390					395					400
Ser	Leu	Lys	Val	Ser	Gly	Asp	Val	Trp	Phe	Gly	Ser	Ser	Ile	Val	Leu
				405					410					415	
Lys	Gly	Lys	Val	Thr	Val	Ala	Ala	Lys	Ser	Gly	Val	Lys	Leu	Glu	Ile
			420					425					430		
Pro	Asp	Arg	Ala	Val	Val	Glu	Asn	Lys	Asn	Ile	Asn	Gly	Pro	Glu	Asp
		435					440					445			
Leu															

(2) INFORMATION FOR SEQ ID NO:1378:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 407 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..407
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500134

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1378:

Met	Thr	Pro	Val	Ser	Gln	Asp	Val	Ala	Glu	Thr	Lys	Asn	Leu	Leu	Asp
1				5					10					15	
Lys	Leu	Val	Val	Leu	Lys	Leu	Asn	Gly	Gly	Leu	Gly	Thr	Thr	Met	Gly
		20						25					30		
Cys	Thr	Gly	Pro	Lys	Ser	Val	Ile	Glu	Val	Arg	Asp	Gly	Leu	Thr	Phe
	35					40					45				
Leu	Asp	Leu	Ile	Val	Ile	Gln	Ile	Glu	Asn	Leu	Asn	Asn	Lys	Tyr	Gly
	50					55				60					
Cys	Lys	Val	Pro	Leu	Val	Leu	Met	Asn	Ser	Phe	Asn	Thr	His	Asp	Asp
65					70					75				80	
Arg	His	Lys	Ile	Val	Glu	Lys	Tyr	Thr	Asn	Ser	Asn	Val	Asp	Ile	His
				85					90					95	

Thr	Phe	Asn	Gln	Ser	Lys	Tyr	Pro	Arg	Val	Val	Ala	Asp	Glu	Phe	Val
		100						105					110		
Pro	Trp	Pro	Ser	Lys	Gly	Lys	Thr	Asp	Lys	Glu	Gly	Trp	Tyr	Pro	Pro
		115					120					125			
Gly	His	Gly	Asp	Val	Phe	Pro	Ala	Leu	Met	Asn	Ser	Gly	Lys	Leu	Asp
	130					135					140				
Thr	Phe	Leu	Ser	Gln	Gly	Lys	Glu	Tyr	Val	Phe	Val	Ala	Asn	Ser	Asp
	145				150					155					160
Asn	Leu	Gly	Ala	Ile	Val	Asp	Leu	Thr	Ile	Leu	Lys	His	Leu	Ile	Gln
				165					170						175
Asn	Lys	Asn	Glu	Tyr	Cys	Met	Glu	Val	Thr	Pro	Lys	Thr	Leu	Ala	Asp
			180					185					190		
Val	Lys	Gly	Gly	Thr	Leu	Ile	Ser	Tyr	Glu	Gly	Lys	Val	Gln	Leu	Leu
	195						200					205			
Glu	Ile	Ala	Gln	Phe	Pro	Asp	Glu	His	Val	Asn	Glu	Phe	Lys	Ser	Ile
	210					215					220				
Glu	Lys	Phe	Lys	Ile	Phe	Asn	Thr	Asn	Asn	Leu	Trp	Val	Asn	Leu	Lys
	225				230					235					240
Ala	Ile	Lys	Lys	Leu	Val	Glu	Ala	Asp	Ala	Leu	Lys	Met	Glu	Ile	Ile
				245				250						255	
Pro	Asn	Pro	Lys	Glu	Val	Asp	Gly	Val	Lys	Val	Leu	Gln	Leu	Glu	Thr
			260					265					270		
Ala	Ala	Gly	Ala	Ala	Ile	Arg	Phe	Asp	Asn	Ala	Ile	Gly	Val	Asn	
		275					280				285				
Val	Pro	Arg	Ser	Arg	Phe	Leu	Pro	Val	Lys	Ala	Ser	Ser	Asp	Leu	Leu
	290					295					300				
Leu	Val	Gln	Ser	Asp	Leu	Tyr	Thr	Leu	Val	Asp	Gly	Phe	Val	Thr	Arg
	305				310					315					320
Asn	Lys	Ala	Arg	Thr	Asn	Pro	Ser	Asn	Pro	Ser	Ile	Glu	Leu	Gly	Pro
				325					330					335	
Glu	Phe	Lys	Lys	Val	Ala	Thr	Phe	Leu	Ser	Arg	Phe	Lys	Ser	Ile	Pro
			340					345					350		
Ser	Ile	Val	Glu	Leu	Asp	Ser	Leu	Lys	Val	Ser	Gly	Asp	Val	Trp	Phe
	355						360				365				
Gly	Ser	Ser	Ile	Val	Leu	Lys	Gly	Lys	Val	Thr	Val	Ala	Ala	Lys	Ser
	370					375					380				
Gly	Val	Lys	Leu	Glu	Ile	Pro	Asp	Arg	Ala	Val	Val	Glu	Asn	Lys	Asn
	385				390					395					400
Ile	Asn	Gly	Pro	Glu	Asp	Leu									
					405										

(2) INFORMATION FOR SEQ ID NO:1379:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1210 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1210
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500135

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1379:

attaaaaatgg	cagttcaagc	tcaacacccat	tcctccaatc	tcctcttcct	caataaaaga	60
aacgggaaag	agaaagaaca	tagtaatttt	acattacaat	cacaagcagc	tggagatttt	120
cttgatcaaa	ccaatatggt	attcaacaat	ggaagttcta	atcagagaaa	aagaagaaga	180
gaaacgaaca	atcatcagtt	attacctatg	cagtcctc	agtttcctca	agttatagac	240
ttatctctat	tacacaacta	caatcatcca	ccgtcgaata	tggttcatac	aggactccga	300
ttatttttccg	gcgaagatca	ggcacaaaag	attagtcacc	tgtctgaaga	tgtttttgct	360
gcacatatca	ataggcaaag	cgaagaactt	gatgagtttc	ttcatgcccc	ggcggaggag	420
ctacggcgta	cattagcgga	gaagaggaag	atgcactata	aagcgcttct	tggtgccgtg	480
gaagagtcgt	tggttcgtaa	gctgaggagg	aaagaggtag	agatagagag	agccacgcgc	540


```
cgtcacaatg agctgggtggc acgtgactcg cagctgagag cggaggtgca agtatggcaa 600
gagagagcta aagcgcacga agacgccgcc gcgtcgctgc agtctcagct ccagcaagcc 660
gttaaccaat gcgccggtgg atgtgtatcg gcgcaggata gtagagcggc ggaggaaggg 720
ctattatgca ccacaatcag cggagtggat gacgccgagt cgggtgtacgt ggatccggag 780
agagtaaagc ggccgaattg caaagcttgc cgggaaagag aggcaacggt ggttgtgttg 840
ccgtgtcggc atctgagcat ctgcccggga tgtgaccgga cagcttttagc ttgcccgttg 900
tgtctcacgt tgcggaattc aagtgttgaa gctatctttt gctaaatggg cctaattcaa 960
gccattagg ttgttatcgt aaatagaact tagtaggtaa cacaaatata aatttcattg 1020
gtatatgata taccgtatat cgaatccact agctattaag gaagccctct aaattttaca 1080
acaaaagaag tttttttttt ttttttttact tttcattact tgggattctt tacacagata 1140
tgggatatgg aaatgttgct attcgtacaa aatagttaac taagctaaga aacccatttt 1200
tgggggggccc
```

(2) INFORMATION FOR SEQ ID NO:1380:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 314 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..314

(D) OTHER INFORMATION: / Ceres Seq. ID 1500136

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1380:

```
Ile Lys Met Ala Val Gln Ala Gln His Ser Ser Asn Leu Leu Phe
1      5      10      15
Leu Asn Lys Arg Asn Gly Lys Glu Lys Glu His Ser Asn Phe Thr Leu
20      25      30
Gln Ser Gln Ala Ala Gly Asp Phe Leu Asp Gln Thr Asn Met Leu Phe
35      40      45
Asn Asn Gly Ser Ser Asn Gln Arg Lys Arg Arg Arg Glu Thr Asn Asn
50      55      60
His Gln Leu Leu Pro Met Gln Ser His Gln Phe Pro Gln Val Ile Asp
65      70      75      80
Leu Ser Leu Leu His Asn Tyr Asn His Pro Pro Ser Asn Met Val His
85      90      95
Thr Gly Leu Arg Leu Phe Ser Gly Glu Asp Gln Ala Gln Lys Ile Ser
100     105     110
His Leu Ser Glu Asp Val Phe Ala Ala His Ile Asn Arg Gln Ser Glu
115     120     125
Glu Leu Asp Glu Phe Leu His Ala Gln Ala Glu Glu Leu Arg Arg Thr
130     135     140
Leu Ala Glu Lys Arg Lys Met His Tyr Lys Ala Leu Leu Gly Ala Val
145     150     155     160
Glu Glu Ser Leu Val Arg Lys Leu Arg Glu Lys Glu Val Glu Ile Glu
165     170     175
Arg Ala Thr Arg Arg His Asn Glu Leu Val Ala Arg Asp Ser Gln Leu
180     185     190
Arg Ala Glu Val Gln Val Trp Gln Glu Arg Ala Lys Ala His Glu Asp
195     200     205
Ala Ala Ala Ser Leu Gln Ser Gln Leu Gln Gln Ala Val Asn Gln Cys
210     215     220
Ala Gly Gly Cys Val Ser Ala Gln Asp Ser Arg Ala Ala Glu Glu Gly
225     230     235     240
Leu Leu Cys Thr Thr Ile Ser Gly Val Asp Asp Ala Glu Ser Val Tyr
245     250     255
Val Asp Pro Glu Arg Val Lys Arg Pro Asn Cys Lys Ala Cys Arg Glu
260     265     270
Arg Glu Ala Thr Val Val Val Leu Pro Cys Arg His Leu Ser Ile Cys
275     280     285
Pro Gly Cys Asp Arg Thr Ala Leu Ala Cys Pro Leu Cys Leu Thr Leu
```

290 295 300
Arg Asn Ser Ser Val Glu Ala Ile Phe Cys
305 310

(2) INFORMATION FOR SEQ ID NO:1381:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 312 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..312

(D) OTHER INFORMATION: / Ceres Seq. ID 1500137

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1381:

Met Ala Val Gln Ala Gln His His Ser Ser Asn Leu Leu Phe Leu Asn
1 5 10 15
Lys Arg Asn Gly Lys Glu Lys Glu His Ser Asn Phe Thr Leu Gln Ser
20 25 30
Gln Ala Ala Gly Asp Phe Leu Asp Gln Thr Asn Met Leu Phe Asn Asn
35 40 45
Gly Ser Ser Asn Gln Arg Lys Arg Arg Arg Glu Thr Asn Asn His Gln
50 55 60
Leu Leu Pro Met Gln Ser His Gln Phe Pro Gln Val Ile Asp Leu Ser
65 70 75 80
Leu Leu His Asn Tyr Asn His Pro Pro Ser Asn Met Val His Thr Gly
85 90 95
Leu Arg Leu Phe Ser Gly Glu Asp Gln Ala Gln Lys Ile Ser His Leu
100 105 110
Ser Glu Asp Val Phe Ala Ala His Ile Asn Arg Gln Ser Glu Glu Leu
115 120 125
Asp Glu Phe Leu His Ala Gln Ala Glu Glu Leu Arg Arg Thr Leu Ala
130 135 140
Glu Lys Arg Lys Met His Tyr Lys Ala Leu Leu Gly Ala Val Glu Glu
145 150 155 160
Ser Leu Val Arg Lys Leu Arg Glu Lys Glu Val Glu Ile Glu Arg Ala
165 170 175
Thr Arg Arg His Asn Glu Leu Val Ala Arg Asp Ser Gln Leu Arg Ala
180 185 190
Glu Val Gln Val Trp Gln Glu Arg Ala Lys Ala His Glu Asp Ala Ala
195 200 205
Ala Ser Leu Gln Ser Gln Leu Gln Gln Ala Val Asn Gln Cys Ala Gly
210 215 220
Gly Cys Val Ser Ala Gln Asp Ser Arg Ala Ala Glu Glu Gly Leu Leu
225 230 235 240
Cys Thr Thr Ile Ser Gly Val Asp Asp Ala Glu Ser Val Tyr Val Asp
245 250 255
Pro Glu Arg Val Lys Arg Pro Asn Cys Lys Ala Cys Arg Glu Arg Glu
260 265 270
Ala Thr Val Val Val Leu Pro Cys Arg His Leu Ser Ile Cys Pro Gly
275 280 285
Cys Asp Arg Thr Ala Leu Ala Cys Pro Leu Cys Leu Thr Leu Arg Asn
290 295 300
Ser Ser Val Glu Ala Ile Phe Cys
305 310

(2) INFORMATION FOR SEQ ID NO:1382:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 269 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..269

(D) OTHER INFORMATION: / Ceres Seq. ID 1500138

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1382:

Met	Leu	Phe	Asn	Asn	Gly	Ser	Ser	Asn	Gln	Arg	Lys	Arg	Arg	Arg	Glu
1			5						10					15	
Thr	Asn	Asn	His	Gln	Leu	Leu	Pro	Met	Gln	Ser	His	Gln	Phe	Pro	Gln
			20					25					30		
Val	Ile	Asp	Leu	Ser	Leu	Leu	His	Asn	Tyr	Asn	His	Pro	Pro	Ser	Asn
		35				40						45			
Met	Val	His	Thr	Gly	Leu	Arg	Leu	Phe	Ser	Gly	Glu	Asp	Gln	Ala	Gln
	50				55						60				
Lys	Ile	Ser	His	Leu	Ser	Glu	Asp	Val	Phe	Ala	His	Ile	Asn	Arg	
65				70					75					80	
Gln	Ser	Glu	Glu	Leu	Asp	Glu	Phe	Leu	His	Ala	Gln	Ala	Glu	Glu	Leu
			85					90						95	
Arg	Arg	Thr	Leu	Ala	Glu	Lys	Arg	Lys	Met	His	Tyr	Lys	Ala	Leu	Leu
			100					105					110		
Gly	Ala	Val	Glu	Glu	Ser	Leu	Val	Arg	Lys	Leu	Arg	Glu	Lys	Glu	Val
		115				120						125			
Glu	Ile	Glu	Arg	Ala	Thr	Arg	His	Asn	Glu	Leu	Val	Ala	Arg	Asp	
	130				135						140				
Ser	Gln	Leu	Arg	Ala	Glu	Val	Gln	Val	Trp	Gln	Glu	Arg	Ala	Lys	Ala
145					150					155				160	
His	Glu	Asp	Ala	Ala	Ala	Ser	Leu	Gln	Ser	Gln	Leu	Gln	Gln	Ala	Val
			165					170						175	
Asn	Gln	Cys	Ala	Gly	Gly	Cys	Val	Ser	Ala	Gln	Asp	Ser	Arg	Ala	Ala
			180					185					190		
Glu	Glu	Gly	Leu	Leu	Cys	Thr	Thr	Ile	Ser	Gly	Val	Asp	Asp	Ala	Glu
		195				200						205			
Ser	Val	Tyr	Val	Asp	Pro	Glu	Arg	Val	Lys	Arg	Pro	Asn	Cys	Lys	Ala
	210				215						220				
Cys	Arg	Glu	Arg	Glu	Ala	Thr	Val	Val	Val	Val	Leu	Pro	Cys	Arg	His
225				230							235				240
Ser	Ile	Cys	Pro	Gly	Cys	Asp	Arg	Thr	Ala	Leu	Ala	Cys	Pro	Leu	Cys
			245					250						255	
Leu	Thr	Leu	Arg	Asn	Ser	Ser	Val	Glu	Ala	Ile	Phe	Cys			
			260					265							

(2) INFORMATION FOR SEQ ID NO:1383:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 719 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..719

(D) OTHER INFORMATION: / Ceres Seq. ID 1500149

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1383:

gttgatatg	cggatctcca	ttcaccaatc	gccttcctgt	cgccctcccg	ctcggtcgg	60
cgaacgcgat	ctgttcccca	acctccgcag	ccgctccacc	gtcctccact	ccggctgccg	120
aatcgaccgg	ccccgatcca	gacgaggagc	tgagggatgg	acgcgaacag	gcgccagagt	180
gggatccagg	agttgctggc	tgcggascag	gaggctcagc	aaattgtgaa	tgcccgctag	240
agctgccaag	tcagcgaggc	tcaggcaagc	aaaagaggag	gctgagcggg	aaatagccga	300
ataccgtgcc	cagatggagg	ctgagtttca	gaggaagggt	gcagagagca	gcggcgactc	360
cggtgcaaac	gtcaagcgtc	tcgaggaaga	aacggcggcg	aagatcgagc	aactcaccca	420
gcaggccgca	agcatctccc	cggatgtcat	tcagatgctt	ctgcggcatg	tcaccaccgt	480
caagaactga	ggagtgtgtg	tcccgaacta	tgctcgcaga	cttgtaccgt	cgatctattt	540

atttttgtca agagtgaag tggtgaggaa taatatgccc gcttgatcc ataattcctg 600
ttcgtaacta cggaataagc cgccgcagct ttagcggcaa acgtgactag tactgtcaga 660
acctaccatt gttatttggt acaattggta aataatattg ttttaaactg gatttttcg

(2) INFORMATION FOR SEQ ID NO:1384:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 75 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..75

(D) OTHER INFORMATION: / Ceres Seq. ID 1500150

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1384:

Leu Tyr Met Arg Ile Ser Ile His Gln Ser Pro Ser Cys Arg Pro Pro
1 5 10 15
Ala Arg Leu Gly Glu Arg Asp Leu Phe Pro Asn Leu Arg Ser Arg Ser
20 25 30
Thr Val Leu His Ser Gly Cys Arg Ile Asp Pro Pro Arg Ser Arg Ser
35 40 45
Gly Ala Glu Gly Trp Thr Arg Thr Gly Ala Arg Val Gly Ser Ser Ser
50 55 60
Cys Trp Leu Arg Xaa Arg Arg Leu Ser Lys Leu
65 70 75

(2) INFORMATION FOR SEQ ID NO:1385:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 97 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..97

(D) OTHER INFORMATION: / Ceres Seq. ID 1500151

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1385:

Cys Ile Cys Gly Ser Pro Phe Thr Asn Arg Leu Pro Val Ala Leu Pro
1 5 10 15
Leu Gly Ser Ala Asn Ala Ile Cys Ser Pro Thr Ser Ala Ala Ala Pro
20 25 30
Pro Ser Ser Thr Pro Ala Ala Glu Ser Thr Arg Pro Asp Pro Asp Gln
35 40 45
Glu Leu Arg Asp Gly Arg Glu Gln Ala Pro Glu Trp Asp Pro Ala Val
50 55 60
Ala Gly Cys Gly Xaa Gly Gly Ser Ala Asn Cys Glu Cys Pro Leu Glu
65 70 75 80
Leu Pro Ser Gln Arg Gly Ser Gly Lys Gln Lys Arg Arg Leu Ser Gly
85 90 95
Lys

(2) INFORMATION FOR SEQ ID NO:1386:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 86 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..86

(D) OTHER INFORMATION: / Ceres Seq. ID 1500152

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1386:

```
Met Pro Ala Arg Ala Lys Ser Ala Arg Leu Arg Gln Ala Lys Glu
1           5           10           15
Glu Ala Glu Arg Glu Ile Ala Glu Tyr Arg Ala Gln Met Glu Ala Glu
20           25           30
Phe Gln Arg Lys Val Ala Glu Ser Ser Gly Asp Ser Gly Ala Asn Val
35           40           45
Lys Arg Leu Glu Glu Glu Thr Ala Ala Lys Ile Glu Gln Leu Thr Gln
50           55           60
Gln Ala Ala Ser Ile Ser Pro Asp Val Ile Gln Met Leu Leu Arg His
65           70           75           80
Val Thr Thr Val Lys Asn
85
```

(2) INFORMATION FOR SEQ ID NO:1387:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 460 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..460

(D) OTHER INFORMATION: / Ceres Seq. ID 1500153

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1387:

```
cttcggtcc tgcattttgt tgtcccctct ccgtagcggg gacgttcgtt cactttctct 60
ctctcgccct ccgtttgccc cgcgtgcgct ctgtgtcgct ccctctcttg tgaggagtga 120
ggacgactgg ggcgaccgcc gccgccgccg ccgccctacg ccagatgccc aggtaggggc 180
cattcgctag ctcttcttctg tgcccttcgc cggcgacgag cattcaccag ttgctgatgc 240
aaggctttca aaagttaaac agtctcactt gatgcaaaag caacacaatc actctaaagg 300
tttggatcag tcatttcaga gcatgggttc gcggtttcca tcccatcagc taagcaatgg 360
cttgatgtgc tctggccgac ctgagcaacc taaagagaag gccccagtca tttgctcctc 420
ggctatgcgt acactggcgg ggacataaag aaatctggag
```

(2) INFORMATION FOR SEQ ID NO:1388:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 62 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..62

(D) OTHER INFORMATION: / Ceres Seq. ID 1500154

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1388:

```
Phe Arg Ser Cys Ile Leu Leu Ser Pro Leu Arg Ser Gly Asp Val Arg
1           5           10           15
Ser Leu Ser Leu Ser Arg Leu Pro Phe Ala Pro Arg Ala Leu Cys Val
20           25           30
Ala Pro Ser Leu Val Arg Ser Glu Asp Asp Trp Gly Asp Arg Arg Arg
35           40           45
Arg Arg Arg Pro Thr Pro Asp Ala Gln Val Gly Ala Ile Arg
50           55           60
```

(2) INFORMATION FOR SEQ ID NO:1389:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 58 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..58

(D) OTHER INFORMATION: / Ceres Seq. ID 1500155

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1389:

```
Met Gln Lys Gln His Asn His Ser Lys Gly Leu Asp Gln Ser Phe Gln
1          5          10          15
Ser Met Gly Ser Arg Phe Pro Ser His Gln Leu Ser Asn Gly Leu Tyr
          20          25          30
Val Ser Gly Arg Pro Glu Gln Pro Lys Glu Lys Ala Pro Val Ile Cys
          35          40          45
Ser Ser Ala Met Arg Thr Leu Ala Gly Thr
          50          55
```

(2) INFORMATION FOR SEQ ID NO:1390:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 41 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..41

(D) OTHER INFORMATION: / Ceres Seq. ID 1500156

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1390:

```
Met Gly Ser Arg Phe Pro Ser His Gln Leu Ser Asn Gly Leu Tyr Val
1          5          10          15
Ser Gly Arg Pro Glu Gln Pro Lys Glu Lys Ala Pro Val Ile Cys Ser
          20          25          30
Ser Ala Met Arg Thr Leu Ala Gly Thr
          35          40
```

(2) INFORMATION FOR SEQ ID NO:1391:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 522 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..522

(D) OTHER INFORMATION: / Ceres Seq. ID 1500157

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1391:

```
aaaacaactg tgtaaagtgc tgaagattgc attttggaga gtcgagtttc aaatagaatc      60
gtgagataga gagtgaaaca gggacaatct gagtgacgta cattatattg acagcrtgcc      120
tggctgtrca ggaggcctac ctggtgacgt cgaggaagta cagcccgggtg cccaggaacc      180
agctgctgag cccgctgata gtgcacgacg gccgcctcgt gcagcgcccg acgcccgtcg      240
tcgcgctcgt caccttcctc tggatgccgt tcggcttcgc gctggcgctc atgcgcgtgt      300
acatcaacct gccgctgccc gagcgcacgc tctactacac ctacaagctc atgggcatca      360
rgctcgtcgt caagddcacc ccgccgccgc cgcccaagaa gggccaccgc ggcgtcctct      420
tcgtctgcaa ccaccgcacc gtgctcgacc ccgtcgaggt ggccgtrgcg ctgcgccgca      480
aggtcagctg cgtcacctac agsatctcca agttctccga gc
```

(2) INFORMATION FOR SEQ ID NO:1392:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 86 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..86

(D) OTHER INFORMATION: / Ceres Seq. ID 1500158

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1392:

Met Pro Phe Gly Phe Ala Leu Ala Leu Met Arg Val Tyr Ile Asn Leu
1 5 10 15
Pro Leu Pro Glu Arg Ile Val Tyr Tyr Thr Tyr Lys Leu Met Gly Ile
20 25 30
Xaa Leu Val Val Lys Xaa Thr Pro Pro Pro Pro Lys Lys Gly His
35 40 45
Pro Gly Val Leu Phe Val Cys Asn His Arg Thr Val Leu Asp Pro Val
50 55 60
Glu Val Ala Xaa Ala Leu Arg Arg Lys Val Ser Cys Val Thr Tyr Xaa
65 70 75 80
Ile Ser Lys Phe Ser Glu
85

(2) INFORMATION FOR SEQ ID NO:1393:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 77 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..77

(D) OTHER INFORMATION: / Ceres Seq. ID 1500159

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1393:

Met Arg Val Tyr Ile Asn Leu Pro Leu Pro Glu Arg Ile Val Tyr Tyr
1 5 10 15
Thr Tyr Lys Leu Met Gly Ile Xaa Leu Val Val Lys Xaa Thr Pro Pro
20 25 30
Pro Pro Pro Lys Lys Gly His Pro Gly Val Leu Phe Val Cys Asn His
35 40 45
Arg Thr Val Leu Asp Pro Val Glu Val Ala Xaa Ala Leu Arg Arg Lys
50 55 60
Val Ser Cys Val Thr Tyr Xaa Ile Ser Lys Phe Ser Glu
65 70 75

(2) INFORMATION FOR SEQ ID NO:1394:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 57 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..57

(D) OTHER INFORMATION: / Ceres Seq. ID 1500160

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1394:

Met Gly Ile Xaa Leu Val Val Lys Xaa Thr Pro Pro Pro Pro Lys
1 5 10 15
Lys Gly His Pro Gly Val Leu Phe Val Cys Asn His Arg Thr Val Leu
20 25 30
Asp Pro Val Glu Val Ala Xaa Ala Leu Arg Arg Lys Val Ser Cys Val
35 40 45
Thr Tyr Xaa Ile Ser Lys Phe Ser Glu
50 55

(2) INFORMATION FOR SEQ ID NO:1395:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 508 base pairs

(B) TYPE: nucleic acid

